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OM nucleic - nucleic search, using sw model

Run on: September 17, 2003, 11:54:34 ; Search time 30.1105 Seconds
(without alignments)
3049.028 Million cell updates/sec

Title: US-09-697-123B-1

Perfect score: 208

Sequence: 1 tcaaggagagcgctacgac.....ccggttgagacgagacat 208

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_NA:*
1: /cgn2.6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2.6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2.6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2.6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2.6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2.6/ptodata/1/ina/backfiles.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	166.4	80.0	970	1	US-08-250-030-1
2	166.4	80.0	970	5	PCT-US95-06790-1
3	166.4	80.0	4403765	3	US-09-103-840A-2
4	166.4	80.0	4411529	3	US-09-103-840A-1
5	142.4	68.5	3447	2	US-08-313-185-57
6	142.4	68.5	3447	3	US-09-082-614A-57
7	49.8	23.9	6085	3	US-09-029-603-4
8	45.4	21.8	4403765	3	US-09-103-840A-2
9	43.8	21.1	981	4	US-09-252-991A-5092
10	43.8	21.1	1149	4	US-09-252-991A-5033
11	43.2	20.8	1781	4	US-09-675-018B-7
12	43.2	20.8	1889	4	US-09-675-018B-9
13	43	20.7	2122	3	US-09-029-603-1
14	42.2	20.3	77536	4	US-09-410-551B-1
15	42	20.2	2244	1	US-08-476-519-10
16	42	20.2	2244	5	PCT-US95-09323-10
17	42	20.2	2334	1	US-08-476-519-1
18	42	20.2	2334	5	PCT-US95-09323-1
19	41.6	20.0	969	4	US-09-252-991A-12911
20	41.6	20.0	1257	4	US-09-252-991A-12881
21	41.4	19.9	276	4	US-09-252-991A-8365
22	41.4	19.9	1731	4	US-09-252-991A-8512
23	41	19.7	4411529	3	US-09-103-840A-1
24	40.6	19.5	1182	4	US-09-252-991A-200
25	40.6	19.5	1698	4	US-09-252-991A-193
26	40.6	19.5	1701	4	US-09-252-991A-219
27	40.6	19.5	1938	4	US-09-252-991A-228

28	40.2	19.3	605	4	US-09-252-991A-8737	Sequence 8737, Ap
29	40.2	19.3	924	4	US-09-252-991A-969	Sequence 969, App
30	40.2	19.3	939	4	US-09-252-991A-925	Sequence 925, App
31	40.2	19.3	1014	4	US-09-252-991A-2663	Sequence 2663, Ap
32	40.2	19.3	1155	4	US-09-252-991A-2762	Sequence 2762, Ap
33	40.2	19.3	1233	4	US-09-252-991A-3203	Sequence 3203, Ap
34	40.2	19.3	1746	4	US-09-252-991A-8843	Sequence 8843, Ap
35	40.2	19.3	2139	4	US-09-252-991A-9211	Sequence 9211, Ap
36	39.8	19.1	768	4	US-09-252-991A-1114	Sequence 1114, Ap
37	39.6	19.0	573	4	US-09-252-991A-5674	Sequence 5674, Ap
38	39.6	19.0	882	4	US-09-252-991A-5644	Sequence 5644, Ap
39	39.6	19.0	1020	4	US-09-252-991A-5550	Sequence 5550, Ap
40	39.6	19.0	1089	4	US-09-252-991A-14778	Sequence 14778, A
41	39.6	19.0	1347	4	US-09-252-991A-14972	Sequence 14972, A
42	39.6	19.0	1482	4	US-09-252-991A-14556	Sequence 14556, A
43	39.6	19.0	1485	4	US-09-252-991A-16168	Sequence 16168, A
44	39.6	19.0	1548	4	US-09-252-991A-16059	Sequence 16059, A
45	39.6	19.0	1587	4	US-09-252-991A-16424	Sequence 16424, A

ALIGNMENTS

RESULT 1
US-08-250-030-1
; Sequence 1, Application US/08250030
; Patent No. 5643723

; GENERAL INFORMATION:

; APPLICANT: Persing, David H.

; TITLE OF INVENTION: Detection of a Genetic Locus Encoding
; TITLE OF INVENTION: Resistance to Rifampin in Mycobacterial Cultures and in
; TITLE OF INVENTION: Clinical Specimens

; NUMBER OF SEQUENCES: 15

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Schwegman, Lundberg & Woessner

; STREET: 3500 IDS Center

; CITY: Minneapolis

; STATE: MN

; COUNTRY: USA

; ZIP: 55402

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/250,030

; FILING DATE: 26-MAY-1994

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Mueiting, Ann M.

; REGISTRATION NUMBER: 33,977

; REFERENCE/DOCKET NUMBER: 150.105US1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 612-339-0331

; TELEFAX: 612-339-3061

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 970 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA

US-08-250-030-1

Query Match 80.0%; Score 166.4; DB 1; Length 970;

Best Local Similarity 87.5%; Pred. No. 5.6e-30;

Matches 182; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 1 TCAAGGAGAGCGCTACGCTGCGCGGTAGGCGCGGTACAGGCTACAGGCTACAGGCTCG 60

|||||

26 TCAAGGAGAGCGCTACGCTGCGCGGTAGGCGCGGTACAGGCTACAGGCTCG 85

DB

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QY 61 GCCTGACGTCGGGATCCGATCACCAGCTCCAGCTCCAGCGTCCAGGAGAGAGCTCGTCGCCA 120
Db 86 GCGTCGATCGCGGAGCGCCATCATCGTCGTCGACGCTGACCGAAGAGAGCTCGTCGCCA 145
QY 121 CCATCGAGTACCTGCTCGCGCTGACGAGGCGCCACACAGTACGCTCCCGGGCGGCA 180
Db 146 CCATCGAATATCTGCTCGCTGACGAGGCTCAGACCAAGTACGCTCCCGGGCGGCG 205
QY 181 CCGAGTGCCTGCTGAGACCGAGACAT 208
Db 206 TCGAGTGCCTGGAACCGAGACAT 233

RESULT 2
PCT-US95-06790-1
; Sequence 1, Application PC/TUS9506790
; GENERAL INFORMATION:
; APPLICANT: Mayo Foundation for Medical Education and Research
; APPLICANT: and Hoffmann-La Roche Inc.
; TITLE OF INVENTION: Detection of a Genetic Locus Encoding
; TITLE OF INVENTION: Resistance to Rifampin
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESS: Schwegman, Lundberg & Woessner
; STREET: 3500 IDS Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/06790
; FILING DATE: 26-MAY-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Raasch, Kevin W.
; REGISTRATION NUMBER: 35,651
; REFERENCE/DOCKET NUMBER: 150.105W01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-339-0331
; TELEFAX: 612-339-3061
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 970 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
PCT-US95-06790-1

Query Match 80.0%; Score 166.4; DB 5; Length 970;
Best Local Similarity 87.5%; Pred. No. 5.6e-30;
Matches 182; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 1 TCAAGGAGAGCGCTACGACTGCGCGGTAGGCGCTACAAAGTCAACAGAGCTCG 60
Db 762648 TCAAGGAGAGCGCTACGACTGCGCGGTAGGCGCTACAAAGTCAACAGAGCTCG 762707
QY 61 GCCTGACGTCGGGATCCGATCACCAGCTCCAGCTCCAGGAGAGAGCTCGTCGCCA 120
Db 762708 GCCTGACGTCGGGATCCGATCACCAGCTCCAGCTCCAGGAGAGAGCTCGTCGCCA 762767
QY 121 CCATCGAGTACCTGCTCGCGCTGACGAGGCGCCACAGTACGCTCCCGGGCGGCA 180
Db 762768 CCATCGAATATCTGCTCGCTGACGAGGCTCAGACCAAGTACGCTCCCGGGCGGCG 762827
QY 181 CCGAGTGCCTGCTGAGACCGAGACAT 208
Db 762828 TCGAGTGCCTGGAACCGAGACAT 762855

RESULT 4
US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match 80.0%; Score 166.4; DB 3; Length 4411529;
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QY 61 GCCTGACGTCGGGATCCGATCACCAGCTCCAGCTCCAGCGTCCAGGAGAGAGCTCGTCGCCA 120
Db 86 GCGTCGATCGCGGAGCGCCATCATCGTCGTCGACGCTGACCGAAGAGAGCTCGTCGCCA 145
QY 121 CCATCGAGTACCTGCTCGCGCTGACGAGGCGCCACACAGTACGCTCCCGGGCGGCA 180
Db 146 CCATCGAATATCTGCTCGCTGACGAGGCTCAGACCAAGTACGCTCCCGGGCGGCG 205
QY 181 CCGAGTGCCTGCTGAGACCGAGACAT 208
Db 206 TCGAGTGCCTGGAACCGAGACAT 233

RESULT 3
US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match 80.0%; Score 166.4; DB 3; Length 4403765;
Best Local Similarity 87.5%; Pred. No. 1e-29;
Matches 182; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 1 TCAAGGAGAGCGCTACGACTGCGCGGTAGGCGCTACAAAGTCAACAGAGCTCG 60
Db 762648 TCAAGGAGAGCGCTACGACTGCGCGGTAGGCGCTACAAAGTCAACAGAGCTCG 762707
QY 61 GCCTGACGTCGGGATCCGATCACCAGCTCCAGCTCCAGGAGAGAGCTCGTCGCCA 120
Db 762708 GCCTGACGTCGGGATCCGATCACCAGCTCCAGCTCCAGGAGAGAGCTCGTCGCCA 762767
QY 121 CCATCGAGTACCTGCTCGCGCTGACGAGGCGCCACAGTACGCTCCCGGGCGGCA 180
Db 762768 CCATCGAATATCTGCTCGCTGACGAGGCTCAGACCAAGTACGCTCCCGGGCGGCG 762827
QY 181 CCGAGTGCCTGCTGAGACCGAGACAT 208
Db 762828 TCGAGTGCCTGGAACCGAGACAT 762855

RESULT 4
US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match 80.0%; Score 166.4; DB 3; Length 4411529;
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Best Local Similarity 87.5%; Pred. No. 1e-29;
Matches 182; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

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DB 760688 TCAAGGAGAAGCGCTACGACCTGCGCGGAGGCGGTACAAAGTCAACAAGAGCTCG 760747
QY 61 GCGTCGACCTGCGGATCCGATACACAGCTCCACGCTGACCGAGGAGAGCTGTCGCCA 120
DB 760748 GCGTCGATGTGGGAGGCCATACGTCGTCGAGGCTGACCGAAGAGAGCTGTCGCCA 760807
QY 121 CCATCGAGTACCTGCTCCGCTGACGAGGGCCAGCACAGTACACGCTCCCGGGCGGCA 180
DB 760808 CCATCGAATATCTGTCGCTGTCACGAGGCTCAGACACAGTACACGCTCCCGGGCGG 760867
QY 181 CCGAGTCCCGGTTGAGACCGACAT 208
DB 760868 TCGAGTCCCGTGGAAACCGACAT 760895

RESULT 5

US-08-313-185-57
; Sequence 57, Application US/08313185
; Patent No. 5851763
; GENERAL INFORMATION:
; APPLICANT: Heym, Beate
; APPLICANT: Cole, Stewart
; APPLICANT: Young, Douglas
; APPLICANT: Zhang, Ying
; APPLICANT: Honore, Nadine
; APPLICANT: Telenti, Amalio
; APPLICANT: Bodmer, Thomas
; TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
; TITLE OF INVENTION: in Mycobacterium Tuberculosis
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/313,185
; FILING DATE: 12-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 02356.0068-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3447 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-313-185-57

Query Match 68.5%; Score 142.4; DB 2; Length 3447;
Best Local Similarity 80.3%; Pred. No. 1.9e-24;
Matches 167; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 1 TCAAGGAGAAGCGCTACGACCTGCGCGGAGGCGGTACAAAGTCAACAAGAGCTCG 60

DB 809 TCAAGGAGAAGCGCTACGACCTGCGCGGAGGCGGTACAAAGTCAACAAGAGCTCG 868
QY 61 GCGTCGACCTGCGGATCCGATACACAGCTCCACGCTGACCGAGGAGAGCTGTCGCCA 120
DB 869 GGTTCACGCGGCTGAGTTGATCAGCTGCTCCACGCTGACCGAAGAGAGTGTGTCGCCA 928
QY 121 CCATCGAGTACCTGCTCCGCTGACGAGGGCCAGCACAGTACACGCTCCCGGGCGGCA 180
DB 929 CCATAGAGTACCTGCTGCTGCTGATGAGGTCAGTGACCAATGACTGTCCCGAGGTGGG 988
QY 181 CCGAGTCCCGGTTGAGACCGACAT 208
DB 989 TAGAAGTGCACGTGGAAGTACGATAT 1016

RESULT 6

US-09-082-614A-57
; Sequence 57, Application US/09082614A
; Patent No. 6124098
; GENERAL INFORMATION:
; APPLICANT: Heym, Beate
; APPLICANT: Cole, Stewart
; APPLICANT: Young, Douglas
; APPLICANT: Zhang, Ying
; APPLICANT: Honore, Nadine
; APPLICANT: Telenti, Amalio
; APPLICANT: Bodmer, Thomas
; TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
; TITLE OF INVENTION: in Mycobacterium Tuberculosis
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/082,614A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/313,185
; FILING DATE: 12-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 02356.0068-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3447 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-082-614A-57

Query Match 68.5%; Score 142.4; DB 3; Length 3447;
Best Local Similarity 80.3%; Pred. No. 1.9e-24;
Matches 167; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 1 TCAAGGAGAAGCGCTACGACCTGCGCGGAGGCGGTACAAAGTCAACAAGAGCTCG 60

Best Local Similarity 54.6%; Pred. No. 0.063;
Matches 112; Conservative 0; Mismatches 87; Indels 6; Gaps 1;
QY 2 CAAGGAGAGCGCTACGACCTGCGCCGGGTAGCGCGCTACAGGTCAACAGAGAGCTCGG 61
Db 388 CGACGAGAGAGACATCAAGCGCGGCTTGGAGTTCTTCGCGAAGATCCCAAGCAGGCGG 447
QY 62 CCTGCACGTCGGCGATCGATCACACGCTCCAGCTGACCGGACCGAGAGAGAGCTGCTGCCAC 121
Db 448 CTTGTGCTGACACACCGGCTGATCGCCACCTTGGAAAGGCGAGGTGGAATCGGCAT 507
QY 122 CATCGAGTACCTGCTGCTCCCTGTCACGAGGCGCCACGACGATGACCGTCCCGCGCGCGAC 181
Db 508 CGTCTGGGACTTCAACGGGCTCAGCTACGCGCCAGCA-----GATCGACCGCGGCGCTT 561
QY 182 CGAGGTGCGGCTTGAGACCGAGGAC 206
Db 562 CGAGGTGCTGATCCCTCGGACGGC 586
RESULT 10
US-09-252-991A-5033
; Sequence 5033, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 5033
; LENGTH: 1149
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-5033
Query Match 21.1%; Score 43.8; DB 4; Length 1149;
Best Local Similarity 54.6%; Pred. No. 0.063;
Matches 112; Conservative 0; Mismatches 87; Indels 6; Gaps 1;
QY 2 CAAGGAGAGCGCTACGACCTGCGCCGGGTAGCGCGCTACAGGTCAACAGAGAGCTCGG 61
Db 657 CGACGAGAGAGACATCAAGCGCGGCTTGGAGTTCTTCGCGAAGATCCCAAGCAGGCGG 716
QY 62 CCTGCACGTCGGCGATCGATCACACGCTCCAGCTGACCGGAGAGAGAGCTGCTGCCAC 121
Db 717 CTTGCTGCTGACCAACCGGCTGATCGCCACCTTGGAAAGGCGGAGGTGGAAGTCTGGCAT 776
QY 122 CATCGAGTACCTGCTGCTCCCTGTCACGAGGCGCCACGACGATGACCGTCCCGGCGCGAC 181
Db 777 CGTCTGGGACTTCAACGGGCTCAGCTACGCGCCAGCA-----GATCGACCGCGGCGCTT 830
QY 182 CGAGGTGCGGCTTGAGACCGAGGAC 206
Db 831 CGAGGTGCTGATCCCTCGGACGGC 855
RESULT 11
US-09-675-018B-7
; Sequence 7, Application US/09675018B
; Patent No. 6573426
; GENERAL INFORMATION:
; APPLICANT: Falco, Saverio Carl
; APPLICANT: Rafalski, J. Antoni
; APPLICANT: Weng, Zude
; TITLE OF INVENTION: A Gene Involved in Pyrimidine Biosynthesis in Plants
; FILE REFERENCE: BB1404 US NA
Best Local Similarity 54.6%; Pred. No. 0.09;
Matches 90; Conservative 0; Mismatches 78; Indels 0; Gaps 0;
QY 41 CAAGGTCAACAAGAGCTCGGCGCTGACGTCGCGGATCCGATCACCAGCTCCACGCTGAC 100
Db 393 CATCGCGCGCAAGGAGGTCAAGGCCCGCACCGCCAAAGTCCATCGAGGGCTCTCTTCAG 452
QY 101 CGAGGAGAGCTGCTGCGCCACCTGCGAGTACCTGCTCGCCCTGACGAGGGCCAGCACAC 160
Db 453 CCGCGGGGACACCGCTCCTCATCATCGAGGACCTCGTCACCATGCGCGCTCCGCTCGA 512
QY 161 GATGACCGTCCCGGGCGGCGAGGTGCGGCTTGAGACCGGACGACAT 208
Db 513 GACGCGCGCGCGCTCGCGCGCGAGGGGCTGCTGCTCGCGCGCGCT 560
RESULT 12
US-09-675-018B-9
; Sequence 9, Application US/09675018B
; Patent No. 6573426
; GENERAL INFORMATION:
; APPLICANT: Falco, Saverio Carl
; APPLICANT: Rafalski, J. Antoni
; APPLICANT: Weng, Zude
; TITLE OF INVENTION: A Gene Involved in Pyrimidine Biosynthesis in Plants
; FILE REFERENCE: BB1404 US NA
; CURRENT APPLICATION NUMBER: US/09/675,018B
; CURRENT FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 60/156,901
; PRIOR FILING DATE: 1999-09-30
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 9
; LENGTH: 1889
; TYPE: DNA
; ORGANISM: Zea mays
US-09-675-018B-9
Query Match 20.8%; Score 43.2; DB 4; Length 1889;
Best Local Similarity 53.6%; Pred. No. 0.09;
Matches 90; Conservative 0; Mismatches 78; Indels 0; Gaps 0;
QY 41 CAAGGTCAACAAGAGCTCGGCGCTGACGTCGCGGATCCGATCACCAGCTCCACGCTGAC 100
Db 393 CATCGCGCGCAAGGAGGTCAAGGCCCGCACCGCCAAAGTCCATCGAGGGCTCTCTTCAG 452
QY 101 CGAGGAGAGCTGCTGCGCCACCTGCGAGTACCTGCTCGCCCTGACGAGGGCCAGCACAC 160
Db 453 CCGCGGGGACACCGCTCCTCATCATCGAGGACCTCGTCACCATGCGCGCTCCGCTCGA 512
QY 161 GATGACCGTCCCGGGCGGCGAGGTGCGGCTTGAGACCGGACGACAT 208
Db 513 GACGCGCGCGCGCTCGCGCGCGAGGGGCTGCTGCTCGCGCGCGCT 560
RESULT 13
US-09-029-603-1
; Sequence 1, Application US/09029603
; Patent No. 6210935
; GENERAL INFORMATION:

; CURRENT APPLICATION NUMBER: US/09/675,018B
; CURRENT FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 60/156,901
; PRIOR FILING DATE: 1999-09-30
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 7
; LENGTH: 1781
; TYPE: DNA
; ORGANISM: Triticum aestivum
US-09-675-018B-7
Query Match 20.8%; Score 43.2; DB 4; Length 1781;
Best Local Similarity 53.6%; Pred. No. 0.09;
Matches 90; Conservative 0; Mismatches 78; Indels 0; Gaps 0;
QY 41 CAAGGTCAACAAGAGCTCGGCGCTGACGTCGCGGATCCGATCACCAGCTCCACGCTGAC 100
Db 371 CATCGCGCGCAAGGAGGTCAAGGCCCGCACCGCCAAAGTCCATCGAGGGCTCTCTTCAG 430
QY 101 CGAGGAGAGCTGCTGCGCCACCTGCGAGTACCTGCTCGCCCTGACGAGGGCCAGCACAC 160
Db 431 CCGCGGGGACACCGCTCCTCATCATCGAGGACCTCGTCACCATGCGCGCTCCGCTCGA 490
QY 161 GATGACCGTCCCGGGCGGCGAGGTGCGGCTTGAGACCGGACGACAT 208
Db 491 GACCGCGCGCGCTCGCGCGCGAGGGGCTGCTGCTCGCGCGCGCT 538
RESULT 14
US-09-675-018B-9
; Sequence 9, Application US/09675018B
; Patent No. 6573426
; GENERAL INFORMATION:
; APPLICANT: Falco, Saverio Carl
; APPLICANT: Rafalski, J. Antoni
; APPLICANT: Weng, Zude
; TITLE OF INVENTION: A Gene Involved in Pyrimidine Biosynthesis in Plants
; FILE REFERENCE: BB1404 US NA
; CURRENT APPLICATION NUMBER: US/09/675,018B
; CURRENT FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 60/156,901
; PRIOR FILING DATE: 1999-09-30
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 9
; LENGTH: 1889
; TYPE: DNA
; ORGANISM: Zea mays
US-09-675-018B-9
Query Match 20.8%; Score 43.2; DB 4; Length 1889;
Best Local Similarity 53.6%; Pred. No. 0.09;
Matches 90; Conservative 0; Mismatches 78; Indels 0; Gaps 0;
QY 41 CAAGGTCAACAAGAGCTCGGCGCTGACGTCGCGGATCCGATCACCAGCTCCACGCTGAC 100
Db 393 CATCGCGCGCAAGGAGGTCAAGGCCCGCACCGCCAAAGTCCATCGAGGGCTCTCTTCAG 452
QY 101 CGAGGAGAGCTGCTGCGCCACCTGCGAGTACCTGCTCGCCCTGACGAGGGCCAGCACAC 160
Db 453 CCGCGGGGACACCGCTCCTCATCATCGAGGACCTCGTCACCATGCGCGCTCCGCTCGA 512
QY 161 GATGACCGTCCCGGGCGGCGAGGTGCGGCTTGAGACCGGACGACAT 208
Db 513 GACGCGCGCGCGCTCGCGCGCGAGGGGCTGCTGCTCGCGCGCGCT 560
RESULT 15
US-09-029-603-1
; Sequence 1, Application US/09029603
; Patent No. 6210935
; GENERAL INFORMATION:

; APPLICANT: Schupp, Thomas
 ; APPLICANT: Engel, Natalie
 ; APPLICANT: Bietenhader, Jurg
 ; APPLICANT: Toupet, Christine
 ; APPLICANT: Pospishech, Andreas
 ; TITLE OF INVENTION: Staurosporin Biosynthesis Gene Clusters
 ; FILE REFERENCE: 4-20555/A/PCT
 ; CURRENT APPLICATION NUMBER: US/09/029,603
 ; CURRENT FILING DATE: 1998-03-20
 ; EARLIER APPLICATION NUMBER: PCT/EP96/03643
 ; EARLIER FILING DATE: 1996-08-19
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 1
 ; LENGTH: 2122
 ; TYPE: DNA
 ; ORGANISM: Streptomyces longisporoflavus
 ; FEATURE:
 ; NAME/KEY: misc_RNA
 ; LOCATION: (1)..(2122)
 ; OTHER INFORMATION: product = 2.1 kb region
 US-09-029-603-1

Query Match 20.7%; Score 43; DB 3; Length 2122;
 Best Local Similarity 52.5%; Pred. No. 0.1;
 Matches 94; Conservative 0; Mismatches 85; Indels 0; Gaps 0;
 QY 8 GAAGCGCTACGACCTGGCGGCTAGGCGGTACAAAGTCAACAAGAAGCTGGCGTGA 67
 DB 1470 GCACCGCTCCGGCTGGCGGTGGCGGAGATGCTGACGTACCGAGCAGACACCGCTGG 1529
 QY 68 CGTGGCGATCGATACACAGCTCCACGCTGACGAGAGAGAGCTGTCGCCACCATGA 127
 DB 1530 CCTGCGCAGAGATGGCAGGCTCGCGCGCTGAGGAGCGCCCGTGGCCATGGACGA 1589
 QY 128 GTACCTGCTCGCTGCAGAGCGCCAGCAGACGATACCGTCCCGGGCGGACCGAGG 186
 DB 1590 GGGCAACTTCGCTTCGGCGAGACTCTCTCAAGCGCTCCGACCTGGCGGGCGTGA 1648

RESULT 14
 US-09-410-551B-1/G
 ; Sequence 1, Application US/09410551B
 ; Patent No. 6503737
 ; GENERAL INFORMATION:
 ; APPLICANT: KOSAN BIOSCIENCES, Inc.
 ; APPLICANT: REEVES, CHRISTOPHER
 ; APPLICANT: CHU, DANIEL
 ; APPLICANT: KHOSLA, CHAITAN
 ; APPLICANT: SANUI, DANIEL
 ; APPLICANT: WU, KAI
 ; TITLE OF INVENTION: POLYKETIDE SYNTHASE ENZYMES AND RECOMBINANT DNA
 ; FILE REFERENCE: CONSTRUCTS THEREFOR
 ; CURRENT APPLICATION NUMBER: US/09/410,551B
 ; CURRENT FILING DATE: 1999-10-01
 ; PRIOR APPLICATION NUMBER: US 60/139,650
 ; PRIOR FILING DATE: 1999-06-17
 ; PRIOR APPLICATION NUMBER: US 60/123,810
 ; PRIOR FILING DATE: 1999-03-11
 ; PRIOR APPLICATION NUMBER: US 60/102,748
 ; PRIOR FILING DATE: 1998-10-02
 ; NUMBER OF SEQ ID NOS: 72
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 77536
 ; TYPE: DNA
 ; ORGANISM: Streptomyces hygroscopicus
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (52275)...(71465)
 US-09-410-551B-1

Query Match 20.3%; Score 42.2; DB 4; Length 77536;
 Best Local Similarity 63.1%; Pred. No. 0.2;
 Matches 65; Conservative 0; Mismatches 38; Indels 0; Gaps 0;
 QY 71 CGCGGATCCGATACACAGCTCCACGCTGACCGAGAGAGCTGTCGCCACCATGAGTA 130
 DB 2431 CGGCGCCACCGACACACCATCAGCTGACCTGGAAACCGCTGACGGCGCCACGACTA 2372
 QY 131 CTTGCTCGCTGCGAGGCGCCAGCAGCAGATGACCGTCCG 173
 DB 2371 CGCGCTCCACCGGAGCGGTGCCAGATCACCACCGTCCGCGCAGC 2329

RESULT 15
 US-08-476-519-10
 ; Sequence 10, Application US/08476519
 ; Patent No. 5750876
 ; GENERAL INFORMATION:
 ; APPLICANT: Barry, Gerard F.
 ; APPLICANT: Kishore, Ganesh M.
 ; APPLICANT: Krohn, Bradley M.
 ; TITLE OF INVENTION: No. 5750876el Isoamylase Gene, Compositions
 ; TITLE OF INVENTION: Containing It and Methods of Using Isoamylases
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Grace L. Bonner, Monsanto Company, BB4F
 ; STREET: 700 Chesterfield Parkway No. 5750876th
 ; CITY: St. Louis
 ; STATE: Missouri
 ; COUNTRY: USA
 ; ZIP: 63198
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC Compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/476,519
 ; FILING DATE:
 ; CLASSIFICATION: 800
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/281902
 ; FILING DATE: 28-JUL-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Bonner, Grace L.
 ; REGISTRATION NUMBER: 32,963
 ; REFERENCE/DOCKET NUMBER: 38-21(13577)A
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (314)537-7286
 ; TELEFAX: (314)537-6047
 ; INFORMATION FOR SEQ ID NO: 10:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2244 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 1..2241
 US-08-476-519-10

Query Match 20.2%; Score 42; DB 1; Length 2244;
 Best Local Similarity 52.9%; Pred. No. 0.17;
 Matches 90; Conservative 0; Mismatches 80; Indels 0; Gaps 0;
 QY 17 CGACCTGCGCGGTAGGCGGTACAAAGTCAACAAGAGCTGGCGTCCAGTCGGGA 76
 DB 1338 CGAGTGGAGACGGCTCTACCGCGACGCGCTGCGAAGAGCAGACAGCTGGCGTGA 1397
 QY 77 TCCGATCACCAGCTCCACGCTGACCGAGAGAGCTGCTGCCACCATGAGTACTGTT 136
 DB 1398 AACGCTACCCCGGCGACCTGCGCCACGCGCTTCGCGGCTCCACGACCTGTAGGGA 1457

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Job time : 50.1605 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 17, 2003, 11:54:34 ; Search time 108.259 Seconds
(without alignments)
4726.283 Million cell updates/sec

Title: US-09-697-123b-1

Perfect score: 208
Sequence: 1 tcaaggagaagcgtacgac.....ccggttgagaccgacacat 208

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Gapop 10.0 , Gapext 1.0

Searched: 1660708 seqs, 1229959015 residues

Total number of hits satisfying chosen parameters: 3321416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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3: /cgn2.6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
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11: /cgn2.6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2.6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
13: /cgn2.6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
14: /cgn2.6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
15: /cgn2.6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
16: /cgn2.6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
17: /cgn2.6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	166.4	80.0	3519	10	US-09-712-363-30
2	83.2	40.0	3495	10	US-09-738-626-547
3	83.2	40.0	5096	10	US-09-984-711-5
4	83.2	40.0	5099	10	US-09-887-052-1
5	83.2	40.0	5099	10	US-09-887-052-3
6	83.2	40.0	5099	10	US-09-887-052-5
7	83.2	40.0	5099	12	US-10-076-406-1
8	83.2	40.0	5099	12	US-10-076-406-3
9	83.2	40.0	5099	12	US-10-076-406-5
10	83.2	40.0	5099	13	US-10-075-460-5
11	83.2	40.0	3309400	10	US-09-738-626-1
12	80.4	38.7	3543	14	US-10-156-761-4898
13	80.4	38.7	9025608	14	US-10-156-761-1
14	45.2	21.7	1596	14	US-10-156-761-4136
15	44.4	21.3	2329	10	US-09-816-828-9
16	44	21.2	603	14	US-10-156-761-1568

17	44	21.2	63158	12	US-10-292-198-1	Sequence 1, Appli
18	44	21.2	9025608	14	US-10-156-761-1	Sequence 1, Appli
19	43.2	20.8	1800	14	US-10-156-761-5464	Sequence 5464, Ap
20	42.4	20.4	1458	14	US-10-156-761-4634	Sequence 4634, Ap
21	42.4	20.4	3759	14	US-10-156-761-2268	Sequence 2268, Ap
22	42	20.2	2730	14	US-10-156-761-3553	Sequence 3553, Ap
23	41.4	19.9	5418	14	US-10-156-761-5959	Sequence 5959, Ap
24	41.2	19.8	1290	14	US-10-156-761-2136	Sequence 2136, Ap
25	41	19.7	1287	14	US-10-156-761-5314	Sequence 5314, Ap
26	41	19.7	1317	14	US-10-028-245-4	Sequence 4, Appli
27	41	19.7	1826	14	US-10-028-245-1	Sequence 1, Appli
28	41	19.7	11058	14	US-10-156-761-3629	Sequence 3629, Ap
29	40.8	19.6	1629	14	US-10-156-761-3330	Sequence 3330, Ap
30	40.4	19.4	1065	14	US-10-156-761-6270	Sequence 6270, Ap
31	40.4	19.4	1188	14	US-10-156-761-1818	Sequence 1818, Ap
32	40.4	19.4	1215	14	US-10-156-761-2811	Sequence 2811, Ap
33	40	19.2	2025	14	US-10-156-761-3283	Sequence 3283, Ap
34	40	19.2	88421	10	US-09-976-059-1	Sequence 1, Appli
35	39.8	19.1	831	14	US-10-156-761-6155	Sequence 6155, Ap
36	39.6	19.0	570	14	US-10-128-714-2426	Sequence 2426, Ap
37	39.6	19.0	570	14	US-10-128-714-7426	Sequence 7426, Ap
38	39.6	19.0	1170	14	US-10-156-761-7006	Sequence 7006, Ap
39	39.4	18.9	711	14	US-10-156-761-379	Sequence 379, App
40	39.4	18.9	1365	14	US-10-156-761-1915	Sequence 1915, Ap
41	39.4	18.9	1395	14	US-10-156-761-2088	Sequence 2088, Ap
42	39.2	18.8	1338	14	US-10-156-761-5115	Sequence 5115, Ap
43	39.2	18.8	1584	14	US-10-156-761-5604	Sequence 5604, Ap
44	39	18.8	402	14	US-10-156-761-3597	Sequence 3597, Ap
45	39	18.8	1542	14	US-10-156-761-5967	Sequence 5967, Ap

ALIGNMENTS

RESULT 1
US-09-712-363-30
; Sequence 30, Application US/09712363
; Patent No. US20020164588A1
; GENERAL INFORMATION:
; APPLICANT: Eisenberg, David
; APPLICANT: Rotstein, Sergio H.
; APPLICANT: Marcotte, Edward M.
; TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND
; FILE REFERENCE: 07419-032001
; CURRENT APPLICATION NUMBER: US/09/712.363
; CURRENT FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: PCT/US00/02246
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,531
; PRIOR FILING DATE: 2000-02-01
; PRIOR APPLICATION NUMBER: 60/117,844
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/118,206
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: 60/126,593
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/134,093
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/134,092
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/165,124
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/165,086
; PRIOR FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 30
; LENGTH: 3519
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-09-712-363-30

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Query Match      80.0%; Score 166.4; DB 10; Length 3519;
Best Local Similarity 87.5%; Pred. No. 8.4e-38;
Matches 182; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 1 TCAGGAGAGCGGTACAGCTGGCCGGGTAGCGCGCTACAGGTCACACAGAGCTCG 60
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Db 884 TCAAGGAGAAGCGCTAGAGCTGGCCGGGTAGCGCGCTATAAGGTCAACAAGAGCTCG 943

QY 61 GCGTCAGCTGGGGATCCAGTCCAGCTCCAGCTGACCGGAGAGCGTCTCGCCA 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 944 GCGTCAGCTGGCGAGCCATCACCTGCTGACCTGACCGAGAGAGCGTCTGGCCA 1003

QY 121 CCATCGAGTACCTGGTCCGCTCAGCAGGGGCCACACAGTACCGTCCCGGGCGGCA 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1004 CCATCGAATATCTGGTCCGCTGTCAGAGGGTCAGACCAAGTACCGTCTCCGGGGCGG 1063

QY 181 CCAGGTGCGGTGACACGAGACAT 208
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Db 1064 TCGAGTGGCGGTGGAACCGAGACAT 1091

RESULT 2
US-09-738-626-547
; Sequence 547, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738, 626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 547
; LENGTH: 3495
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-547

Query Match      40.0%; Score 83.2; DB 10; Length 3495;
Best Local Similarity 67.0%; Pred. No. 2.1e-14;
Matches 134; Conservative 0; Mismatches 63; Indels 3; Gaps 1;

QY 9 AAGCGTACAGCTGGCCGGGTAGCGCGCTACAAGTCAACAAGAGCTCGGCCCTGCAC 68
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 877 AAGCGTACAGCTGGCTCGCGTGTGCTTACAAGATCAACCGCAAGCTCGGCCCT--- 933

QY 69 GTGGCGATCCGATCCAGCTCCAGCTGACCGGAGGAGCTGTCGCCACCATCGAG 128
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Db 934 GTGGCGACCATCATGATGCTTTACTGAGAGGACATCGCAACCATCATCGAG 993

QY 129 TACTGTGTCGGCTGACGAGGCCACACAGTACCGCTCCCGGGCGGACCGAGGTG 188
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Db 994 TACTGTGTCGCTGACGAGGTGAGCGGCTCATGACTTCTCCAAATGTTGAAGATC 1053

QY 189 CCGGTTGAGACCGACAT 208
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Db 1054 CCAGTCGAGACCGATGACAT 1073
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RESULT 3
US-09-984-711-5
; Sequence 5, Application US/09984711
; Patent No. US20020119549A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: STEPHAN, Hans
; APPLICANT: KREUTZER, Caroline
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE IPOL GENE
; FILE REFERENCE: 204209US0
; CURRENT APPLICATION NUMBER: US/09/984,711
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: DE10108230.9
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 5096
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
; OTHER INFORMATION:
US-09-984-711-5

Query Match      40.0%; Score 83.2; DB 10; Length 5096;
Best Local Similarity 67.0%; Pred. No. 2.1e-14;
Matches 134; Conservative 0; Mismatches 63; Indels 3; Gaps 1;

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Db 1578 AAGCGTACAGCTGGCTCGCGTGTGCTTACAAGATCAACCGCAAGCTCGGCCCT--- 1634

QY 69 GTGGCGATCCGATCCAGCTCCAGCTGACCGGAGGAGCTGTCGCCACCATCGAG 128
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1635 GTGGCGACCATCATGATGCTTTACTGAGAGGACATCGCAACCATCATCGAG 1694

QY 129 TACTGTGTCGGCTGACGAGGCCACACAGTACCGCTCCCGGGCGGACCGAGGTG 188
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Db 1695 TACTGTGTCGCTGACGAGGTGAGCGGCTCATGACTTCTCCAAATGTTGAAGATC 1754

QY 189 CCGGTTGAGACCGACAT 208
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Db 1755 CCAGTCGAGACCGATGACAT 1774

RESULT 4
US-09-887-052-1
; Sequence 1, Application US/09887052
; Patent No. US20020119537A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE IPOL GENE
; FILE REFERENCE: 204212US0X
; CURRENT APPLICATION NUMBER: US/09/887,052
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: DE10107229.5
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 5099
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; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
US-09-887-052-1

Query Match 40.0%; Score 83.2; DB 10; Length 5099;
Best Local Similarity 67.0%; Pred. No. 2.1e-14;
Matches 134; Conservative 0; Mismatches 63; Indels 3; Gaps 1;

QY 9 AAGCGCTACGACCTGCCCGGTAGCGCGCTACAAAGTCAACAAGAGCTCGGCTGCAC 68
|||||
Db 1578 AAGCGCTACGACCTGCCCGGTAGCGCGCTACAAAGTCAACAAGAGCTCGGCTGCAC 68
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QY 69 GTCGGCGATCCGATCACAGCTCCACGCTGACCGAGGAGAGCTGTCGCCACCATCGAG 128
|||||
Db 1635 GGTGGCGACACAGATGGTTGATGACTTTACTGAAGAGGACATCGCAACACCATCGAG 1694
|||||

QY 129 TACCTGTGCGCTGCACGAGGGCCAGCAGCAGATGACCGTCCCGGGCGGACCGAGGTG 188
|||||
Db 1695 TACCTGTGCGCTGCACGAGGGCCAGCAGCAGATGACCGTCCCGGGCGGACCGAGGTG 188
|||||

QY 189 CCGGTTGAGACCGACGACAT 208
|||||
Db 1755 CCAGTCGAGACCGATGACAT 1774
|||||

RESULT 5
US-09-887-052-3
; Sequence 3, Application US/09887052
; Patent No. US20020119537A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE rpoB GENE
; FILE REFERENCE: 204212US0X
; CURRENT APPLICATION NUMBER: US/09/887,052
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: DE10107229.5
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 5099
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
US-09-887-052-3

Query Match 40.0%; Score 83.2; DB 10; Length 5099;
Best Local Similarity 67.0%; Pred. No. 2.1e-14;
Matches 134; Conservative 0; Mismatches 63; Indels 3; Gaps 1;

QY 9 AAGCGCTACGACCTGCCCGGTAGCGCGCTACAAAGTCAACAAGAGCTCGGCTGCAC 68
|||||
Db 1578 AAGCGCTACGACCTGCCCGGTAGCGCGCTACAAAGTCAACAAGAGCTCGGCTGCAC 68
|||||

QY 69 GTCGGCGATCCGATCACAGCTCCACGCTGACCGAGGAGAGCTGTCGCCACCATCGAG 128
|||||
Db 1635 GGTGGCGACACAGATGGTTGATGACTTTACTGAAGAGGACATCGCAACACCATCGAG 1694
|||||

QY 129 TACCTGTGCGCTGCACGAGGGCCAGCAGCAGATGACCGTCCCGGGCGGACCGAGGTG 188
|||||
Db 1695 TACCTGTGCGCTGCACGAGGGCCAGCAGCAGATGACCGTCCCGGGCGGACCGAGGTG 188
|||||

QY 189 CCGGTTGAGACCGACGACAT 208
|||||

Db 1755 CCAGTCGAGACCGATGACAT 1774

RESULT 6
US-09-887-052-5
; Sequence 5, Application US/09887052
; Patent No. US20020119537A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE rpoB GENE
; FILE REFERENCE: 204212US0X
; CURRENT APPLICATION NUMBER: US/09/887,052
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: DE10107229.5
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 5099
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
US-09-887-052-5

Query Match 40.0%; Score 83.2; DB 10; Length 5099;
Best Local Similarity 67.0%; Pred. No. 2.1e-14;
Matches 134; Conservative 0; Mismatches 63; Indels 3; Gaps 1;

QY 9 AAGCGCTACGACCTGCCCGGTAGCGCGCTACAAAGTCAACAAGAGCTCGGCTGCAC 68
|||||
Db 1578 AAGCGCTACGACCTGCCCGGTAGCGCGCTACAAAGTCAACAAGAGCTCGGCTGCAC 68
|||||

QY 69 GTCGGCGATCCGATCACAGCTCCACGCTGACCGAGGAGAGCTGTCGCCACCATCGAG 128
|||||
Db 1635 GGTGGCGACACAGATGGTTGATGACTTTACTGAAGAGGACATCGCAACACCATCGAG 1694
|||||

QY 129 TACCTGTGCGCTGCACGAGGGCCAGCAGCAGATGACCGTCCCGGGCGGACCGAGGTG 188
|||||
Db 1695 TACCTGTGCGCTGCACGAGGGCCAGCAGCAGATGACCGTCCCGGGCGGACCGAGGTG 188
|||||

QY 189 CCGGTTGAGACCGACGACAT 208
|||||
Db 1755 CCAGTCGAGACCGATGACAT 1774
|||||

RESULT 7
US-10-076-406-1
; Sequence 1, Application US/10076406
; Publication No. US20030166884A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: Nucleotide sequences coding for the rpoB gene
; FILE REFERENCE: 219774US0XIP
; CURRENT APPLICATION NUMBER: US/10/076,406
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: DE 10107229.5
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 09/887052
; PRIOR FILING DATE: 2001-06-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 5099

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; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
; OTHER INFORMATION:
US-10-076-406-1

Query Match          40.0%; Score 83.2; DB 12; Length 5099;
Best Local Similarity 67.0%; Pred. No. 2.1e-14;
Matches 134; Conserved 0; Mismatches 63; Indels 3; Gaps 1;

QY 9 AAGCGCTACGACCTGGCCGGGTAGGCGGCTACAAAGGTCACAAAGAGCTCGGCTGCAC 68
Db 1578 AAGCGCTACGACCTGGCTGGCTGCTTACAGATCAACCCGAGCTCGGCTT--- 1634
QY 69 GTCGGGATCCGATCACCAGCTCCAGCTGACCGAGGAGAGAGCTGCGCCACCATCGAG 128
Db 1635 GGTGGCGACCGATGATGTTGCTGCTTACAGATCAACCCGAGCTCGGCTT--- 1634
QY 129 TACCTGGTCCGCTGACGAGGCGCCAGCACAGATGACCGTCCCGGGCGGCACCGAGGTG 188
Db 1695 TACCTGGTCCGCTGACGAGGCGCCAGCACAGATGACCGTCCCGGGCGGCACCGAGGTG 188
QY 189 CCGGTTGAGACCGAGCAT 208
Db 1755 CCAGTCGAGACCGATGACAT 1774

RESULT 8
US-10-076-406-3
; Sequence 3, Application US/10076406
; Publication No. US20030166884A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: Nucleotide sequences coding for the rpoB gene
; FILE REFERENCE: 219774USOXIP
; CURRENT APPLICATION NUMBER: US/10/076,406
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: DE 10107229.5
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 09/887052
; PRIOR FILING DATE: 2001-06-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 5099
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
; OTHER INFORMATION:
; NAME/KEY: mutation
; LOCATION: (1987)..(1987)
; OTHER INFORMATION: Substitution of adenine by thymine
; NAME/KEY: mutation
; LOCATION: (1288)..(1288)
; OTHER INFORMATION: Substitution of cytosine by thymine
; NAME/KEY: mutation
; LOCATION: (715)..(715)
; OTHER INFORMATION: Substitution of cytosine by thymine
US-10-076-406-3

Query Match          40.0%; Score 83.2; DB 12; Length 5099;
Best Local Similarity 67.0%; Pred. No. 2.1e-14;
Matches 134; Conserved 0; Mismatches 63; Indels 3; Gaps 1;

QY 9 AAGCGCTACGACCTGGCCGGGTAGGCGGCTACAAAGGTCACAAAGAGCTCGGCTGCAC 68
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Db 1578 AAGCGCTACGACCTGGCTGGCTGCTTACAGATCAACCCGAGCTCGGCTT--- 1634
QY 69 GTCGGGATCCGATCACCAGCTCCAGCTGACCGAGGAGAGAGCTGCGCCACCATCGAG 128
Db 1635 GGTGGCGACCGATGATGTTGCTGCTTACAGATCAACCCGAGCTCGGCTGAG 1694
QY 129 TACCTGGTCCGCTGACGAGGCGCCAGCACAGATGACCGTCCCGGGCGGCACCGAGGTG 188
Db 1695 TACCTGGTCCGCTGACGAGGCGCCAGCACAGATGACCGTCCCGGGCGGCACCGAGGTG 188
QY 189 CCGGTTGAGACCGAGCAT 208
Db 1755 CCAGTCGAGACCGATGACAT 1774

RESULT 9
US-10-076-406-5
; Sequence 5, Application US/10076406
; Publication No. US20030166884A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: Nucleotide sequences coding for the rpoB gene
; FILE REFERENCE: 219774USOXIP
; CURRENT APPLICATION NUMBER: US/10/076,406
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: DE 10107229.5
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 09/887052
; PRIOR FILING DATE: 2001-06-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 5099
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
; OTHER INFORMATION:
; NAME/KEY: mutation
; LOCATION: (2016)..(2016)
; OTHER INFORMATION: Substitution of cytosine by thymine
US-10-076-406-5

Query Match          40.0%; Score 83.2; DB 12; Length 5099;
Best Local Similarity 67.0%; Pred. No. 2.1e-14;
Matches 134; Conserved 0; Mismatches 63; Indels 3; Gaps 1;

QY 9 AAGCGCTACGACCTGGCCGGGTAGGCGGCTACAAAGGTCACAAAGAGCTCGGCTGCAC 68
Db 1578 AAGCGCTACGACCTGGCTGGCTGCTTACAGATCAACCCGAGCTCGGCTT--- 1634
QY 69 GTCGGGATCCGATCACCAGCTCCAGCTGACCGAGGAGAGAGCTGCGCCACCATCGAG 128
Db 1635 GGTGGCGACCGATGATGTTGCTGCTTACAGATCAACCCGAGCTCGGCTGAG 1694
QY 129 TACCTGGTCCGCTGACGAGGCGCCAGCACAGATGACCGTCCCGGGCGGCACCGAGGTG 188
Db 1695 TACCTGGTCCGCTGACGAGGCGCCAGCACAGATGACCGTCCCGGGCGGCACCGAGGTG 188
QY 189 CCGGTTGAGACCGAGCAT 208
Db 1755 CCAGTCGAGACCGATGACAT 1774

RESULT 10
US-10-075-460-5
; Sequence 5, Application US/10075460
```

```
; Publication No. US2002015557A1
; GENERAL INFORMATION:
; APPLICANT: MOCKEL, BERTINA
; APPLICANT: BATHÉ, BRIGITTE
; APPLICANT: HANS, STEFAN
; APPLICANT: KREUTZER, CAROLINE
; APPLICANT: HERMANN, THOMAS
; APPLICANT: PEPPERLE, WALTER
; APPLICANT: BLINDER, MICHAEL
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE rpsL GENE
; FILE REFERENCE: 2184720SUX
; CURRENT APPLICATION NUMBER: US/10/075,460
; CURRENT FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: DE 10107230.9
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: DE 10162386.0
; PRIOR FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 5099
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
; OTHER INFORMATION:
US-10-075-460-5

Query Match 40.0%; Score 83.2; DB 13; Length 5099;
Best Local Similarity 67.0%; Pred. No. 2.1e-14;
Matches 134; Conservative 0; Mismatches 63; Indels 3; Gaps 1;

QY 9 AAGCGTAGACCTGGCCGGGTAGCGCGTACACAGGTCAACAGAGCTCGCCCTGCAC 68
DB 1578 AAGCGTAGACCTGGCTGCGGTGCTTACAGATCAACCCAGCTCGCCCT--- 1634
QY 69 GTGCGGATCCGATCACCAGCTCCACGCTGACCGAGGAGAGCTGCTGCCACCATCGAG 128
DB 1635 GTGCGGACCATGATGTTGCTGCTTACTGAGAGGACATCGCAACCATCATCGAG 1694
QY 129 TACCTGGTCCGCTGACGAGGGCCAGACAGATGACCGTCCCGGGCGGCACCGAGGTG 188
DB 1695 TACCTGGTGGCTGACGAGGTGAGCGGCTCATGACTTCTCCAAATGGTGAAGAGATC 1754
QY 189 CCGGTTGACACCGAGCAT 208
DB 1755 CCACTCGAGACCGATGACAT 1774

RESULT 11
US-09-738-626-1
; Sequence 1, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: JOCHIAL, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENO, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
```

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; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 1
; LENGTH: 3309400
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-1

Query Match 40.0%; Score 83.2; DB 10; Length 3309400;
Best Local Similarity 67.0%; Pred. No. 1.7e-14;
Matches 134; Conservative 0; Mismatches 63; Indels 3; Gaps 1;

QY 9 AAGCGTAGACCTGGCCGGGTAGCGCGTACACAGGTCAACAGAGCTCGCCCTGCAC 68
DB 513789 AAGCGTAGACCTGGCTGCGGTGCTTACAGATCAACCCAGCTCGCCCT--- 513845
QY 69 GTGCGGATCCGATCACCAGCTCCACGCTGACCGAGGAGAGCTGCTGCCACCATCGAG 128
DB 513846 GTGCGGACCATGATGTTGATGACTCTTCTGAGAGGACATCGCAACCATCATCGAG 513905
QY 129 TACCTGGTCCGCTGACGAGGGCCAGACAGATGACCGTCCCGGGCGGCACCGAGGTG 188
DB 513906 TACCTGGTGGCTGCTGACGAGGTGAGCGGCTCATGACTTCTCCAAATGGTGAAGAGATC 513965
QY 189 CCGGTTGACACCGAGCAT 208
DB 513966 CCACTCGAGACCGATGACAT 513985

RESULT 12
US-10-156-761-4898
; Sequence 4898, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 4898
; LENGTH: 3543
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3543)
US-10-156-761-4898

Query Match 38.7%; Score 80.4; DB 14; Length 3543;
Best Local Similarity 65.4%; Pred. No. 1.3e-13;
Matches 136; Conservative 0; Mismatches 66; Indels 6; Gaps 1;

QY 1 TCAAGGAGAGCGCTACGACCTGGCCGGGTAGCGCGTACAGGTCAACAGAGAGCTCG 60
DB 926 TCAACCCGAAGCGCTACGACCTCGCGAGGTGCGCGGTACAGGTCAACAGAGAGCTGG 985
QY 61 GCTTGCACCTCGCGGATCCGATTCACAGTCCACGCTGACCGAGAGAGAGCTGCTGCCA 120
DB 986 G-----CGCGGAGGCGCGCTGGACCGCGGATCTCGACGAGGACATCATCTCT 1039
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1	172.8	83.1	970	1	US-08-250-030-1	Sequence 1, Appli
2	172.8	83.1	970	5	PCI-US95-06790-1	Sequence 1, Appli
3	172.8	83.1	4403765	3	US-09-103-840A-2	Sequence 2, Appli
4	172.8	83.1	4411529	3	US-09-103-840A-1	Sequence 1, Appli
5	134.4	64.6	3447	2	US-08-313-185-57	Sequence 57, Appl
6	134.4	64.6	3447	3	US-09-082-6114A-57	Sequence 57, Appl
C 7	44	21.2	4403765	3	US-09-103-840A-2	Sequence 2, Appl
C 8	44	21.2	4411529	3	US-09-103-840A-1	Sequence 1, Appl
C 9	40.4	19.4	77536	4	US-09-410-551B-1	Sequence 1, Appli
C 10	39.6	19.0	1218	4	US-09-252-991A-9482	Sequence 9482, Ap
11	39.6	19.0	1290	4	US-09-252-991A-9349	Sequence 9349, Ap
12	39.6	19.0	2196	4	US-09-252-991A-9319	Sequence 9319, Ap
13	39.6	18.9	1894	3	US-09-329-350-32	Sequence 32, Appl
14	39	18.8	1100	3	US-09-248-335-53	Sequence 53, Appl
15	38.8	18.7	924	4	US-09-252-991A-969	Sequence 969, App
16	38.8	18.7	939	4	US-09-252-991A-925	Sequence 925, App
17	38.6	18.6	1326	4	US-09-252-991A-10931	Sequence 10931, A
18	38.6	18.6	2211	4	US-09-252-991A-11256	Sequence 11256, A
C 19	38.6	18.6	2289	4	US-09-252-991A-10995	Sequence 10995, A
20	38.4	18.5	1221	6	5212296-16	Patent No. 5212296
21	38.4	18.5	1839	4	US-09-252-991A-2563	Sequence 2563, Ap
22	38.4	18.5	1879	6	5212296-5	Patent No. 5212296
C 23	38.4	18.5	2907	4	US-09-252-991A-2354	Sequence 2354, Ap
C 24	38.2	18.4	768	4	US-09-252-991A-1114	Sequence 1114, Ap
C 25	38	18.3	657	4	US-09-252-991A-12503	Sequence 12503, A
C 26	38	18.3	1050	4	US-09-252-991A-13134	Sequence 13134, A
27	38	18.3	1089	4	US-09-252-991A-14778	Sequence 14778, A

Best Local Similarity 89.4%; Pred. No. 1.7e-33;
Matches 186; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 1 TCAAGGAGAAGCGCTACGACCTGCTCGGTGGGTGCGGTACAAAGAGAGCTCG 60
DB 760688 TCAAGGAGAAGCGCTACGACCTGCTCGGTGGGTGCGGTATTAAGGTCAACAAGAGCTCG 760747
QY 61 GCCTGACCGCGCGCCAGCCCATCACAGCTCGACGCTGACCGGAGAGAGCTGCTGCGCA 120
DB 760748 GCGTGGATGTCGGCGAGCCCATCACGCTGCGGTGGGTGCGGTGACCGGAGAGAGCTGCTGCGCA 760807
QY 121 CCATCGAATACCTGCTCGCTTGCACGAGGGCCAGACCGCGATGACCGCTCCCGGGCGGTG 180
DB 760808 CCATCGAATATCTGCTCGCTTGCACGAGGGTTCAGAGGGTTCAGACCGATGACCGTCCCGGGCGGTG 180
QY 181 TCGAGTGGCGGTGCGAGACCGAGACAT 208
DB 760868 TCGAGTGGCGGTGCGAGACCGAGACAT 760895

RESULT 5

US-08-313-185-57
; Sequence 57, Application US/08313185
; Patent No. 5851763
; GENERAL INFORMATION:
; APPLICANT: Heym, Beate
; APPLICANT: Cole, Stewart
; APPLICANT: Young, Douglas
; APPLICANT: Zhang, Ying
; APPLICANT: Honore, Nadine
; APPLICANT: Telenti, Amalio
; APPLICANT: Bodmer, Thomas
; TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
; TITLE OF INVENTION: in Mycobacterium Tuberculosis
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Parabow, Garrett &
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/313,185
; FILING DATE: 12-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 02356.0068-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3447 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-313-185-57

Query Match 54.6%; Score 134.4; DB 2; Length 3447;
Best Local Similarity 77.9%; Pred. No. 1.9e-24;
Matches 162; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 1 TCAAGGAGAAGCGCTACGACCTGCTCGGTGGGTGCGGTACAAAGTCAACAAGAGCTCG 60

DB 809 TCAGGAGAAAGCTACGACCTGCGCGAGGTGCTGTACAGGTCAACAAGAGCTCG 868
QY 61 GCCTGACCGCGCGCCAGCCCATCACAGCTCGACGCTGACCGGAGAGAGCTGCTGCGCA 120
DB 869 GGTTCACGCGCGGTGAGTTGATCACGCTGCTCCACGCTGACCGAGAGAGTGTGCTGCGCA 928
QY 121 CCATCGAATACCTGCTCGCTTGCACGAGGGCCAGACCGCGATGACCGCTCCCGGGCGGTG 180
DB 929 CCATAGAGTACCTGCTGCTGCTGATGAGGGTTCAGTTCGACATGACTGTCCCAAGGTGGGG 988
QY 181 TCGAGTGGCGGTGCGAGACCGAGACAT 208
DB 989 TAGAGTGGCCAGTGGAAACTGACGATAT 1016

RESULT 6

US-09-082-614A-57
; Sequence 57, Application US/09082614A
; Patent No. 6124098
; GENERAL INFORMATION:
; APPLICANT: Heym, Beate
; APPLICANT: Cole, Stewart
; APPLICANT: Young, Douglas
; APPLICANT: Zhang, Ying
; APPLICANT: Honore, Nadine
; APPLICANT: Telenti, Amalio
; APPLICANT: Bodmer, Thomas
; TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
; TITLE OF INVENTION: in Mycobacterium Tuberculosis
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Parabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/082,614A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/313,185
; FILING DATE: 12-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 02356.0068-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3447 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-082-614A-57

Query Match 64.6%; Score 134.4; DB 3; Length 3447;
Best Local Similarity 77.9%; Pred. No. 1.9e-24;
Matches 162; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 1 TCAAGGAGAAGCGCTACGACCTGCTCGGTGGGTGCGGTACAAAGTCAACAAGAGCTCG 60

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Db 809 TCAGGAGAAAGCTACGACTGGCCAGGTGGTTCGTATACAGGTCAACAAAGAGCTCG 868
QY 61 GCTTGAAGCGGGCCAGCCACACACAGCTGACGCTGACGAGGAGACGTCGTCGCCA 120
Db 869 GCTTGAAGCGGGGAGGTGATCATCAGCTGTCACGCTGACGAGGAGGATGTCGTCGCCA 928
QY 121 CCATCGAATACCTGCTCGCTGACGAGGGCCAGCCGCGATGACCGCTCCGGGCGGTG 180
Db 929 CCATAGACTACTGGTTCGCTGATGAGGGTCAGTCGCAATGACTGTCACAGTGGG 988
QY 181 TCGAGTCCGCGTCGACGACGAGCAT 208
Db 989 TAGAAGTCCAGTGGAACTGAGGATAT 1016

RESULT 7
US-09-103-840A-2/c
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match 21.28; Score 44; DB 3; Length 4403765;
Best Local Similarity 55.1%; Pred. No. 0.043; Indels 0; Gaps 0;
Matches 86; Conservative 0; Mismatches 70;

QY 50 CAAGAAGCTCGGCTGAAACGCCGCCAGCCATCACCAGCTCGACGCTGACCGGAGAGA 109
Db 3046005 CAAGAAGCTCGGCTGTCGACACCCATTCTGCTGTCAGCCAGCCGACCGGGGACA 3045946
QY 110 CGTGTGCGCCACCATGCAATACCTGTCGCTTGCAGAGGGGCCAGACCGGATGACCGC 169
Db 3045945 GGCACCTCGAGATCGCCGACATGCTGATCGCTCGGGTGCCTTGACATGCTGGTGATCGA 3045886
QY 170 TCGGGCGGTGTCGAGTGCCTGCGGTCCGAGACCGACA 205
Db 3045885 CTCGGTGGCGGTGTCGTCGCCGCCGCGGAGCTCGA 3045850

RESULT 8
US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
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; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match 21.28; Score 44; DB 3; Length 4411529;
Best Local Similarity 55.1%; Pred. No. 0.043; Indels 0; Gaps 0;
Matches 86; Conservative 0; Mismatches 70;

QY 50 CAAGAAGCTCGGCTGAAACGCCGCCAGCCATCACCAGCTCGACGCTGACCGGAGAGA 109
Db 3051107 CAAGAAGCTCGGCTGTCGACACCCGATTCTGCTGTCAGCCAGCCGACCGGGGACA 3051048
QY 110 CGTGTGCGCCACCATGCAATACCTGTCGCTTGCAGAGGGGCCAGACCGGATGACCGC 169
Db 3051047 GGCACCTCGAGATCGCCGACATGCTGATCGCTCGGGTGCCTTGACATGCTGGTGATCGA 3050988
QY 170 TCGGGCGGTGTCGAGTGCCTGCGGTCCGAGACCGACA 205
Db 3050987 CTCGGTGGCGGTGTCGTCGCCGCCGCGGAGCTCGA 3050952

RESULT 9
US-09-410-551B-1/c
; Sequence 1, Application US/09410551B
; Patent No. 6503737
; GENERAL INFORMATION:
; APPLICANT: KOSAN BIOSCIENCES, Inc.
; APPLICANT: REEVES, CHRISTOPHER
; APPLICANT: CHU, DANIEL
; APPLICANT: KHOSLA, CHAITAN
; APPLICANT: SANTI, DANIEL
; APPLICANT: WO, KAI
; TITLE OF INVENTION: POLYKETIDE SYNTHASE ENZYMES AND RECOMBINANT DNA
; TITLE OF INVENTION: CONSTRUCTS THEREFOR
; FILE REFERENCE: 30062-20026.00
; CURRENT APPLICATION NUMBER: US/09/410,551B
; CURRENT FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: US 60/139,650
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: US 60/123,810
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 60/102,748
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 77536
; TYPE: DNA
; ORGANISM: Streptomyces hygroscopicus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (52275)...(71465)
US-09-410-551B-1

Query Match 19.4%; Score 40.4; DB 4; Length 77536;
Best Local Similarity 61.3%; Pred. No. 0.21; Indels 0; Gaps 0;
Matches 65; Conservative 0; Mismatches 41;

QY 68 CGCGCGCCAGCCCATCACCAGCTGACGCTGACCGAGGAGGAGCTGTCGCCACCATCGA 127
Db 2434 CACCGCGCCAGCCAGCACCATCAGCTGACCTGGAACCCGTCGACGCGGCCACCGA 2375
QY 128 ATACTGTGCTGCTTGCACAGGAGGCCAGCCGCGATGACCGCTCG 173
Db 2374 CTACGCGCTCCACCGCGCGCTGCCAGATCACCAGCTCCGCCACG 2329

RESULT 10
US-09-252-991A-9482/c
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; Sequence 9482, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 9482
; LENGTH: 1218
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-9482

Query Match          19.0%; Score 39.6; DB 4; Length 1218;
Best Local Similarity 56.0%; Pred. No. 0.22;
Matches 75; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

QY 13 GCTACGACCTGGCTCGGTGCGGTGCTGCTACAGAGTCAACAGAGCTGCGCTGAACGGCG 72
Db 221 GCTACACCTGGCGGCGCATGGCGGCTTCATGTCGGCTGTCACAGACCTGACCGGG 162
QY 73 GCCAGGCCATCACCAGCTGCGACGCTGACCGAGGAGAGACGTCGTCGCCACCATCGAATACC 132
Db 161 GCTGGAACGCGGTGCGGTATATCTTCATCGCGGTGCGCATCGCGGCCACCGCTTTCGGGC 102
QY 133 TGGTCGCGCTTGCAC 146
Db 101 TCGGCGCGGGGCGC 88

RESULT 11
US-09-252-991A-9349
; Sequence 9349, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 9349
; LENGTH: 1290
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-9349

Query Match          19.0%; Score 39.6; DB 4; Length 1290;
Best Local Similarity 56.0%; Pred. No. 0.22;
Matches 75; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

QY 13 GCTACGACCTGGCTCGGTGCGGTGCTGCTACAGAGTCAACAGAGCTGCGCTGAACGGCG 72
Db 1121 GCTACACCTGGCGGCGCATGGCGGCTTCATGTCGGCTGTCACAGACCTGACCGGGG 1180
QY 73 GCCAGGCCATCACCAGCTGCGACGCTGACCGAGGAGAGACGTCGTCGCCACCATCGAATACC 132
Db 1191 GCTGGAACGCGGTGCGGCTATATCTTCATCGCGGTGCGCATCGCGGCCACCGCTTTCGGGC 1240
QY 133 TGGTCGCGCTTGCAC 146
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Db 1241 TCGGCGCGGGGCGC 1254

RESULT 12
US-09-252-991A-9319
; Sequence 9319, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 9319
; LENGTH: 2196
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-9319

Query Match          19.0%; Score 39.6; DB 4; Length 2196;
Best Local Similarity 56.0%; Pred. No. 0.23; 59; Indels 0; Gaps 0;
Matches 75; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

QY 13 GCTACGACCTGGCTCGGTGCGGTGCTGCTACAGAGTCAACAGAGCTGCGCTGAACGGCG 72
Db 1911 GCTACACCTGGCGGCGCATGGCGGCTTCATGTCGGCTGTCACAGACCTGACCGGGG 1970
QY 73 GCCAGGCCATCACCAGCTGCGACGCTGACCGAGGAGAGACGTCGTCGCCACCATCGAATACC 132
Db 1971 GCTGGAACGCGGTGCGGTATATCTTCATCGCGGTGCGCATCGCGGCCACCGCTTTCGGGC 2030
QY 133 TGGTCGCGCTTGCAC 146
| | | | |
Db 2031 TCGGCGCGGGGCGC 2044

RESULT 13
US-09-329-350-32
; Sequence 32, Application US/09329350
; Patent No. 6184019
; GENERAL INFORMATION:
; APPLICANT: Miettinen-Oinonen, Arja
; APPLICANT: Londresborough, John
; APPLICANT: Vehmaanper, Jari
; APPLICANT: Haakana, Heli
; APPLICANT: M nyl , Arja
; APPLICANT: Lantto, Raija
; APPLICANT: Elovainio, Minna
; APPLICANT: Joutsjoki, Vesa
; APPLICANT: Paloheimo, Marja
; APPLICANT: Suominen, Pirkko
; TITLE OF INVENTION: NOVEL CELLULASES, THE GENES ENCODING THEM AND
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
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Run on: September 17, 2003, 11:54:34 ; Search time 108.259 Seconds
(without alignments)
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Perfect score: 208
Sequence: 1 tcaaggagacgcctacgac.....ccgctcgagacgacacat 208

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1660708 seqs, 1229959015 residues
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Minimum DB seq length: 0
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Listing first 45 summaries

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2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
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17: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				Query		Description	
Result No.	Score	Match	Length	DB	ID		
1	172.8	83.1	3519	10	US-09-712-363-30	Sequence 30, Appl	
2	94.4	45.4	3495	10	US-09-738-626-547	Sequence 547, Appl	
3	94.4	45.4	5096	10	US-09-984-711-5	Sequence 5, Appl	
4	94.4	45.4	5099	10	US-09-887-052-1	Sequence 1, Appl	
5	94.4	45.4	5099	10	US-09-887-052-3	Sequence 3, Appl	
6	94.4	45.4	5099	10	US-09-887-052-5	Sequence 5, Appl	
7	94.4	45.4	5099	12	US-10-076-406-1	Sequence 1, Appl	
8	94.4	45.4	5099	12	US-10-076-406-3	Sequence 3, Appl	
9	94.4	45.4	5099	12	US-10-076-406-5	Sequence 5, Appl	
10	94.4	45.4	5099	13	US-10-075-460-5	Sequence 5, Appl	
11	94.4	45.4	3309400	10	US-09-738-626-1	Sequence 1, Appl	
12	72.4	34.8	3543	14	US-10-156-761-4898	Sequence 4898, Appl	
13	72.4	34.8	9025608	14	US-10-156-761-1	Sequence 1, Appl	
14	44.6	21.4	603	14	US-10-156-761-1568	Sequence 1568, Appl	
15	44.6	21.4	9025608	14	US-10-156-761-1	Sequence 1, Appl	
16	41.6	20.0	2230	12	US-10-361-460-78	Sequence 78, Appl	

17	41.2	19.8	1644	14	US-10-156-761-1757	Sequence 1757, Appl
18	41	19.7	1266	9	US-09-815-242-7920	Sequence 7920, Appl
19	40.6	19.5	1233	14	US-10-022-809-1	Sequence 1, Appl
20	40	19.2	1428	14	US-10-156-761-2812	Sequence 2812, Appl
21	40	19.2	1458	14	US-10-156-761-4634	Sequence 4634, Appl
22	39.6	19.0	1320	14	US-10-156-761-6285	Sequence 6285, Appl
23	39.6	19.0	2329	10	US-09-816-828-9	Sequence 9, Appl
24	39.4	18.9	1894	8	US-08-841-636A-32	Sequence 32, Appl
25	39.4	18.9	11058	14	US-10-156-761-3629	Sequence 3629, Appl
26	39.2	18.8	3759	14	US-10-156-761-2268	Sequence 2268, Appl
27	38.8	18.7	1215	14	US-10-156-761-2811	Sequence 2811, Appl
28	38.6	18.6	1509	12	US-09-967-464-64	Sequence 64, Appl
29	38.6	18.6	1584	12	US-10-045-612A-29	Sequence 29, Appl
30	38.6	18.6	4396	10	US-09-880-107-2329	Sequence 2329, Appl
31	38.6	18.6	4396	14	US-10-171-581-46	Sequence 46, Appl
32	38.2	18.4	1389	14	US-10-158-761-5431	Sequence 5431, Appl
33	38.2	18.4	1395	14	US-10-205-032-21	Sequence 21, Appl
34	38.2	18.4	1509	12	US-09-967-464-68	Sequence 68, Appl
35	38.2	18.4	60196	14	US-10-205-032-1	Sequence 1, Appl
36	38	18.3	1392	14	US-10-156-761-3990	Sequence 3990, Appl
37	38	18.3	1698	14	US-10-156-761-1532	Sequence 1532, Appl
38	38	18.3	1806	12	US-10-259-165-239	Sequence 239, Appl
39	37.8	18.2	471	14	US-10-156-761-2536	Sequence 2536, Appl
40	37.8	18.2	1164	9	US-09-815-242-7696	Sequence 7696, Appl
41	37.8	18.2	2487	14	US-10-156-761-3753	Sequence 3753, Appl
42	37.8	18.2	3731	9	US-09-822-268A-1	Sequence 1, Appl
43	37.4	18.0	339	14	US-10-156-761-5500	Sequence 5500, Appl
44	37.2	17.9	993	14	US-10-156-761-4673	Sequence 4673, Appl
45	37.2	17.9	14520	14	US-10-156-761-2885	Sequence 2885, Appl

ALIGNMENTS

RESULT 1
US-09-712-363-30
; Sequence 30, Application US/09712363
; Patent No. US20020164588A1
; GENERAL INFORMATION:
; APPLICANT: Eisenberg, David
; APPLICANT: Rotstein, Sergio H.
; APPLICANT: Marcotte, Edward M.
; TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND
; TITLE OF INVENTION: INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS
; FILE REFERENCE: 07419-032001
; CURRENT APPLICATION NUMBER: US/09712,363
; CURRENT FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: PCT/US00/02246
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,531
; PRIOR FILING DATE: 2000-02-01
; PRIOR APPLICATION NUMBER: 60/117,844
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/118,206
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: 60/126,593
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/134,093
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/134,092
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/165,124
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/165,086
; PRIOR FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 3519
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-09-712-363-30

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Query Match      83.1%; Score 172.8; DB 10; Length 3519;
Best Local Similarity 89.4%; Pred. No. 3.6e-41;
Matches 186; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

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Db 884 TCAAGGAGACGCTACGACCTGGCTGGCTGGGTACAGGTCAACAGAGCTCG 943

Qy 61 GCGTGAAGCGGCGAGCCCTACACAGCTGACGCTGACCGAGGAGAGCTCGTCCCA 120
    |||||
Db 944 GCGTGAAGCGGCGAGCCCTACACAGCTGACGCTGACCGAGGAGAGCTCGTCCCA 1003

Qy 121 CCATCGAATACCTGGTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 180
    |||||
Db 1004 CCATCGAATACCTGGTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 1063

Qy 181 TCGAGGTCCGCTGAGACCGACGACAT 208
    |||||
Db 1064 TCGAGGTCCGCTGAGAAACGACGACAT 1091

RESULT 2
US-09-738-626-547
; Sequence 547, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOH, AKIHITO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 547
; LENGTH: 3495
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-547

Query Match      45.4%; Score 94.4; DB 10; Length 3495;
Best Local Similarity 70.5%; Pred. No. 2.5e-18;
Matches 141; Conservative 0; Mismatches 56; Indels 3; Gaps 1;

Qy 9 AAGCGCTACGACCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGA 68
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Db 877 AAGCGCTACGACCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGA 936

Qy 69 GCGGCGACGACCTACGACCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGA 128
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Db 937 GCGGCGACGACCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGA 993

Qy 129 TACTGTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 188
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Db 994 TACTGTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 1053

Qy 189 CCGGTGAGACCGGACGACAT 208
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Db 1054 CCGGTGAGACCGGACGACAT 1073
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RESULT 3
US-09-984-711-5
; Sequence 5, Application US/09984711
; Patent No. US20020119549A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: STEPHAN, Hans
; APPLICANT: KREUTZER, Caroline
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE TP5L GENE
; FILE REFERENCE: 20420950
; CURRENT APPLICATION NUMBER: US/09/984,711
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: DE10108230.9
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 5096
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
; OTHER INFORMATION:
US-09-984-711-5

Query Match      45.4%; Score 94.4; DB 10; Length 5096;
Best Local Similarity 70.5%; Pred. No. 2.5e-18;
Matches 141; Conservative 0; Mismatches 56; Indels 3; Gaps 1;

Qy 9 AAGCGCTACGACCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGA 68
    |||||
Db 1578 AAGCGCTACGACCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGA 1637

Qy 69 GCGGCGACGACCTACGACCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGA 128
    |||||
Db 1638 GCGGCGACGACCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGA 1694

Qy 129 TACTGTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 188
    |||||
Db 1695 TACTGTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 1754

Qy 189 CCGGTGAGACCGGACGACAT 208
    |||||
Db 1755 CCGGTGAGACCGGACGACAT 1774

RESULT 4
US-09-887-052-1
; Sequence 1, Application US/09887052
; Patent No. US20020119537A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE TP5L GENE
; FILE REFERENCE: 2042120X
; CURRENT APPLICATION NUMBER: US/09/887,052
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: DE10107229.5
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 5099
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; Publication No. US2002015557A1
; GENERAL INFORMATION:
; APPLICANT: MCKEL, BETTINA
; APPLICANT: BATHE, BRIGITTE
; APPLICANT: HANS, STEFAN
; APPLICANT: KREUTZER, CAROLINE
; APPLICANT: HERMANN, THOMAS
; APPLICANT: PFEFFERLE, WALTER
; APPLICANT: BINDER, MICHAEL
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE TP5L GENE
; FILE REFERENCE: 2184720S0X
; CURRENT APPLICATION NUMBER: US/10/075.460
; CURRENT FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: DE 10107230.9
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: DE 10162386.0
; PRIOR FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 5099
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
; OTHER INFORMATION:
; US-10-075-460-5

Query Match      45.4%; Score 94.4; DB 13; Length 5099;
Best Local Similarity 70.5%; Pred. No. 2.5e-18;
Matches 141; Conservative 0; Mismatches 56; Indels 3; Gaps 1;

QY      9 AAGCGCTACGACCTGGCTCGGTCGGTACAGGTCAACAAGAGCTCGGCTGAAC 68
DQ      1578 AAGCGCTACGACCTGGCTCGGTCGGTACAGGTCAACAAGAGCTCGGCTGAAC 1637
QY      69 GCCGGCCAGCCATCACCAGCTCGACGTCGACGAGGAGAGCGTCGTCGCCACCATCGAA 128
DQ      1638 GCGACCCAGCATGGTTGAT--GACTCTTACTGAGAGAGATCGCAACCATCGAG 1694
QY      129 TACCTGTCGCTTCGACAGAGGCCGACACCGCATGACCGTCCGGGGGGTGTGAGGTG 188
DQ      1695 TACCTGTCGCTTCGACAGAGGCCGACACCGCATGACCTTCTCCAAATGTTGAAGATC 1754
QY      189 CCGCTCGAGACCGAGACAT 208
DQ      1755 CCAGTCGAGACCGATGACAT 1774

RESULT 11
US-09-738-626-1
; Sequence 1, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIO
; APPLICANT: OKHIAL, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENOH, AKIHITO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
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; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 1
; LENGTH: 3309400
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; US-09-738-626-1

Query Match      45.4%; Score 94.4; DB 10; Length 3309400;
Best Local Similarity 70.5%; Pred. No. 2.7e-18;
Matches 141; Conservative 0; Mismatches 56; Indels 3; Gaps 1;

QY      9 AAGCGCTACGACCTGGCTCGGTCGGTACAGGTCAACAAGAGCTCGGCTGAAC 68
DQ      513789 AAGCGCTACGACCTGGCTCGGTCGGTACAGGTCAACAAGAGCTCGGCTGAAC 513848
QY      69 GCCGGCCAGCCATCACCAGCTCGACGTCGACGAGGAGAGCGTCGTCGCCACCATCGAA 128
DQ      513849 GCGACCCAGCATGGTTGAT--GACTCTTACTGAGAGAGATCGCAACCATCGAG 513905
QY      129 TACCTGTCGCTTCGACAGAGGCCGACACCGCATGACCGTCCGGGGGGTGTGAGGTG 188
DQ      513906 TACCTGTCGCTTCGACAGAGGCCGACACCGCATGACTTCTCCAAATGTTGAAGATC 513965
QY      189 CCGCTCGAGACCGAGACAT 208
DQ      513966 CCAGTCGAGACCGATGACAT 513985

RESULT 12
US-10-156-761-4898
; Sequence 4898, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 4898
; LENGTH: 3543
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3543)
; US-10-156-761-4898

Query Match      34.8%; Score 72.4; DB 14; Length 3543;
Best Local Similarity 63.0%; Pred. No. 6.4e-12;
Matches 131; Conservative 0; Mismatches 71; Indels 6; Gaps 1;

QY      1 TCAAGGAGAGCGCTACGACCTCGGCTCGGTCGGTACAGGTCAACAAGAGCTCG 60
DQ      926 TCAACCCGAGAGCGCTACGACCTCGGTCGGTACAGGTCAACAAGAGCTCG 985
QY      61 GCCTGAGAGCGGCGGCGAGCCCATCACACGCTCGAGCGCTGACCGAGGAGAGCTCGTCCCA 120
DQ      986 GCGGCGAGGC-----GCGCTGTCGAGCGGCGGATCTCTGACCGTCGAGGACATCATCTCGT 1039
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QY 121 CCATGAATACCTGCTCGCTTGCAGAGGCGCCAGACCGCATGACGCTCCGGGGGTG 180
Db 1040 CGATCAAGTACCTGCTGAGCTGCACCGCGGTGAGACCGAGACCGTTGGGCGAACAACGGCA 1099
QY 181 TCAGAGTCCGGTCCGAGACCGAGACAT 208
Db 1100 CCTCGATGCTGCTGAGACCGAGACAT 1127

RESULT 13
US-10-156-761-1
; Sequence 1, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
; LENGTH: 9025608
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1

Query Match 34.8%; Score 72.4; DB 14; Length 9025608;
Best Local Similarity 63.0%; Pred. No. 7e-12; Indels 6; Gaps 1;
Matches 131; Conservative 0; Mismatches 71;

QY 1 TCAAGGAGAGCGCTAGACCTGCTCGCTGGTGGTGTACAGCTGACCGAGAGAGAGCTCG 60
Db 5970494 TCAACCGAAGCGCTAGACCTGCTCGAAGTGGCGGCTACAGCTCAACAGAGAGCTCG 5970553
QY 61 GCCTGACCGCGCGCCAGCCCATACACAGCTGACCGAGAGAGAGAGCTGCTGCGCA 120
Db 5970554 CGCGCGAGCGC-----GCCGCTGGACGCGCGGATCCTGACCGTCCGAGGACATCATCTG 5970607
QY 121 CCATGAATACCTGCTCGCTTGCAGAGGCGCCAGACCGCATGACGCTCCGGGGGTG 180
Db 5970608 CGATCAAGTACCTGCTGAGCTGCACCGCGGTGAGACCGAGACCGTTGGGCGAACAACGGCA 5970667
QY 181 TCAGAGTCCGGTCCGAGACCGAGACAT 208
Db 5970668 CCTCGATGCTGCTGAGACCGAGACAT 1127
```

```
RESULT 14
US-10-156-761-1568
; Sequence 1568, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRO
```

```
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1568
; LENGTH: 603
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(603)
US-10-156-761-1568

Query Match 21.4%; Score 44.6; DB 14; Length 603;
Best Local Similarity 55.5%; Pred. No. 0.00078;
Matches 86; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 40 ACAAGGTCAACAAGAAGCTCGGCTGAACGCGCGGCCAGCCCATCACAGCTCGAGCTGA 99
Db 191 AGAAGGTCAACACAGCTGTCGCCATGACTCGCGCGCATCACCATCAGATCCGGCTCT 250
QY 100 CCGAGAGAGAGCTGCTCGCCACCATCGAATACCTGCTCCGCTTCACAGAGGCGGACCG 159
Db 251 CCCTGTACTCTTCGCGACCCCGCGGCTGCTCTGCTTCTGCTCTGCGAGAGCTGT 310
QY 160 CGATGACCGCTCCGCGGCGGTGTCGAGGTGCGCGTC 194
Db 311 CGCAGGCGCGCTCGCGGCTGCTCTCGCGGAC 345

RESULT 15
US-10-156-761-1/c
; Sequence 1, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
; LENGTH: 9025608
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1

Query Match 21.4%; Score 44.6; DB 14; Length 9025608;
Best Local Similarity 55.5%; Pred. No. 0.00087;
Matches 86; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 40 ACAAGGTCAACAAGAAGCTCGGCTGAACGCGCGGCCAGCCCATCACAGCTCGAGCTGA 99
Db 1943983 AGAAGGTCAACACAGCTGTCGCCATGACTCGCGCGCATCACCATCAGATCCGGCTCT 1943924
```

QY

100 CCGAGGACGCTGTGCCCATCGAATACCTGGTCGGTGCACGAGGCCACCG 159
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Dd 1943923 CCTGTACTCTTCGGCACCCCGGGCCAGACC GGTTCTGGTTCTCTGGACGACCTGT 1943864

Qy 160 CGATGACCGCTCCGGCGGTGTCGAGGTGCCGTC 194
||| ||| ||| ||| ||| ||| ||| |||
Db 1943863 CCGAGGCGCCCTCGGCGGTGTCCTCCGGAC 1943829

Search completed: September 17, 2003, 13:05:24
Job time : 135.259 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 17, 2003, 11:54:34 ; Search time 30,1105 Seconds
(without alignments)
3049.028 Million cell updates/sec

Title: US-09-697-123b-11

Perfect score: 208

Sequence: 1 tcaagagaagcgctacgac.....ccggtcgagaccagacat 208

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_NA.*

- 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/PCRUS_COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	171.2	82.3	970	1	US-08-250-030-1
2	171.2	82.3	970	5	PCR-US95-06790-1
3	171.2	82.3	4403765	3	US-09-103-840A-2
4	171.2	82.3	4411529	3	US-09-103-840A-1
5	136	65.4	3447	2	US-08-313-185-57
6	136	65.4	3447	3	US-09-082-614A-57
7	44	21.2	4403765	3	US-09-103-840A-2
8	44	21.2	4411529	3	US-09-103-840A-1
9	42	20.2	903	4	US-08-252-991A-10682
10	42	20.2	933	4	US-08-252-991A-10768
11	42	20.2	1239	4	US-09-252-991A-10390
12	40.6	19.5	918	4	US-09-252-991A-16461
13	40.6	19.5	1005	4	US-08-252-991A-16346
14	40.6	19.5	1098	4	US-08-252-991A-16142
15	40.4	19.4	77536	4	US-09-410-551B-1
16	40	19.2	6085	3	US-09-029-603-4
17	39.6	19.0	1089	4	US-09-252-991A-14778
18	39.6	19.0	1347	4	US-09-252-991A-14972
19	39.6	19.0	1482	4	US-09-252-991A-14656
20	39.4	18.9	1894	3	US-09-329-350-32
21	39.4	18.9	77536	4	US-09-410-551B-1
22	39.2	18.8	1470	4	US-08-252-991A-896
23	39.2	18.8	1662	4	US-09-252-991A-1137
24	39.2	18.8	1839	4	US-08-252-991A-945
25	39	18.8	1100	3	US-08-248-335-53
26	38.8	18.7	924	4	US-09-252-991A-969
27	38.8	18.7	939	4	US-09-252-991A-925

c	28	38.6	18.6	480	4	US-09-252-991A-8286	Sequence 8286, Ap
	29	38.6	18.6	1326	4	US-09-252-991A-10931	Sequence 10931, A
	30	38.6	18.6	1506	4	US-09-252-991A-8077	Sequence 8077, Ap
c	31	38.6	18.6	1506	4	US-09-252-991A-8236	Sequence 8236, Ap
c	32	38.6	18.6	2211	4	US-09-252-991A-11256	Sequence 11256, A
	33	38.6	18.6	2289	4	US-09-252-991A-10995	Sequence 10995, A
	34	38.4	18.5	1221	6	5212296-16	Patent No. 5212296
	35	38.4	18.5	1839	4	US-09-252-991A-2563	Sequence 2563, Ap
	36	38.4	18.5	1879	6	5212296-5	Patent No. 5212296
	37	38.4	18.5	2676	4	US-09-252-991A-12118	Sequence 12118, A
c	38	38.4	18.5	2907	4	US-09-252-991A-2354	Sequence 2354, Ap
c	39	38.4	18.5	3618	4	US-09-252-991A-12305	Sequence 12305, A
	40	38.2	18.4	402	4	US-09-252-991A-8726	Sequence 8726, Ap
c	41	38.2	18.4	768	4	US-09-252-991A-1114	Sequence 1114, Ap
	42	38.2	18.4	1248	3	US-09-105-537-7	Sequence 7, Appli
	43	38.2	18.4	1299	4	US-09-252-991A-8945	Sequence 8945, Ap
c	44	38.2	18.4	1503	4	US-09-252-991A-9139	Sequence 9139, Ap
	45	38.2	18.4	2040	4	US-09-252-991A-8829	Sequence 8829, Ap

ALIGNMENTS

RESULT 1

US-08-250-030-1
; Sequence 1, Application US/08250030
; Patent No. 5643723
; GENERAL INFORMATION:
; APPLICANT: Persing, David H.
; TITLE OF INVENTION: Detection of a Genetic Locus Encoding
; TITLE OF INVENTION: Resistance to Rifampin in Mycobacterial Cultures and in
; TITLE OF INVENTION: Clinical Specimens
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg & Woessner
; STREET: 3500 IDS Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/250,030
; FILING DATE: 26-MAY-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueting, Ann M.
; REGISTRATION NUMBER: 33,977
; REFERENCE/DOCKET NUMBER: 150.105US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-339-0331
; TELEFAX: 612-339-3061
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 970 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA

Query Match 82.3%; Score 171.2; DB 1; Length 970;
Best Local Similarity 88.9%; Pred. No. 5.6e-32;
Matches 185; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 1 TCAAGGAGAGCGCTACGACCTGCGCGGTGGCGGTACAGGTCAACAAGACTCG 60
|||||
DB 26 TCAAGGAGAGCGCTACGACCTGCGCGGTGGCGGTATAGGTCAACAAGACTCG 85
|||||

Best Local Similarity 88.9%; Pred. No. 1.1e-31;
Matches 185; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 1 TCAAGGAGAAGCGCTACGACCTGCGCGGGTGGCGCGGTACAAGTCAACAAGAAGCTCG 60
|||||
Db 760688 TCAAGGAGAAGCGCTACGACCTGCGCGGGTGGCGCGGTACAAGTCAACAAGAAGCTCG 760747
|||||

QY 61 GCCTGTAACCGCGCGCCAGCCCATCACAGCTCGACGCTGACCGAGAGAGAGCTGTCGCCA 120
|||||
Db 760748 GCGTGCATGTCGGCGAGCCCATCACGTCGTCGACGCTGACCGAGAGAGAGCTGTCGCCA 760807
|||||

QY 121 CCATCGAATACCTGCTCGCGCTTGCCAGGAGGCGCCAGCGCGTACCGCTCCCGGGCGGTG 180
|||||
Db 760808 CCATCGAATATCTGCTCGCGCTTGCCAGGAGGCTCAGACCATGATGACCGTCCCGGGCGGTG 760867
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QY 181 TCGAGTGCGCGTTCGAGACCGACGACAT 208
|||||
Db 760868 TCGAGTGCGCGTTCGAGACCGACGACAT 760895
|||||

RESULT 5

US-08-313-185-57
; Sequence 57, Application US/08313185
; Patent No. 5851763
; GENERAL INFORMATION:
; APPLICANT: Heym, Beate
; APPLICANT: Cole, Stewart
; APPLICANT: Young, Douglas
; APPLICANT: Zhang, Ying
; APPLICANT: Honore, Nadine
; APPLICANT: Telenti, Amelio
; APPLICANT: Bodmer, Thomas
; TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
; TITLE OF INVENTION: in Mycobacterium Tuberculosis
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/313,185
; FILING DATE: 12-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 02356.0068-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3447 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-313-185-57

Query Match 65.4%; Score 136; DB 2; Length 3447;
Best Local Similarity 78.4%; Pred. No. 1.1e-23;
Matches 163; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 1 TCAAGGAGAAGCGCTACGACCTGCGCGGGTGGCGCGGTACAAGTCAACAAGAAGCTCG 60
|||||

Db 809 TCAAGGAGAAGCGCTACGACCTGCGCGGGTGGCGGTACAAGTCAACAAGAAGCTCG 868
|||||

QY 61 GCCTGTAACCGCGCGCCAGCCCATCACAGCTGACGCTGACCGAGAGAGAGCTGTCGCCA 120
|||||

Db 869 GGTTCGACGCGGTGAGTTGATCATACGTCGTCCTCCACGCTGACCGAAGAGGATGTCGTCGCCA 928
|||||

QY 121 CCATCGAATACCTGCTCGCGCTTGCCAGGAGGCGCCAGCGCGTACCGCTCCCGGGCGGTG 180
|||||

Db 929 CCATAGAGTACCTGCTGCTGCTGATGAGGCTCAGTCGACATGACTGTCCAGGTGGGG 988
|||||

QY 181 TCGAGTGCGCGTTCGAGACCGACGACAT 208
|||||

Db 989 TAGAAGTGCCAGTGGAAACTGACGATAT 1016
|||||

RESULT 6

US-09-082-614A-57
; Sequence 57, Application US/09082614A
; Patent No. 6124098
; GENERAL INFORMATION:
; APPLICANT: Heym, Beate
; APPLICANT: Cole, Stewart
; APPLICANT: Young, Douglas
; APPLICANT: Zhang, Ying
; APPLICANT: Honore, Nadine
; APPLICANT: Telenti, Amelio
; APPLICANT: Bodmer, Thomas
; TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
; TITLE OF INVENTION: in Mycobacterium Tuberculosis
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/082,614A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/313,185
; FILING DATE: 12-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 02356.0068-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3447 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-082-614A-57

Query Match 65.4%; Score 136; DB 3; Length 3447;
Best Local Similarity 78.4%; Pred. No. 1.1e-23;
Matches 163; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 1 TCAAGGAGAAGCGCTACGACCTGCGCGGGTGGCGCGGTACAAGTCAACAAGAAGCTCG 60
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Query Match          19.5%; Score 40.6; DB 4; Length 1005;
Best Local Similarity 50.8%; Pred. No. 0.23;
Matches 97; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

QY      17  CGACCTGGCCGCGGTGGCCGGTACAAAGGTCAACAAGATCGGCGCTGAACGCGCGCCA 76
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      712  CGCCCTGGCCGGGTGCTGATCCACATGAACTACGGCACCTTGACTTTACGCCGGGTT 771

QY      77  GCOCATCACCACTCGACGGTGAACCGAGGAAGACGTGTCGCCACCATCGAATACTGGT 136
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      772  CATCATCGGCATCAAGGCGTTTCACCGCGCGGTGCTCGCGCGGATCGGCTGCCCGG 831

QY      137  CCGCTGTCACGAGGCGCAGACCGCGATGACCCGCTCCGGCGGTGTCAGGTGCCGTGCA 196
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      832  GCGATGCTCGCGCGCCCTGCTGGAGTGGCCGAGCGGCAGTTCGCGGGATGTGCAA 891

QY      197  GACGCGACGACA 207
      ||| ||| |||
Db      892  CACCGACTACA 902

RESULT 14
US-09-252-991A-16142/c
US-Sequence 16142, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 16142
; LENGTH: 1098
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-16142

```

```

; APPLICANT: SANTI, DANIEL
; APPLICANT: WU, KAI
; TITLE OF INVENTION: POLYKETIDE SYNTHASE ENZYMES AND RECOMBINANT DNA
; TITLE OF INVENTION: CONSTRUCTS THEREFOR
; FILE REFERENCE: 30062-20026.00
; CURRENT APPLICATION NUMBER: US/09/410,551B
; CURRENT FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: US 60/139,650
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: US 60/123,810
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 60/102,748
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 77536
; TYPE: DNA
; ORGANISM: Streptomyces hygroscopicus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (52275)...(71465)
US-09-410-551B-1

Query Match          19.4%; Score 40.4; DB 4; Length 77536;
Best Local Similarity 61.3%; Pred. No. 0.37;
Matches 65; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY      68  CGCGCGCCAGCCATCACCGCTGACGCTGACCGAGGAGAGAGCTGTCGCCACCATGGA 127
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      2434  CACCGGCGCCACCGACACCCACATFACGCTGACCTGGAAGACCCGTCGAGCGGCGCACCGGA 2375
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY      128  ATACCTGGTCGCTTGCACGAGGCGCCAGCCGCGATGACCGCTCCG 173
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      2374  CTAGCGCTCCACCGCGACGCTGCCAGATCACCGCTCCGCCACG 2329
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

Search completed: September 17, 2003, 12:28:50
Job time : 53.1605 secs

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[illegible]

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43      40.0      19.5      15.5      12      08 10 17.5 144 543
sequence 343, 443, 453

ALIGNMENTS

RESULT 1
US-09-712-363-30
; Sequence 30, Application US/09712363
; Patent NO. US20020164588A1
; GENERAL INFORMATION:
; APPLICANT: Eisenberg, David
; APPLICANT: Rotstein, Sergio H.
; APPLICANT: Marcotte, Edward M.
; TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND
; TITLE OF INVENTION: INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS
; FILE REFERENCE: 07419-032001
; CURRENT APPLICATION NUMBER: US/09/712,363

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? PRIOR APPLICATION NUMBER: 60/111,844
? PRIOR FILING DATE: 1999-01-29
? PRIOR APPLICATION NUMBER: 60/118,206,
? PRIOR FILING DATE: 1999-02-01
? PRIOR APPLICATION NUMBER: 60/126,593
? PRIOR FILING DATE: 1999-03-26
? PRIOR APPLICATION NUMBER: 60/134,093
? PRIOR FILING DATE: 1999-05-14
? PRIOR APPLICATION NUMBER: 60/134,092
? PRIOR FILING DATE: 1999-05-14
? PRIOR APPLICATION NUMBER: 60/165,124
? PRIOR FILING DATE: 1999-11-12
? PRIOR APPLICATION NUMBER: 60/165,086
? PRIOR FILING DATE: 1999-11-12
? NUMBER OF SEQ ID NOS: 292
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 30
? LENGTH: 3519
? TYPE: DNA
? ORGANISM: Mycobacterium tuberculosis
US-09-712-363-30

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Query Match	82.3%;	Score	171.2;	DB	10;	Length	3519;
Best Local Similarity	88.9%;	Pred.	No. 1.2e-39;				
Matches	185;	Conservative	0;	Mismatches	23;	Indels	0;
Gaps	0;						
QY	1	TCAGAGAGAGCGCTACGACCTGCCCGGTGGCGGTACAAAGTCAACAAGAAGCTCG	60				
Db	884	TCAGAGAGAGCGCTACGACCTGCCCGGTGGCGGTATAGGTCAACAAGAAGCTCG	943				
QY	61	GCTTGACGCGCGGCAGCCCATCACCAGTCTGACGCGCTGACGAGGAAGACGTCGTGCGCA	120				
Db	944	GGCTGCATGTCGCGAGCGCCATCACGCTCTGACGCGCTGACGAGGAAGACGTCGTGCGCA	1003				
QY	121	CCATCAATACCTGCTCGCTTGACAGAGGGCCAGACCGCGATGACGCGTCCGSGCGGTG	180				
Db	1004	CCATCAATATCTGGTCCGCTTGACAGGGTCAGACCCAGCATGACGCTCCGSGCGGTG	1063				
QY	181	TCGAGGTGCGGTCGAGACCGACAT	208				
Db	1064	TCGAGGTGCGGTTGAAACCGACACAT	1091				

RESULT 2
US-09-738-626-547
; Sequence 547, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIALI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 547
; LENGTH: 3495
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-547

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RESULT 3
US-09-984-711-5
; Sequence 5, Application US/09984711
; Patent No. US20020119549A1
; GENERAL INFORMATION:
; APPLICANT: MORCKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: STEPHAN, Hans
; APPLICANT: KREUTZER, Caroline
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE rpsL GENE
; FILE REFERENCE: 204209US0
; CURRENT APPLICATION NUMBER: US/09/984,711
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: DE10108230.9
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 5096
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
; OTHER INFORMATION:
US-09-984-711-5

Query Match 43.1%; Score 89.6; DB 10; Length 5096;
Best Local Similarity 69.0%; P: 0.0; M: 2e-16;
Matches 138; Conservative 0; Mismatches 59; Indels 3; Gaps 1;

QY 9 AAGCGCTACGACTGGCCGGGTGGCGGGTCAAGGTCAACAAGAGCTCGGCCTGAAC 68
|||
DB 1578 AAGCGCTACGACTGGCTGGCTGGTGGTGTACAGATCACCGCAGCTCGGCTTGGT 1637
|||
QY 69 GCCGGGCCAGCCCATCACAGCTGACCGCTGACGGAGGAGACGTGTCGCCACCATCGAA 128
|||
DB 1638 GCGCACCAACGATGGTTTGTAT---GACTCTTACTGAAGAGGACATCGCAACCCATCGAG 1694
|||
QY 129 TACCTGTGTGGCTTGCACGAGGGCCACAGCGGCGATGACCGGTCCGGCGGTGTGAGGTG 188
|||
DB 1695 TACCTGTGTGGCTTGCAGCGCAGGTACGCGGTCACTGACTTCTCCAAATGTGAGAGATC 1754
|||
QY 189 CCGGTGAGACGACGACAT 208
|||
DB 1755 CCAGTTCGAGACGATGAT 1774
|||

```

```

RESULT 4
US-09-887-052-1
; Sequence 1, Application US/09887052
; Patent No. US20020119537A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE IPOB GENE
; FILE REFERENCE: 204212050X
; CURRENT APPLICATION NUMBER: US/09/887,052
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: DE10107229.5
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 5099

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; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
US-09-887-052-1

Query Match      43.1%; Score 89.6; DB 10; Length 5099;
Best Local Similarity 69.0%; Pred. No. 2e-16;
Matches 138; Conservative 0; Mismatches 59; Indels 3; Gaps 1;

QY 9 AAGCGCTACGACCTGGCCGGTGGCCGGTACAAAGTCAACGAAGCTCGGCCTGAAC 68
    |||||
Db 1578 AAGCGCTACGACCTGGCTCGCTGGTGTACAGATCAACGCGAGCTCGGCCTTGGT 1637

QY 69 GCGGCCAGCCCAATCACCAGCTGACGAGTGCAGGAGGAGAGAGTCTGCCACCATCGAA 128
    |||||
Db 1638 GCGGACCAAGATGTTTGAAT---GACTCTTACTGAAGAGGACATCGCAACCATCGAG 1694

QY 129 TACCTGGTCCGCTTCACAGAGGGCCAGCCGATGACCGCTCCGGGGGTGTCTGAGGTG 188
    |||||
Db 1695 TACCTGGTCCGCTTCACAGAGGGCCAGCGGTGACGCGTCTCTCCAAATGGTGAAGATC 1754

QY 189 CCGGTCGAGACCGAGCAT 208
    |||||
Db 1755 CCAGTCGAGACCGATGACAT 1774

; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
US-09-887-052-3

Query Match      43.1%; Score 89.6; DB 10; Length 5099;
Best Local Similarity 69.0%; Pred. No. 2e-16;
Matches 138; Conservative 0; Mismatches 59; Indels 3; Gaps 1;

QY 9 AAGCGCTACGACCTGGCCGGTGGCCGGTACAAAGTCAACGAAGCTCGGCCTGAAC 68
    |||||
Db 1578 AAGCGCTACGACCTGGCTCGCTGGTGTACAGATCAACGCGAGCTCGGCCTTGGT 1637

QY 69 GCGGCCAGCCCAATCACCAGCTGACGAGTGCAGGAGGAGAGAGTCTGCCACCATCGAA 128
    |||||
Db 1638 GCGGACCAAGATGTTTGAAT---GACTCTTACTGAAGAGGACATCGCAACCATCGAG 1694

QY 129 TACCTGGTCCGCTTCACAGAGGGCCAGCCGATGACCGCTCCGGGGGTGTCTGAGGTG 188
    |||||
Db 1695 TACCTGGTCCGCTTCACAGAGGGCCAGCGGTGACGCGTCTCTCCAAATGGTGAAGATC 1754

QY 189 CCGGTCGAGACCGAGCAT 208
    |||||
Db 1755 CCAGTCGAGACCGATGACAT 1774

; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
US-09-887-052-5

Query Match      43.1%; Score 89.6; DB 10; Length 5099;
Best Local Similarity 69.0%; Pred. No. 2e-16;
Matches 138; Conservative 0; Mismatches 59; Indels 3; Gaps 1;

QY 9 AAGCGCTACGACCTGGCCGGTGGCCGGTACAAAGTCAACGAAGCTCGGCCTGAAC 68
    |||||
Db 1578 AAGCGCTACGACCTGGCTCGCTGGTGTACAGATCAACGCGAGCTCGGCCTTGGT 1637

QY 69 GCGGCCAGCCCAATCACCAGCTGACGAGTGCAGGAGGAGAGAGTCTGCCACCATCGAA 128
    |||||
Db 1638 GCGGACCAAGATGTTTGAAT---GACTCTTACTGAAGAGGACATCGCAACCATCGAG 1694

QY 129 TACCTGGTCCGCTTCACAGAGGGCCAGCCGATGACCGCTCCGGGGGTGTCTGAGGTG 188
    |||||
Db 1695 TACCTGGTCCGCTTCACAGAGGGCCAGCGGTGACGCGTCTCTCCAAATGGTGAAGATC 1754

QY 189 CCGGTCGAGACCGAGCAT 208
    |||||
Db 1755 CCAGTCGAGACCGATGACAT 1774

; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
US-09-887-052-7

Query Match      43.1%; Score 89.6; DB 10; Length 5099;
Best Local Similarity 69.0%; Pred. No. 2e-16;
Matches 138; Conservative 0; Mismatches 59; Indels 3; Gaps 1;

QY 9 AAGCGCTACGACCTGGCCGGTGGCCGGTACAAAGTCAACGAAGCTCGGCCTGAAC 68
    |||||
Db 1578 AAGCGCTACGACCTGGCTCGCTGGTGTACAGATCAACGCGAGCTCGGCCTTGGT 1637

QY 69 GCGGCCAGCCCAATCACCAGCTGACGAGTGCAGGAGGAGAGAGTCTGCCACCATCGAA 128
    |||||
Db 1638 GCGGACCAAGATGTTTGAAT---GACTCTTACTGAAGAGGACATCGCAACCATCGAG 1694

QY 129 TACCTGGTCCGCTTCACAGAGGGCCAGCCGATGACCGCTCCGGGGGTGTCTGAGGTG 188
    |||||
Db 1695 TACCTGGTCCGCTTCACAGAGGGCCAGCGGTGACGCGTCTCTCCAAATGGTGAAGATC 1754

QY 189 CCGGTCGAGACCGAGCAT 208
    |||||
Db 1755 CCAGTCGAGACCGATGACAT 1774
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Db 1755 CCAGTCGAGACCGATGACAT 1774

RESULT 6
US-09-887-052-5
; Sequence 5, Application US/09887052
; Patent No. US20020119537A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE rpoB GENE
; FILE REFERENCE: 204212USOX
; CURRENT APPLICATION NUMBER: US/09/887,052
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: DE10107229.5
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 5099
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
US-09-887-052-5

Query Match      43.1%; Score 89.6; DB 10; Length 5099;
Best Local Similarity 69.0%; Pred. No. 2e-16;
Matches 138; Conservative 0; Mismatches 59; Indels 3; Gaps 1;

QY 9 AAGCGCTACGACCTGGCCGGTGGCCGGTACAAAGTCAACGAAGCTCGGCCTGAAC 68
    |||||
Db 1578 AAGCGCTACGACCTGGCTCGCTGGTGTACAGATCAACGCGAGCTCGGCCTTGGT 1637

QY 69 GCGGCCAGCCCAATCACCAGCTGACGAGTGCAGGAGGAGAGAGTCTGCCACCATCGAA 128
    |||||
Db 1638 GCGGACCAAGATGTTTGAAT---GACTCTTACTGAAGAGGACATCGCAACCATCGAG 1694

QY 129 TACCTGGTCCGCTTCACAGAGGGCCAGCCGATGACCGCTCCGGGGGTGTCTGAGGTG 188
    |||||
Db 1695 TACCTGGTCCGCTTCACAGAGGGCCAGCGGTGACGCGTCTCTCCAAATGGTGAAGATC 1754

QY 189 CCGGTCGAGACCGAGCAT 208
    |||||
Db 1755 CCAGTCGAGACCGATGACAT 1774

; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
US-10-076-406-1

Query Match      43.1%; Score 89.6; DB 10; Length 5099;
Best Local Similarity 69.0%; Pred. No. 2e-16;
Matches 138; Conservative 0; Mismatches 59; Indels 3; Gaps 1;

QY 9 AAGCGCTACGACCTGGCCGGTGGCCGGTACAAAGTCAACGAAGCTCGGCCTGAAC 68
    |||||
Db 1578 AAGCGCTACGACCTGGCTCGCTGGTGTACAGATCAACGCGAGCTCGGCCTTGGT 1637

QY 69 GCGGCCAGCCCAATCACCAGCTGACGAGTGCAGGAGGAGAGAGTCTGCCACCATCGAA 128
    |||||
Db 1638 GCGGACCAAGATGTTTGAAT---GACTCTTACTGAAGAGGACATCGCAACCATCGAG 1694

QY 129 TACCTGGTCCGCTTCACAGAGGGCCAGCCGATGACCGCTCCGGGGGTGTCTGAGGTG 188
    |||||
Db 1695 TACCTGGTCCGCTTCACAGAGGGCCAGCGGTGACGCGTCTCTCCAAATGGTGAAGATC 1754

QY 189 CCGGTCGAGACCGAGCAT 208
    |||||
Db 1755 CCAGTCGAGACCGATGACAT 1774

; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
US-10-076-406-1

Query Match      43.1%; Score 89.6; DB 10; Length 5099;
Best Local Similarity 69.0%; Pred. No. 2e-16;
Matches 138; Conservative 0; Mismatches 59; Indels 3; Gaps 1;

QY 9 AAGCGCTACGACCTGGCCGGTGGCCGGTACAAAGTCAACGAAGCTCGGCCTGAAC 68
    |||||
Db 1578 AAGCGCTACGACCTGGCTCGCTGGTGTACAGATCAACGCGAGCTCGGCCTTGGT 1637

QY 69 GCGGCCAGCCCAATCACCAGCTGACGAGTGCAGGAGGAGAGAGTCTGCCACCATCGAA 128
    |||||
Db 1638 GCGGACCAAGATGTTTGAAT---GACTCTTACTGAAGAGGACATCGCAACCATCGAG 1694

QY 129 TACCTGGTCCGCTTCACAGAGGGCCAGCCGATGACCGCTCCGGGGGTGTCTGAGGTG 188
    |||||
Db 1695 TACCTGGTCCGCTTCACAGAGGGCCAGCGGTGACGCGTCTCTCCAAATGGTGAAGATC 1754

QY 189 CCGGTCGAGACCGAGCAT 208
    |||||
Db 1755 CCAGTCGAGACCGATGACAT 1774
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/ TYPE: DNA
/ ORGANISM: Corynebacterium glutamicum
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (702)..(4196)
/ OTHER INFORMATION:
US-10-076-406-1

Query Match 43.1%; Score 89.6; DB 12; Length 5099;
Best Local Similarity 59.0%; Pred. No. 2e-16;
Matches 138; Conservative 0; Mismatches 59; Indels 3; Gaps 1;

QY 9 AAGCGCTACGACCTGGCGCGGTGGCGGTACAGGTCAACGAGTCAACGAGCTCGGCTTGGT 1637
Db |||||
1578 AAGCGCTACGACCTGGCGCGGTGGCGGTACAGGTCAACGAGTCAACGAGCTCGGCTTGGT 1637

QY 69 GCCGCCAGCCATCACCAGCTCGACGCTGACCGAGGAGACGCTGCTGCCACCATCGAA 128
Db |||||
1638 GCCGACCACGATGTTTGAT---GACTCTTACTGAAGGAGCATCGCAACCATCGAG 1694

QY 129 TACCTGGTCCGCTTGACAGAGGCCAGACCGCGGTGATCCGCTCCGGCGGCTGTCAGGTG 188
Db |||||
1695 TACCTGGTCCGCTTGACAGAGGCCAGACCGCGGTGATCCGCTCCGGCGGCTGTCAGGTG 188

QY 189 CCGGTCGAGACCGACGACAT 208
Db |||||
1755 CCAGTCGAGACCGATGACAT 1774

RESULT 8
US-10-076-406-3
/ Sequence 3, Application US/10076406
/ Publication No. US20030166884A1
/ GENERAL INFORMATION:
/ APPLICANT: MOECKEL, Bettina
/ APPLICANT: BATHE, Brigitte
/ APPLICANT: HERMANN, Thomas
/ APPLICANT: PFEFFERLE, Walter
/ APPLICANT: BINDER, Michael
/ TITLE OF INVENTION: Nucleotide sequences coding for the rpoB gene
/ FILE REFERENCE: 219774USOXCIP
/ CURRENT APPLICATION NUMBER: US/10/076,406
/ PRIOR FILING DATE: 2002-02-19
/ PRIOR APPLICATION NUMBER: DE 10107229.5
/ PRIOR FILING DATE: 2001-02-16
/ PRIOR APPLICATION NUMBER: US 09/887052
/ PRIOR FILING DATE: 2001-06-25
/ NUMBER OF SEQ ID NOS: 12
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 3
/ LENGTH: 5099
/ TYPE: DNA
/ ORGANISM: Corynebacterium glutamicum
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (702)..(4196)
/ OTHER INFORMATION:
/ NAME/KEY: mutation
/ LOCATION: (2188)..(1288)
/ OTHER INFORMATION: Substitution of adenine by thymine
/ NAME/KEY: mutation
/ LOCATION: (715)..(715)
/ OTHER INFORMATION: Substitution of cytosine by thymine
US-10-076-406-3

Query Match 43.1%; Score 89.6; DB 12; Length 5099;
Best Local Similarity 59.0%; Pred. No. 2e-16;
Matches 138; Conservative 0; Mismatches 59; Indels 3; Gaps 1;

QY 9 AAGCGCTACGACCTGGCGCGGTGGCGGTACAGGTCAACGAGTCAACGAGCTCGGCTTGGT 1637
Db |||||
1578 AAGCGCTACGACCTGGCGCGGTGGCGGTACAGGTCAACGAGTCAACGAGCTCGGCTTGGT 1637

QY 69 GCCGCCAGCCATCACCAGCTCGACGCTGACCGAGGAGACGCTGCTGCCACCATCGAA 128
Db |||||
1638 GCCGACCACGATGTTTGAT---GACTCTTACTGAAGGAGCATCGCAACCATCGAG 1694

QY 129 TACCTGGTCCGCTTGACAGAGGCCAGACCGCGGTGATCCGCTCCGGCGGCTGTCAGGTG 188
Db |||||
1695 TACCTGGTCCGCTTGACAGAGGCCAGACCGCGGTGATCCGCTCCGGCGGCTGTCAGGTG 188

QY 189 CCGGTCGAGACCGACGACAT 208
Db |||||
1755 CCAGTCGAGACCGATGACAT 1774
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Db |||||
1578 AAGCGCTACGACCTGGCGCGGTGGCGGTACAGGTCAACGAGTCAACGAGCTCGGCTTGGT 1637

QY 69 GCCGCCAGCCATCACCAGCTCGACGCTGACCGAGGAGACGCTGCTGCCACCATCGAA 128
Db |||||
1638 GCCGACCACGATGTTTGAT---GACTCTTACTGAAGGAGCATCGCAACCATCGAG 1694

QY 129 TACCTGGTCCGCTTGACAGAGGCCAGACCGCGGTGATCCGCTCCGGCGGCTGTCAGGTG 188
Db |||||
1695 TACCTGGTCCGCTTGACAGAGGCCAGACCGCGGTGATCCGCTCCGGCGGCTGTCAGGTG 188

QY 189 CCGGTCGAGACCGACGACAT 208
Db |||||
1755 CCAGTCGAGACCGATGACAT 1774

RESULT 9
US-10-076-406-5
/ Sequence 5, Application US/10076406
/ Publication No. US20030166884A1
/ GENERAL INFORMATION:
/ APPLICANT: MOECKEL, Bettina
/ APPLICANT: BATHE, Brigitte
/ APPLICANT: HERMANN, Thomas
/ APPLICANT: PFEFFERLE, Walter
/ APPLICANT: BINDER, Michael
/ TITLE OF INVENTION: Nucleotide sequences coding for the rpoB gene
/ FILE REFERENCE: 219774USOXCIP
/ CURRENT APPLICATION NUMBER: US/10/076,406
/ CURRENT FILING DATE: 2002-02-19
/ PRIOR APPLICATION NUMBER: DE 10107229.5
/ PRIOR FILING DATE: 2001-02-16
/ PRIOR APPLICATION NUMBER: US 09/887052
/ PRIOR FILING DATE: 2001-06-25
/ NUMBER OF SEQ ID NOS: 12
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 5
/ LENGTH: 5099
/ TYPE: DNA
/ ORGANISM: Corynebacterium glutamicum
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (702)..(4196)
/ OTHER INFORMATION:
/ NAME/KEY: mutation
/ LOCATION: (2016)..(2016)
/ OTHER INFORMATION: Substitution of cytosine by thymine
US-10-076-406-5

Query Match 43.1%; Score 89.6; DB 12; Length 5099;
Best Local Similarity 59.0%; Pred. No. 2e-16;
Matches 138; Conservative 0; Mismatches 59; Indels 3; Gaps 1;

QY 9 AAGCGCTACGACCTGGCGCGGTGGCGGTACAGGTCAACGAGTCAACGAGCTCGGCTTGGT 1637
Db |||||
1578 AAGCGCTACGACCTGGCGCGGTGGCGGTACAGGTCAACGAGTCAACGAGCTCGGCTTGGT 1637

QY 69 GCCGCCAGCCATCACCAGCTCGACGCTGACCGAGGAGACGCTGCTGCCACCATCGAA 128
Db |||||
1638 GCCGACCACGATGTTTGAT---GACTCTTACTGAAGGAGCATCGCAACCATCGAG 1694

QY 129 TACCTGGTCCGCTTGACAGAGGCCAGACCGCGGTGATCCGCTCCGGCGGCTGTCAGGTG 188
Db |||||
1695 TACCTGGTCCGCTTGACAGAGGCCAGACCGCGGTGATCCGCTCCGGCGGCTGTCAGGTG 188

QY 189 CCGGTCGAGACCGACGACAT 208
Db |||||
1755 CCAGTCGAGACCGATGACAT 1774

RESULT 10
US-10-075-460-5
/ Sequence 5, Application US/10075460
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; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 1
; LENGTH: 3309400
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-1

Query Match          43.1%; Score 89.6; DB 10; Length 3309400;
Best Local Similarity 69.0%; Pred. No. 1.9e-16;
Matches 138; Conservative 0; Mismatches 59; Indels 3; Gaps 1;

QY 9 AAGCGCTACGACCTGGCCGGTGGCGGGGTACAAGGTCAACAAGAAAGCTCGGCTGAAC 68
Db 513789 AAGCGCTACGACCTGGCTGGCTGGTGTGTGTACAGATCAACCGCAAGCTCGGCTTGGT 513848

QY 69 GCGGGCCAGCCCATACACAGCTTCGACGCGTACCGAGGAAGAGCTGTGCGCCACCATCGAA 128
Db 513849 GCGCACCACGATGGTTGTAT---GACTCTTACTAGAGAGGACATCGCAACCACCATCGAG 513905

QY 129 TACTGTGTGGCTTGCACGAGGGCCACGACGCGATGACCGTCCGCGCGGTGTCGAGGTG 188
Db 513906 TACTGTGTGGCTTGCACGAGGTGAGCGGTGATGACTTCTCCAAATGGTGAAGATC 513965

QY 189 CCGGTCGAGACGAGACAT 208
Db 513966 CCAGTCGAGACGATGACAT 513985

RESULT 12
US-10-156-761-4898
; Sequence 4898, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 4898
; LENGTH: 3543
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3543)
US-10-156-761-4898

Query Match          36.3%; Score 75.6; DB 14; Length 3543;
Best Local Similarity 63.9%; Pred. No. 1.9e-12;
Matches 133; Conservative 0; Mismatches 69; Indels 6; Gaps 1;

QY 1 TCAGAGGAAGCGCTACGACCTGGCCGGGTGGCGCGGTACAAGGTCAACAAGAAAGCTCG 60
Db 926 TCACCCGAGCGCTACGACCTTCGCGAAGTTCGGCGCTCAAGGTCAACGAGAGCTG 985

QY 61 GCCTGAACGCCGCCAGCCCATACCAAGCTCGAGCTGACCGAGGAAGACGCTCGTGCCTA 120
Db 986 GCGCGCAGGC-----GCCGCTGAGACCGGGGATCTCGACCTCGAGGACATCATCTCGT 1039

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OM nucleic - nucleic search, using sw model

Run on: September 17, 2003, 11:54:34 ; Search time 29.9657 Seconds
(without alignments)
3049.028 Million cell updates/sec

Title: US-09-697-123B-12
Perfect score: 207
Sequence: 1 tcaaggagacgcgtacgac.....ccggtgagaccgacacat 207

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PTCUS_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	154.4	74.6	970	1	US-08-250-030-1
2	154.4	74.6	970	5	PCT-US95-06790-1
3	154.4	74.6	4403765	3	US-09-103-840A-2
4	154.4	74.6	4411529	3	US-09-103-840A-1
5	135.2	65.3	3447	2	US-08-313-185-57
6	135.2	65.3	3447	3	US-09-082-614A-57
c 7	38.2	18.5	276	4	US-09-252-991A-8365
8	38.2	18.5	1731	4	US-09-252-991A-8512
9	37.2	18.0	1926	4	US-09-079-955-10
10	37.2	18.0	3000	3	US-09-192-104-1
11	37.2	18.0	3000	4	US-09-543-446-1
12	36.6	17.7	537	4	US-09-252-991A-8177
13	36.6	17.7	1239	4	US-09-252-991A-8289
14	36	17.4	543	4	US-09-252-991A-2614
15	36	17.4	2205	4	US-09-252-991A-2535
c 16	36	17.4	2388	4	US-09-252-991A-2384
c 17	35.8	17.3	540	4	US-09-252-991A-550
18	35.8	17.3	1002	4	US-09-252-991A-542
c 19	35.8	17.3	1245	4	US-09-252-991A-594
20	35.8	17.3	2067	4	US-09-252-991A-527
c 21	35.4	17.1	480	4	US-09-252-991A-8286
22	35.4	17.1	1506	4	US-09-252-991A-8077
c 23	35.4	17.1	1506	4	US-09-252-991A-8236
c 24	35.4	17.1	4403765	3	US-09-103-840A-2
c 25	35.4	17.1	4411529	3	US-09-103-840A-1
26	35.2	17.0	1014	4	US-09-252-991A-2663
27	35.2	17.0	1155	4	US-09-252-991A-2762

c 28	35.2	17.0	1233	4	US-09-252-991A-3203	Sequence 3203, Ap
c 29	35	16.9	633	4	US-09-252-991A-488	Sequence 488, App
c 30	35	16.9	879	4	US-09-252-991A-359	Sequence 359, App
c 31	35	16.9	1164	4	US-09-252-991A-385	Sequence 385, App
c 32	35	16.9	1419	4	US-09-252-991A-440	Sequence 440, App
c 33	34.8	16.8	657	4	US-09-252-991A-12503	Sequence 12503, A
c 34	34.8	16.8	1050	4	US-09-252-991A-13134	Sequence 13134, A
c 35	34.8	16.8	1707	4	US-09-252-991A-12666	Sequence 12666, A
c 36	34.8	16.8	1836	4	US-09-252-991A-13295	Sequence 13295, A
c 37	34.8	16.8	6085	3	US-08-029-603-4	Sequence 4, Appli
c 38	34.6	16.7	1818	4	US-09-252-991A-3290	Sequence 3290, Ap
c 39	34.6	16.7	2115	4	US-09-252-991A-3388	Sequence 3388, Ap
c 40	34.6	16.7	77536	4	US-09-410-551B-1	Sequence 1, Appli
c 41	34.2	16.5	44377	2	US-08-804-227C-7	Sequence 7, Appli
c 42	34.2	16.5	44377	2	US-08-804-198-1	Sequence 1, Appli
c 43	34	16.4	849	4	US-09-252-991A-12573	Sequence 12573, A
c 44	34	16.4	969	4	US-09-252-991A-12911	Sequence 12911, A
c 45	34	16.4	1257	4	US-09-252-991A-12881	Sequence 12881, A

ALIGNMENTS

RESULT 1
US-08-250-030-1
; Sequence 1, Application US/08250030
; Patent No. 5643723
; GENERAL INFORMATION:
; APPLICANT: Persing, David H.
; TITLE OF INVENTION: Detection of a Genetic Locus Encoding
; TITLE OF INVENTION: Resistance to Rifampin in Mycobacterial Cultures and in
; TITLE OF INVENTION: Clinical Specimens
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Schwegman, Lundberg & Woessner
; STREET: 3500 IDS Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/250,030
; FILING DATE: 26-MAY-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueing, Ann M.
; REGISTRATION NUMBER: 33,977
; REFERENCE/DOCKET NUMBER: 150.105U51
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-339-0331
; TELEFAX: 612-339-3061
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 970 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-250-030-1

Query Match 74.6%; Score 154.4; DB 1; Length 970;
Best Local Similarity 87.0%; Pred. No. 1.4e-33;
Matches 181; Conservative 0; Mismatches 26; Indels 1; Gaps 1;

Qy 1 TCAGGAGAGCGGTACGACTGCGTCCGCGCGGTTCACAGGTCAACAAAAGCTCG 59

Db 26 TCAGGAGAGCGGTACGACTGCGCGCGGTTCACAGGTCAACAAAAGCTCG 85

QY 60 GTCGAGAGCGTCGCGAGCCGATCACCAGTTCGAGCGCTGACCGAGAGGATGCTGCGCCA 119
Db 86 GCGTCGATGTCGCGAGCCCATCAGTCGTCGAGCTGACCGAAGAGACGCTGCGCCA 145
QY 120 CCATCGAGTACCTGGTTGGCTGCGACGAGGCGCAGACCGATGATCCCGCGCGCA 179
Db 146 CCATCGATATCTGGTCCGCTGCGACGAGGGTCAGACCGGATGACCGTTCGCGCGCGG 205
QY 180 CCGAGGTCCGCGTGGAGACCGAGCAT 207
Db 206 TCGAGGTCCGCGTGGAAACCGAGCAT 233

RESULT 2

PCT-US95-06790-1
; Sequence 1, Application PC/TUS9506790
; GENERAL INFORMATION:
; APPLICANT: Mayo Foundation for Medical Education and Research
; APPLICANT: and Hoffmann-La Roche Inc.
; TITLE OF INVENTION: Detection of a Genetic Locus Encoding
; TITLE OF INVENTION: Resistance to Rifampin
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg & Woessner
; STREET: 3500 IDS Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/06790
; FILING DATE: 26-MAY-1995

; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Raasch, Kevin W.
; REGISTRATION NUMBER: 35,651
; REFERENCE/DOCKET NUMBER: 150.105W01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-339-0331
; TELEFAX: 612-339-3061
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 970 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
PCT-US95-06790-1

Query Match 74.6%; Score 154.4; DB 5; Length 970;
Best Local Similarity 87.0%; Pred. No. 1.4e-33;
Matches 181; Conservative 0; Mismatches 26; Indels 1; Gaps 1;

QY 1 TCAAGGAGAGCGCTACGACCTGG-TCGCGTCGCGCGCTTACAGGTCACAAAAGCTCG 59
Db 26 TCAAGGAGAGCGCTACGACCTGGCGCGCTGCTGCTATAGGTCACAGAGCTCG 85
QY 60 GTCGAGTCCGCGAGCCGATCACCAGTTCGAGCGTACCGAAGAGATGTCGCGCCA 119
Db 86 GCGTCATGTCGGAGCCCATCAGTCGTCGAGCGTACCGAGAGAGCTGCTGCGCCA 145
QY 120 CCATCGATGCTGGTTGGCTGCGACGAGGCGCAGACCGATGACCGTCCCGCGCGCA 179
Db 146 CCATCGAATATCTGGTCCGCTGCGACGAGGGTCAGACCGATGACCGTTCGCGCGCGG 205
QY 180 CCGAGGTCCGCGTGGAGACCGAGCAT 207
Db 206 TCGAGGTCCGCGTGGAAACCGAGCAT 233

RESULT 3

US-09-103-840A-2

; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2

; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match 74.6%; Score 154.4; DB 3; Length 4403765;
Best Local Similarity 87.0%; Pred. No. 5.7e-33;
Matches 181; Conservative 0; Mismatches 26; Indels 1; Gaps 1;

QY 1 TCAAGGAGAGCGCTACGACCTGG-TCGCGTCGCGCGCTTACAGGTCACAAAAGCTCG 59
Db 762648 TCAAGGAGAGCGCTACGACCTGGCGCGCTGCTGCTATAGGTCACAGAGCTCG 762707

QY 60 GTCGAGTCCGCGAGCCGATCACCAGTTCGAGCGTACCGAAGAGATGTCGCGCCA 119
Db 762708 GCGTCATGTCGGAGCCCATCAGTCGTCGAGCGTACCGAAGAGAGCTGCTGCGCCA 762767

QY 120 CCATCGATGCTGGTTGGCTGCGACGAGGCGCAGACCGATGACCGTCCCGCGCGCA 179
Db 762768 CCATCGAATATCTGGTCCGCTTGCAGAGGGTCAGACCGATGACCGTTCGCGCGCGG 762827

QY 180 CCGAGGTCCGCGTGGAGACCGAGCAT 207
Db 762828 TCGAGGTCCGCGTGGAAACCGAGCAT 762855

RESULT 4

US-09-103-840A-1

; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1

; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37RV
US-09-103-840A-1

Query Match 74.6%; Score 154.4; DB 3; Length 4411529;

Best Local Similarity 87.0%; Pred. No. 5.7e-33;
Matches 161; Conservative 0; Mismatches 26; Indels 1; Gaps 1;

QY 1 TCAAGGAGAACGCTAGCACTGG-TCCGGTCGGCGGTTACAAAGGTCAACAAAAGCTCG 59
Db TCAAGGAGAACGCTAGCACTGGCGCGGTCGGTTCGCTATTAAGGTCAACAAAAGCTCG 760747
QY 60 GTCGTGAAGTCGGGACCGATCAACAGTTGAGCGCTGACGAGAGGATGTCGCGCA 119
Db GGTTCGATGTCGGGACCGATCAACAGTTGAGCGCTGACGAGAGGATGTCGCGCA 760807
QY 120 CCATCGAGTACCTGGTTCGGCTGCAGAGGCGCACAGCATGACCGTTCGCGGCGCA 179
Db CCATCGAGTACCTGGTTCGGCTGCAGAGGCGCACAGCATGACCGTTCGCGGCGCA 760808
QY 180 CCGAGGTCGGGTCGGGACCGAGCAT 207
Db TCGAGGTCGGGTCGGGACCGAGCAT 760895

RESULT 5

US-08-313-185-57
; Sequence 57, Application US/08313185
; Patent No. 5851763
; GENERAL INFORMATION:
; APPLICANT: Heym, Beate
; APPLICANT: Cole, Stewart
; APPLICANT: Young, Douglas
; APPLICANT: Zhang, Ying
; APPLICANT: Honore, Nadine
; APPLICANT: Telenti, Amelio
; APPLICANT: Bodmer, Thomas
; TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
; TITLE OF INVENTION: in Mycobacterium Tuberculosis
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/313,185
; FILING DATE: 12-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 02356.0068-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3447 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-313-185-57

Query Match 65.3%; Score 135.2; DB 2; Length 3447;
Best Local Similarity 81.2%; Pred. No. 3e-28;
Matches 169; Conservative 0; Mismatches 38; Indels 1; Gaps 1;

QY 1 TCAAGGAGAACGCTAGCACTGGTC-GGGTCGGCGGTTACAAAGGTCAACAAAAGCTCG 59

Db 809 TCAAGGAGAACGCTAGCACTGGCGCGGTTGCTGTACAGGTCAACAAAAGCTCG 868
QY 60 GTCGTGAAGTCGGGACCGATCAACAGTTGAGCGCTGACGAGAGGATGTCGCGCA 119
Db GGTTCGATGTCGGGACCGATCAACAGTTGAGCGCTGACGAGAGGATGTCGCGCA 928
QY 120 CCATCGAGTACCTGGTTCGGCTGCAGAGGCGCACAGCATGACCGTTCGCGGCGCA 179
Db CCATCGAGTACCTGGTTCGGCTGCAGAGGCGCACAGCATGACCGTTCGCGGCGCA 928
QY 180 CCGAGGTCGGGTCGGGACCGAGCAT 207
Db TAGAGTCCAGTGGAACTGACGATAT 1016

RESULT 6

US-09-082-614A-57
; Sequence 57, Application US/09082614A
; Patent No. 6124098
; GENERAL INFORMATION:
; APPLICANT: Heym, Beate
; APPLICANT: Cole, Stewart
; APPLICANT: Young, Douglas
; APPLICANT: Zhang, Ying
; APPLICANT: Honore, Nadine
; APPLICANT: Telenti, Amelio
; APPLICANT: Bodmer, Thomas
; TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
; TITLE OF INVENTION: in Mycobacterium Tuberculosis
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/082,614A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/313,185
; FILING DATE: 12-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 02356.0068-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3447 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-082-614A-57

Query Match 65.3%; Score 135.2; DB 3; Length 3447;
Best Local Similarity 81.2%; Pred. No. 3e-28;
Matches 169; Conservative 0; Mismatches 38; Indels 1; Gaps 1;

QY 1 TCAAGGAGAACGCTAGCACTGGTC-GGGTCGGCGGTTACAAAGGTCAACAAAAGCTCG 59

```

; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-8512

Query Match      18.5%; Score 38.2; DB 4; Length 1731;
Best Local Similarity 51.5%; Pred. No. 0.087;
Matches 88; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

QY 34 CGGTTACAAGGTCACAAAAAGTCGGTCTGAACGTCGGCGAGCCGATCACACAGTTCGAC 93
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 114 CCGCCATCAGGACGACGATGGCCCTCGCGACGACGAGTGGCCATTGCGTCCAGGSGTCTGCA 173
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 94 GCTGACCGAGAGGAGTGCCTCGCCACCATCCAGTACCTGCTTGGCGTGCACGAGGCGCA 153
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 174 GTGTGTTCTATGAGCACTCTAGTTCGCGCGCTTCTATGGCGGTTGCGCCAGATCGCCA 233
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 154 GACCAAGATGACCGTTTCCCGCGGCGACCGAGGTGCGGTTGGAGACGACGCA 204
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 234 GCTCTCCAGGCCATCGCAGGCGCACTCTGTTCTGTTGAGACGCGACA 284
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 9
US-09-079-955-10
; Sequence 10, Application US/09079955A
; Patent No. 6465209
; GENERAL INFORMATION:
; APPLICANT: Alexander Blinkovsky
; APPLICANT: Kimberly Brown
; APPLICANT: Elizabeth Golightly
; APPLICANT: Tony Byun
; APPLICANT: Thomas Mathiasen
; APPLICANT: Lene V. Kofod
; APPLICANT: Mikio Fujii
; APPLICANT: Chigusa Shizuoka
; TITLE OF INVENTION: Methods For Producing Protein
; TITLE OF INVENTION: Hydrolysates
; FILE REFERENCE: 5253.500-US
; CURRENT APPLICATION NUMBER: US/09/079,955A
; CURRENT FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Fast-SEQ for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 1926
; TYPE: DNA
; ORGANISM: Sphingomonas capsulata
US-09-079-955-10

Query Match      18.0%; Score 37.2; DB 4; Length 1926;
Best Local Similarity 54.3%; Pred. No. 0.17;
Matches 75; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 67 CGTCCGCGAGCCGATCACCACTTCGAGCTGACCGAAGAGATGTCGTCGCCACCATCGA 126
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1179 CGCCGCAAGCCCAAGCCCTATTCTCGCTAACCGGTAACGAGGACTATTACACCGAAGG 1238
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 127 GTACTCGGTTGCGCTGTCACGAGGCGCACCAAGATGACCGGTTCCCGCGCGCACCGAGGT 186
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1239 CGCGCTGGTGTGCTGCGAAGCGGACAGATCATCCGCGATGSCACCGCGGCGCAAGAGGG 1298
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 187 GCGGTGGAGACCGACGA 204
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1299 CCTGGATGATTCGCGCAA 1316
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 10
US-09-192-104-1
; Sequence 1, Application US/09192104B
; Patent No. 6184020
; GENERAL INFORMATION:
; APPLICANT: Alexander Blinkovsky
; APPLICANT: Tony Byun
; APPLICANT: Alan V. Klotz
; APPLICANT: Alan Sloma
; APPLICANT: Maria Tang

```



```

Query Match      18.0%; Score 37.2; DB 4; Length 3000;
Best Local Similarity 54.3%; Pred. Nismat.0.18;
Matches 75; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY      67  CGTCGGCGACCGATCACCGATTGACGCTGACCGAGAGGATGCTCGCCACCATCGA 126
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      1848  CGCCCGCAAGCCCAAGCCCTATTCTCGTCTACCCGTAACGAGGACTATTACACCGAAGG 1907
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY      127  GTACCTGTCGGCTGCACGAGGCGACACCGATGACCGTTCGCCGGCGCACCGAGGT 186
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      1908  CGCCTGTGCTGCTGGAAGCGGACCATCATCCCGGATGCGACCGCGGCGCAGAGGG 1967
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY      187  GCGGTGGAGACGACGA 204
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      1968  CTTGGATGATTCGCCAA 1985
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 12
US-09-252-991A-8177
; Sequence 8177, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONA
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 8177
; LENGTH: 537
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-8177

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Query Match      17.7%; Score 36.6; DB 4; Length 537;
Best Local Similarity 54.0%; Pred. No. 0.2;
Matches 75; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY      69  TCGCGGAGCGGATCACACAGTTCGAGCGTGACCGAAGAGGATGTCGTCCGCCACCATGAGT 128
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      107  TCGCGGTCCAGGCGGACAGCGCGGAACTGGACGACAGCAGGCGGCTCGCGTCTACGCGG 166
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY      129  ACCCTGGTTCGGCTGCACGAGGCGCAGACCGACGATGACCGTTCCTCCGCGCGCACCCGAGGTGC 188
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      167  GCGAGCTGCTGGTGACCCAGGCGACGACCAAGCTGACCGGCAACACCTGACCCCTGAAGC 226
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY      189  CGGTGGAGACCGAGACAT 207
      || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      227  AGGACAAGAACGGCGACAT 245
      || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 13
US-09-252-991A-8289
; Sequence 8289, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONA
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; SEQUENCE ID NOS: 33142
; SEQ ID NO 8289

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OM nucleic - nucleic search, using sw model

Run on: September 17, 2003, 11:54:34 ; Search time 107.739 Seconds
(without alignments)
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Gapop 10.0 , Gapext 1.0

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:
15: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:
16: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:
17: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	154.4	74.6	3519	10	US-09-712-363-30
2	77.6	37.5	3495	10	US-09-738-626-547
3	77.6	37.5	5096	10	US-09-984-711-5
4	77.6	37.5	5099	10	US-09-887-052-1
5	77.6	37.5	5099	10	US-09-887-052-3
6	77.6	37.5	5099	10	US-09-887-052-5
7	77.6	37.5	5099	12	US-10-076-406-1
8	77.6	37.5	5099	12	US-10-076-406-3
9	77.6	37.5	5099	12	US-10-076-406-5
10	77.6	37.5	5099	13	US-10-075-460-5
11	77.6	37.5	3309400	10	US-09-738-626-1
12	71.6	34.6	3543	14	US-10-156-761-4898
13	71.6	34.6	9025608	14	US-10-156-761-1
14	39.2	18.9	1317	14	US-10-028-245-4
15	39.2	18.9	1826	14	US-10-028-245-1
16	37.6	18.2	1458	14	US-10-156-761-4634

Sequence 2879, Ap
Sequence 15102, A
Sequence 2811, Ap
Sequence 1, Appli
Sequence 2883, Ap
Sequence 15102, A
Sequence 1, Appli
Sequence 1459, Ap
Sequence 4015, Ap
Sequence 2885, Ap
Sequence 2136, Ap
Sequence 2212, Ap
Sequence 4136, Ap
Sequence 2845, Ap
Sequence 7920, Ap
Sequence 3987, Ap
Sequence 6238, Ap
Sequence 3212, Ap
Sequence 2223, Ap
Sequence 114750,
Sequence 2959, Ap
Sequence 59, Appli
Sequence 1, Appli
Sequence 1984, Ap
Sequence 3873, Ap
Sequence 5121, Ap
Sequence 2515, Ap
Sequence 1, Appli
Sequence 5299, Ap

ALIGNMENTS

RESULT 1
US-09-712-363-30
; Sequence 30, Application US/09712363
; Patent No. US20020164588A1
; GENERAL INFORMATION:
; APPLICANT: Eisenberg, David
; APPLICANT: Rotstein, Sergio H.
; APPLICANT: Marcotte, Edward M.
; TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND
; FILE REFERENCE: 07419-032001
; CURRENT APPLICATION NUMBER: US/09/712,363
; CURRENT FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: PCT/US00/02246
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,531
; PRIOR FILING DATE: 2000-02-01
; PRIOR APPLICATION NUMBER: 60/117,844
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/118,206,
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: 60/126,593
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/134,093
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/134,092
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/165,124
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/165,086
; PRIOR FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 3519
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-09-712-363-30

```

RESULT 3
US-09-984-711-5
; Sequence 5, Application US/09984711
; Patent No. US20020119549A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: STEPHAN, Hans
; APPLICANT: KREUTZER, Caroline
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE rpsL GENE
; FILE REFERENCE: 204209US0
; CURRENT APPLICATION NUMBER: US/09/984,711
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: DE10108230.9
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 5096
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
; OTHER INFORMATION:
US-09-984-711-5

Query Match          37.5%; Score 77.6; DB 10; Length 5096;
Best Local Similarity 68.5%; Pred. No. 5.4e-15;
Matches 137; Conservative 0; Mismatches 59; Indels 4; Gaps 2;

QY      9  AAGCGCTACGACTGG-TCGCGTCGCGCGGTACAGGTCACAAAAAGCTCGGTCTGAC 67
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db      1578 AAGCGCTACGACTGGCTCGCGTTGTCGTTACAGATCAACCGCAAGCTCGGCGCTT--- 1634
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
QY      68  GTCGGCGAGCGGATCACCAGTTGACGCTGACCGAAGAGGATGTCGTGCCACCATCGAG 127
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db      1635 GGTGGCGACCAAGATGCTTTGATGACTCTTACTGAGAGGACATCGCAACCATCGAG 1694
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
QY      128 TACCTGTTGGCTGCACGAGGGCCAGACACGATGACCGTTCCCGGGCGACCGAGGTG 187
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db      1695 TACCTGTTGGCTGCACGCGAGTGTAGCGCGTCATGACTTCTCCAAATGGTGAAGAGATC 1754
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
QY      188 CCGTGGAGACGACGACAT 207
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db      1755 CAGTCGAGACGATGACAT 1774
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||

RESULT 4
US-09-887-052-1
; Sequence 1, Application US/09887052
; Patent No. US20020119537A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE rpoB GENE
; FILE REFERENCE: 204212US0X
; CURRENT APPLICATION NUMBER: US/09/887,052
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: DE10107229.5
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 5099

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; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
; OTHER INFORMATION:
US-10-076-406-1

Query Match 37.5%; Score 77.6; DB 12; Length 5099;
Best Local Similarity 68.5%; Pred. No. 5.4e-15;
Matches 137; Conservative 0; Mismatches 59; Indels 4; Gaps 2;

QY 9 AAGCGCTACGACCTGG-TCCGTCGCGCGCTTACAGGTCAACAAAAGTCTCGTCTGAAC 67
|||||
Db 1578 AAGCGCTACGACCTGGTGGCTGCTTACAGGTCAACAAAAGTCTCGTCTGAAC 1634
|||||
QY 68 GTCGGGAGCCGATCACCAGTTCGACGTCGACCGAGAGGATGTCGTCGCCACCATCGAG 127
|||||
Db 1635 GTCGGGAGCCGATCACCAGTTCGACGTCGACCGAGAGGATGTCGTCGCCACCATCGAG 1694
|||||
QY 128 TACCTGGTTCGCTGACGAGGCGCCAGACCGATGACCGTTCGCGCGCACCGAGGTG 187
|||||
Db 1695 TACCTGGTTCGCTGACGAGGCGCCAGACCGATGACCGTTCGCGCGCACCGAGGTG 1754
|||||
QY 188 CCGGTGGAGACCGAGCAT 207
|||
Db 1755 CCAGTCGAGACCGATGACAT 1774

RESULT 8

US-10-076-406-3

; Sequence 3, Application US/10076406
; Publication No. US20030166884A1

; GENERAL INFORMATION:

; APPLICANT: MOECKEL, Bettina

; APPLICANT: BATHE, Brigitte

; APPLICANT: HERMANN, Thomas

; APPLICANT: PFEFFERLE, Walter

; APPLICANT: BINDER, Michael

; TITLE OF INVENTION: Nucleotide sequences coding for the rpoB gene

; FILE REFERENCE: 219774USOXIP

; CURRENT APPLICATION NUMBER: US/10/076,406

; PRIOR FILING DATE: 2002-02-19

; PRIOR FILING DATE: 2001-02-16

; PRIOR APPLICATION NUMBER: US 09/887052

; PRIOR FILING DATE: 2001-06-25

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 3

; LENGTH: 5099

; TYPE: DNA

; ORGANISM: Corynebacterium glutamicum

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (702)..(4196)

; OTHER INFORMATION:

; NAME/KEY: mutation

; LOCATION: (1987)..(1987)

; OTHER INFORMATION: Substitution of adenine by thymine

; NAME/KEY: mutation

; LOCATION: (1288)..(1288)

; OTHER INFORMATION: Substitution of cytosine by thymine

; NAME/KEY: mutation

; LOCATION: (715)..(715)

; OTHER INFORMATION: Substitution of cytosine by thymine

; US-10-076-406-3

Query Match 37.5%; Score 77.6; DB 12; Length 5099;
Best Local Similarity 68.5%; Pred. No. 5.4e-15;
Matches 137; Conservative 0; Mismatches 59; Indels 4; Gaps 2;

QY 9 AAGCGCTACGACCTGG-TCCGTCGCGCGCTTACAGGTCAACAAAAGTCTCGTCTGAAC 67

Db 1578 AAGCGCTACGACCTGGTGGCTGCTTACAGGTCAACCCCAGCTCGGCCTT--- 1634
|||||
QY 68 GTCGGGAGCCGATCACCAGTTCGACGTCGACCGAGAGGATGTCGTCGCCACCATCGAG 127
|||||
Db 1635 GTCGGGAGCCGATCACCAGTTCGACGTCGACCGAGAGGATGTCGTCGCCACCATCGAG 1694
|||||
QY 128 TACCTGGTTCGCTGACGAGGCGCCAGACCGATGACCGTTCGCGCGCACCGAGGTG 187
|||||
Db 1695 TACCTGGTTCGCTGACGAGGCGCCAGACCGATGACCGTTCGCGCGCACCGAGGTG 1754
|||||
QY 188 CCGGTGGAGACCGAGCAT 207
|||
Db 1755 CCAGTCGAGACCGATGACAT 1774

RESULT 9

US-10-076-406-5

; Sequence 5, Application US/10076406

; Publication No. US20030166884A1

; GENERAL INFORMATION:

; APPLICANT: MOECKEL, Bettina

; APPLICANT: BATHE, Brigitte

; APPLICANT: HERMANN, Thomas

; APPLICANT: PFEFFERLE, Walter

; APPLICANT: BINDER, Michael

; TITLE OF INVENTION: Nucleotide sequences coding for the rpoB gene

; FILE REFERENCE: 219774USOXIP

; CURRENT APPLICATION NUMBER: US/10/076,406

; PRIOR FILING DATE: 2002-02-19

; PRIOR FILING DATE: 2001-02-16

; PRIOR APPLICATION NUMBER: US 09/887052

; PRIOR FILING DATE: 2001-06-25

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 5

; LENGTH: 5099

; TYPE: DNA

; ORGANISM: Corynebacterium glutamicum

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (702)..(4196)

; OTHER INFORMATION:

; NAME/KEY: mutation

; LOCATION: (2016)..(2016)

; OTHER INFORMATION: Substitution of cytosine by thymine

; US-10-076-406-5

Query Match 37.5%; Score 77.6; DB 12; Length 5099;
Best Local Similarity 68.5%; Pred. No. 5.4e-15;
Matches 137; Conservative 0; Mismatches 59; Indels 4; Gaps 2;

QY 9 AAGCGCTACGACCTGG-TCCGTCGCGCGCTTACAGGTCAACAAAAGTCTCGTCTGAAC 67
|||||
Db 1578 AAGCGCTACGACCTGGTGGCTGCTTACAGGTCAACCCCAGCTCGGCCTT--- 1634
|||||
QY 68 GTCGGGAGCCGATCACCAGTTCGACGTCGACCGAGAGGATGTCGTCGCCACCATCGAG 127
|||||
Db 1635 GTCGGGAGCCGATCACCAGTTCGACGTCGACCGAGAGGATGTCGTCGCCACCATCGAG 1694
|||||
QY 128 TACCTGGTTCGCTGACGAGGCGCCAGACCGATGACCGTTCGCGCGCACCGAGGTG 187
|||||
Db 1695 TACCTGGTTCGCTGACGAGGCGCCAGACCGATGACCGTTCGCGCGCACCGAGGTG 1754
|||||
QY 188 CCGGTGGAGACCGAGCAT 207
|||
Db 1755 CCAGTCGAGACCGATGACAT 1774

RESULT 10

US-10-075-460-5

; Sequence 5, Application US/10075460

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; Publication No. US2002015557A1
; GENERAL INFORMATION:
; APPLICANT: MOCKEL, BETTINA
; APPLICANT: BATHE, BRIGITTE
; APPLICANT: HANS, STEFAN
; APPLICANT: KREUTZER, CAROLINE
; APPLICANT: HERMANN, THOMAS
; APPLICANT: PEPPERLE, WALTER
; APPLICANT: BINDER, MICHAEL
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE rpsL GENE
; FILE REFERENCE: 2184720USX
; CURRENT APPLICATION NUMBER: US/10/075,460
; CURRENT FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: DE 10107230.9
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: DE 10162386.0
; PRIOR FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 5099
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
; OTHER INFORMATION:
US-10-075-460-5

Query Match      37.5%; Score 77.6; DB 13; Length 5099;
Best Local Similarity 68.5%; Pred. No. 5.4e-15;
Matches 137; Conservative 0; Mismatches 59; Indels 4; Gaps 2;

QY 9 AAGCGTAGACCTGG-TCGCGTCGCCGCTTACAGGTCACAAAAAGCTCGGTCTGAC 67
DB 1578 AAGCGTAGACCTGGCTCGGCTTACAGGTCACAAAAAGCTCGGTCTGAC 1634
QY 68 GTGCGGAGCGGATCACCGAGTTCGACGCTCACGAGAGGATGTCGTCGCCACCATCGAG 127
DB 1635 GTGCGGAGCGGATGTTGATGACTCTTACTGAGAGGACATCGCAACCATCGAG 1694
QY 128 TACCTGGTTCGCTCGACGAGGCGCACACGATGACGCTTCCCGGCGGACCGAGGTG 187
DB 1695 TACCTGGTTCGCTCGACGAGGTCGCGGCTCATGACTTCTCCAAATGGTGAAGAGATC 1754
QY 188 CCGGTGGAGACCGAGACAT 207
DB 1755 CCACTCGAGACCGATGACAT 1774

RESULT 11
US-09-738-626-1
; Sequence 1, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIALI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAORO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
```

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; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 1
; LENGTH: 3309400
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-1

Query Match      37.5%; Score 77.6; DB 10; Length 3309400;
Best Local Similarity 68.5%; Pred. No. 1.1e-14;
Matches 137; Conservative 0; Mismatches 59; Indels 4; Gaps 2;

QY 9 AAGCGTAGACCTGG-TCGCGTCGCCGCTTACAGGTCACAAAAAGCTCGGTCTGAC 67
DB 513789 AAGCGTAGACCTGGCTCGGCTTACAGGTCACAAAAAGCTCGGTCTGAC 513845
QY 68 GTGCGGAGCGGATCACCGAGTTCGACGCTCACGAGAGGATGTCGTCGCCACCATCGAG 127
DB 513846 GTGCGGAGCGGATGTTGATGACTCTTACTGAGAGGACATCGCAACCATCGAG 513905
QY 128 TACCTGGTTCGCTCGACGAGGCGCACACGATGACGCTTCCCGGCGGACCGAGGTG 187
DB 513906 TACCTGGTTCGCTCGACGAGGTCGCGGCTCATGACTTCTCCAAATGGTGAAGAGATC 513965
QY 188 CCGGTGGAGACCGAGACAT 207
DB 513966 CCACTCGAGACCGATGACAT 513985

RESULT 12
US-10-156-761-4898
; Sequence 4898, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 4898
; LENGTH: 3543
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3543)
US-10-156-761-4898

Query Match      34.6%; Score 71.6; DB 14; Length 3543;
Best Local Similarity 65.9%; Pred. No. 4.1e-13;
Matches 137; Conservative 0; Mismatches 64; Indels 7; Gaps 2;

QY 1 TCAGGAGAGAGCGCTACGACCT-GTCTCGCTCGCGCTTACAGGTCAACAAAAAGCTCG 59
DB 926 TCACCGGAGAGCGCTACGACCTCGCGGAGGTTCGCGGCTTACAGGTCAACAAAAAGCTCG 985
QY 60 GTCTGACGTCGCGGAGCGGATCACCAGTTCACCGTTCACCGAGAGAGGATGTCGTGCA 119
DB 986 G-----CGCGAGGCGCGCTGACCGCGGATCTCTGACCGAGGACATCTCTCT 1039
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 17, 2003, 11:54:34 ; Search time 32.2819 Seconds
(without alignments)
3049.028 Million cell updates/sec

Title: US-09-697-123B-13

Perfect score: 223

Sequence: 1 tcaaggagaagcgctacgac.....ccggtgaaacgacgacat 223

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_NA.*

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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
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4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PCBUS_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	123.8	55.5	970	1	US-08-250-030-1
2	123.8	55.5	970	5	PCR-US95-06790-1
3	123.8	55.5	4403765	3	US-09-103-840A-2
4	123.8	55.5	4411529	3	US-09-103-840A-1
5	111	49.8	3447	2	US-08-313-185-57
6	111	49.8	3447	3	US-08-313-185-57
7	41.4	18.6	1119	4	US-09-082-614A-57
8	41.4	18.6	1239	4	US-09-252-991A-9448
9	41.2	18.5	3306	1	US-08-252-991A-9383
10	39.6	17.8	77536	4	US-08-261-206A-71
11	39	17.5	483	4	US-09-410-551B-1
12	38.8	17.4	491	1	US-08-133-711-36
13	38.2	17.1	2673	4	US-09-252-991A-2993
14	38.2	17.1	2715	4	US-09-252-991A-2686
15	38.2	17.1	2814	4	US-09-252-991A-2875
16	38	17.0	462	4	US-09-252-991A-3347
17	38	17.0	1818	4	US-09-252-991A-3290
18	38	17.0	2115	4	US-09-252-991A-3388
19	37.6	16.9	4403765	3	US-09-103-840A-2
20	37.6	16.9	4411529	3	US-09-103-840A-1
21	37.4	16.8	1326	4	US-09-252-991A-10931
22	37.4	16.8	2211	4	US-09-252-991A-11256
23	37.4	16.8	2289	4	US-09-252-991A-10995
24	37.2	16.7	1089	4	US-09-252-991A-1923
25	37.2	16.7	2295	4	US-09-252-991A-2036
26	37.2	16.7	3231	1	US-08-074-121-4
27	37.2	16.7	3231	5	PCR-US94-06447-4

c	28	37	16.6	528	4	US-09-252-991A-3140	Sequence 3140, Ap
c	29	37	16.6	912	4	US-09-252-991A-3042	Sequence 3042, Ap
c	30	37	16.6	936	4	US-09-252-991A-2918	Sequence 2918, Ap
	31	37	16.6	1482	4	US-09-252-991A-2824	Sequence 2824, Ap
	32	36.8	16.5	1014	4	US-09-252-991A-2663	Sequence 2663, Ap
	33	36.8	16.5	1155	4	US-09-252-991A-2762	Sequence 2762, Ap
c	34	36.8	16.5	1233	4	US-09-252-991A-3203	Sequence 3203, Ap
	35	36.6	16.4	734	4	US-09-221-017B-1070	Sequence 1070, Ap
	36	36.6	16.4	765	3	US-08-718-904-79	Sequence 79, Appl
	37	36.6	16.4	765	4	US-09-449-249-79	Sequence 79, Appl
c	38	36.6	16.4	1458	4	US-09-252-991A-8297	Sequence 8297, Ap
	39	36.6	16.4	1899	4	US-09-252-991A-8019	Sequence 8019, Ap
c	40	36.4	16.3	2208	4	US-09-252-991A-13998	Sequence 13998, A
	41	36.4	16.3	2439	4	US-09-252-991A-14139	Sequence 14139, A
	42	36.4	16.3	2994	4	US-09-252-991A-14228	Sequence 14228, A
	43	36.2	16.2	1272	2	US-08-972-258-1	Sequence 1, Appl
	44	36.2	16.2	1272	3	US-09-263-128-1	Sequence 1, Appl
	45	36.2	16.2	1395	4	US-09-252-991A-16537	Sequence 16537, A

ALIGNMENTS.

RESULT 1

US-08-250-030-1

; Sequence 1, Application US/08250030

; Patent No. 5643723

; GENERAL INFORMATION:

; APPLICANT: Persing, David H.

; TITLE OF INVENTION: Detection of a Genetic Locus Encoding

; TITLE OF INVENTION: Resistance to Rifampin in Mycobacterial Cultures and in

; NUMBER OF SEQUENCES: 15

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Schwegman, Lundberg & Woessner

; STREET: 3500 IDS Center

; CITY: Minneapolis

; STATE: MN

; COUNTRY: USA

; ZIP: 55402

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/250,030

; FILING DATE: 26-MAY-1994

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Mueiting, Ann M.

; REGISTRATION NUMBER: 33,977

; REFERENCE/DOCKET NUMBER: 150.105US1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 612-339-0331

; TELEFAX: 612-339-3061

; INFORMATION FOR SEQ ID NO: 1:

; LENGTH: 970 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA

US-08-250-030-1

Query Match 55.5%; Score 123.8; DB 1; Length 970;
Best Local Similarity 76.7%; Pred. No. 1.9e+22;
Matches 171; Conservative 0; Mismatches 37; Indels 15; Gaps 1;

QY 1 TCAAGGAGAGCGCTAGCCTGGCCCGCGTGGCCCGCTACAGGTCACAAAGACTGG 60

Db 26 TCAAGGAGAGCGCTAGCCTGGCCCGCGTGGCCCGCTACAGGTCACAAAGACTCG 85


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Best Local Similarity 76.7%; Pred. No. 5.9e-22;
Matches 171; Conservative 0; Mismatches 37; Indels 15; Gaps 1;

QY 1 TCAAGGAGAGCGCTACGACCTGGCCCGCGCTCGCGCGCTACAAGGTCAACAAGAAGCTGG 60
Db 760698 TCAAGGAGAGCGCTACGACCTGGCCCGCGCTCGCGCTATTAAGTCAACAAGAAGCTGG 760747
QY 61 GCCTGACACCGCATCCGATCAACACACCGAGCGTGCACGAGAGACGCTGTCGCCCA 120
Db 760748 GCGTGCATGTGCGGAGCCCATCACGCTGCTGACGCTGACCGAAGAGACGCTGTCGCCCA 760807
QY 121 CCATCGAGTACCTGGTTCGCTGCATGACACACGCTCTCTCAGGTGGCCAGGCCGCCGTTATGA 180
Db 760808 CCATCGAATATCTGTCGCTGTCACGAGG-----GTCAGACCACGATGA 760852
QY 181 CTGTCCCCCGCGGGTCGAGGTGCGCGGTGGGAACCGACGACAT 223
Db 760853 CCGTTCGCGGCGGCTGAGGTGCGCGGTGGAAACCGACGACAT 760895

RESULT 5
US-08-313-185-57
; Sequence 57, Application US/08313185
; Patent No. 5851763
; GENERAL INFORMATION:
; APPLICANT: Heym, Beate
; APPLICANT: Cole, Stewart
; APPLICANT: Young, Douglas
; APPLICANT: Zhang, Ying
; APPLICANT: Honore, Nadine
; APPLICANT: Telenti, Amalio
; APPLICANT: Bodmer, Thomas
; TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
; TITLE OF INVENTION: in Mycobacterium Tuberculosis
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/313.185
; FILING DATE: 12-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/POCKET NUMBER: 02356.0068-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3447 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-313-185-57

Query Match 49.8%; Score 111; DB 2; Length 3447;
Best Local Similarity 73.1%; Pred. No. 3.4e-19;
Matches 163; Conservative 0; Mismatches 45; Indels 15; Gaps 1;

QY 1 TCAAGGAGAGCGCTACGACCTGGCCCGCGCTCGCGCGCTACAAGGTCAACAAGAAGCTGG 60

```



```
;
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Acromonium chrysogenum
; FEATURE:
; NAME/KEY:
; LOCATION: 1..3306
; OTHER INFORMATION: /label= PKG_gene
; OTHER INFORMATION: /note= "Nucleotide sequence of region A in Figure
; OTHER INFORMATION: 59. The sequence is presented as Figure 61."
; FEATURE:
; NAME/KEY: exon
; LOCATION: 1252..1317
; FEATURE:
; NAME/KEY: exon
; LOCATION: 1463..1883
; FEATURE:
; NAME/KEY: exon
; LOCATION: 1948..2715
; FEATURE:
; NAME/KEY: CDS
; LOCATION: Join(1252..1317, 1463..1883, 1948..2714)
US-08-261-206A-71
```

```
Query Match 18.5%; Score 41.2; DB 1; Length 3306;
Best Local Similarity 49.1%; Pred. No. 0.085;
Matches 109; Conservative 0; Mismatches 113; Indels 0; Gaps 0;

QY 1 TCAGGAGAGCGCTACGACTGCGCGCGCGGTACAGGTCAACAGAGAGCTGG 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1455 TCAGGAGAGCTGACTTCAACTGCGCGCGCGGTACAGGTCAACAGAGAGCTGG 1514

QY 61 GCCTGAACACCGATCATCGATCACCACACGCGCTGACCGAGAGAGCTGGTGC 120
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1515 GCATGTCGTCCTCCACCATGATGACGCGCTGACATGCGCGCAAGCGGTCA 1574

QY 121 CCATCGAGTACCTGTTGCGTGCACACGCGCTCTCAGGTGGCGGCCCGCTTATGA 180
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1575 TCCTCATGTCCACCTTGGCGCGCGCGCAACGCGCACCCCAAGTATCTCGTCAGC 1634

QY 181 CTGTCCCGCGGGTGCAGTGCCTGAGTGGGAGAACCGAGACA 222
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1635 CCGTGTCCCGGAGCTGAGAGAGTGTCTGGCAAGAGGTCA 1676
```

```
RESULT 10
US-09-410-551B-1/c
; Sequence 1, Application US/09410551B
; Patent No. 6503737
; GENERAL INFORMATION:
; APPLICANT: KOSAN BIOSCIENCES, INC.
; APPLICANT: REEVES, CHRISTOPHER
; APPLICANT: CHU, DANIEL
; APPLICANT: KHOSLA, CHAITAN
; APPLICANT: SANTI, DANIEL
; APPLICANT: WU, KAI
; TITLE OF INVENTION: POLYPEPTIDE SYNTHASE ENZYMES AND RECOMBINANT DNA
; TITLE OF INVENTION: CONSTRUCTS THEREFOR
; FILE REFERENCE: 30062-20026.00
; CURRENT APPLICATION NUMBER: US/09/410,551B
; CURRENT FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: US 60/139,650
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: US 60/123,810
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 60/102,748
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 77536
; TYPE: DNA
; ORGANISM: Streptomyces hygroscopicus
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (52275)....(71465)
US-09-410-551B-1

Query Match 17.8%; Score 39.6; DB 4; Length 77536;
Best Local Similarity 53.2%; Pred. No. 0.33;
Matches 84; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

QY 2 CAAGGAGAGCGCTACGACTGCGCGCGGTGCGCGGTACAGGTCAACAGAGAGCTGG 61
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 24392 CAAGGAGAGCGGACAGAGTGTCTGCGCGGTGCGCGGTGCGCGGTGCGCGGTG 24333

QY 62 CCGTGAACCGGATCATCGATCACCACCGAGCGTACCGAGAGAGAGAGCTGCGCCAC 121
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 24332 CCACCCGACGCGCGCGGTGCGCGGTGCGCGGTGCGCGGTGCGCGGTGCGCGGT 24273

QY 122 CATCGAGTACCTGTTGCGCTGCACACGCGCTCTCAGG 159
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 24272 GCTCACCGGCTGCGCGGTGCGCGGTGCGCGGTGCGCGGTGCGCGGTGCGCGGT 24235

RESULT 11
US-09-252-991A-12631
; Sequence 12631, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 12631
; LENGTH: 483
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-12631
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Query Match 17.5%; Score 39; DB 4; Length 483;
Best Local Similarity 49.3%; Pred. No. 0.23;
Matches 102; Conservative 0; Mismatches 105; Indels 0; Gaps 0;

QY 1 TCAGGAGAGCGCTACGACTGCGCGGTGCGCGGTGCGCGGTGCGCGGTGCGCGGTG 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 98 TCCTACTGAAACCCACAACTTCCACTGGAAGTACACGCGCGCGGTGCGCGGTGCG 157

QY 61 GCCTGAACCGGATCATCGATCACCACGAGCGTACCGAGAGAGAGAGCTGCGCGCA 120
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 158 ACCTGATGTTGGAAGCGGACGATACACGAGTGGCGGTGCGGTGCGGTGCGGTGCG 217

QY 121 CCATCGAGTACCTGTTGCGCTGCACACGCGCTCTCAGGTGCGCGGTGCGCGGTG 180
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 218 GCATCGGCGCGCTGGGCTTCCCGCGCGCGGTGCGCGGTGCGCGGTGCGGTGCGT 277

QY 181 CTGTCCCGCGCGGTGCGAGTGCCTGG 207
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 278 CCATCAAGGAGGAGGAGGCGTTCCTGG 304

RESULT 12
US-08-133-711-36
; Sequence 36, Application US/08133711
; Patent No. 5525463
; GENERAL INFORMATION:
; APPLICANT: Zolig, Werner
; TITLE OF INVENTION: Methods and reagents for detection of
; TITLE OF INVENTION: pathogens using superoxide dismutase gene
```

```
; TITLE OF INVENTION: Targeting
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: NJ
; COUNTRY: U.S.A.
; ZIP: 07110-1199
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/133,711
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 92810780.4
; FILING DATE: 13-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Patricia S. Rocha
; REGISTRATION NUMBER: 31,054
; REFERENCE/DOCKET NUMBER: 4095/95
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201) 235 5000
; TELEFAX: (201) 235 3500
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORGANISM: Mycobacterium kansasii/SOD gene
; US-08-133-711-36

Query Match 17.4%; Score 38.8; DB 1; Length 491;
Best Local Similarity 48.6%; Pred. No. 0.26;
Matches 106; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

QY 1 TCACGAGAGAGCGGTACGACTCGGCCGCGTCCGCGCTACAAAGGTCAACAGAGAGCTGG 60
DB 100 TTCTGCTGACGAGAGAACTTGGCTTCAACCTCGCGCGCCAGCTCAACACACAGATCT 159
QY 61 GCTGTACACAGATCACTCGATCAACACAGAGAGCTGACGAGAGAGAGCTGCTCGCCA 120
DB 160 GTGAGAGAGACTTCTCCCAAGGAGCGGACAGCGAGCGGCACTCGCGCGGCCA 219
QY 121 CCATCGAGTACCTGGTTCGCTGCACACGCTCTCAGGGTGGCCAGGCCGCCGTTATGA 180
DB 220 TCGAGAGAGCGTTCGGGTCTTCGACAAAGTTTCGTGCCAATTCACAGCGCGCGGCCA 279
QY 181 CRTGCCCCGGGGGTGCGAGGTCCCGGTGGAAACCGAC 218
DB 280 CGGTGAGGGGTGCGGCTGGCGGCGCTGGGTGGGAC 317

RESULT 13
US-09-252-991A-2993/c
; Sequence 2993, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 482
; SEQ ID NO 2686
; LENGTH: 2715
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-2686

Query Match 17.1%; Score 38.2; DB 4; Length 2715;
Best Local Similarity 49.7%; Pred. No. 0.46;
Matches 97; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 26 CCGCGCTCGCGCGCTACAAAGGTCAACAGAGAGCTGGGCTGAACACCGATCATCCGATCAC 85
DB 423 CTGGCTCGCGCGCGCTACAAAGGTCAACAGAGAGCTGGGCTGAACACCGATCATCCGATCAC 482
QY 86 CACACAGAGCTGACCGAGAGAGAGAGCTGCTGCCACCATCGAGTACCTGTTCCGCTTCCA 145
DB 483 CAACGAGTTCGCGGAGCGTGTGCGAGTGTATGTCGCAACGAGGCGCTGTTCCGCGCGCA 542
QY 146 CCACGCTCTCAGGGTGGCCAGGCCCGCTTATGACTGTCCCGCGGGGTGAGGTGCC 205
DB 543 GTGAGCGGCGGAAACAGTGTATGCTTACCTGACCGGGTCCGCGCGGCTCAAGGTTC 602
QY 206 GGTGGAACCGGACCA 220
DB 603 GTGAGCGGCGGAAACAGTGTATGCTTACCTGACCGGGTCCGCGCGGCTCAAGGTTC 602
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; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 2993
; LENGTH: 2673
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-2993

Query Match 17.1%; Score 38.2; DB 4; Length 2673;
Best Local Similarity 49.7%; Pred. No. 0.46;
Matches 97; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 26 CCGCGCTCGCGCGCTACAAAGGTCAACAGAGAGCTGGGCTGAACACCGATCATCCGATCAC 85
DB 2362 CTGGCTCGCGCGCGCTGCGCAGCAGCAGAGGCGGAGATGCGCGGCCATCCGATCGC 2303
QY 86 CACACAGAGCTGACCGAGAGAGAGAGCTGCTGCCACCATCGAGTACCTGTTCCGCTTCCA 145
DB 2302 CAACGAGTTCGCGGAGCGTGTGCGAGTGTATGTCGCAACGAGGCGCTGTTCCGCGCGCA 2243
QY 146 CCACGCTCTCAGGGTGGCCAGGCCCGCTTATGACTGTCCCGCGGGGTGAGGTGCC 205
DB 2242 GGTGAGCGGCGGAAACAGTGTATGCTTACCTGACCGGGTCCGCGCGGCTCAAGGTTC 2183
QY 206 GGTGGAACCGGACCA 220
DB 2182 GTGAGCGGCGGAAACAGTGTATGCTTACCTGACCGGGTCCGCGCGGCTCAAGGTTC 2183

RESULT 14
US-09-252-991A-2686
; Sequence 2686, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 2686
; LENGTH: 2715
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-2686
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RESULT 15

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US-09-252-991A-2875
; Sequence 2875, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 2875
; LENGTH: 2814
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-2875

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Query Match	17.1%;	Score 38.2;	DB 4;	Length 2814;
Best Local Similarity	49.7%;	Pred. No. 0.47;		
Matches 97;	Conservative 0;	Mismatches 98;	Indels 0;	Gaps 0;
QY	26	CCGCGTCGGCGCGCTACAAGGTCAACAAGAGCTGGGCGCTGAACCGCATATCCGATCCAC	85	
Db	481	CTGGCTCGGCGCGACCTGGCCACGACGAGGCCGAGATCCCGCGCCATCGCATGCG	540	
QY	86	CACACAGAGCGCTGACCGAAGAGACGTCGTCGCCACCATCGAGTACCTGGTTGCGCTGCA	145	
Db	541	CAACGAGTCCGCGACGCGTGGTGCAGTGTATGTCGCGCAACGAGCGCGTGTTCGCGCGCGA	600	
QY	146	CCAGCGCTCTCFAGGGTGGCCAGCCGCCCGCTTATGACTGTCCCGCGGGGTGAGGTGCC	205	
Db	601	GGTGACGCGGACAGTTGATCGCGCTACCTCGACCGGTCCGCGCGGTCAAGGTTC	660	
QY	206	GGTGAACACCGACA	220	
Db	661	GGTGACCAACCGCGA	675	

Search completed: September 17, 2003, 12:29:21
Job time : 48.3319 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 17, 2003, 11:54:34 : Search time 116.066 Seconds
(without alignments)
4726.283 Million cell updates/sec

Title: US-09-697-123B-13

Perfect score: 223

Sequence: 1 tcgaagaagcgtacgac.....ccggtggaaccgacgacat 223

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1660708 seqs, 1229959015 residues

Total number of hits satisfying chosen parameters: 3321416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_NA:

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2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
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6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq.*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
15: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
16: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
17: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	123.8	55.5	3519	10	US-09-712-363-30
2	65.6	29.4	3543	14	US-10-156-761-4898
3	65.6	29.4	9025608	14	US-10-156-761-1
4	62.8	28.2	3495	10	US-09-738-626-547
5	62.8	28.2	5096	10	US-09-984-711-5
6	62.8	28.2	5099	10	US-09-887-052-1
7	62.8	28.2	5099	10	US-09-887-052-3
8	62.8	28.2	5099	10	US-09-887-052-5
9	62.8	28.2	5099	12	US-10-076-406-1
10	62.8	28.2	5099	12	US-10-076-406-3
11	62.8	28.2	5099	12	US-10-076-406-5
12	62.8	28.2	5099	13	US-10-075-460-5
13	62.8	28.2	3309400	10	US-09-738-626-1
14	42.4	19.0	704	13	US-10-062-254-109
15	42.4	19.0	752	13	US-10-062-254-111
16	41	18.4	278	9	US-09-294-093B-1392

17	41	18.4	1029	14	US-10-156-761-6689
18	41	18.4	2532	14	US-10-156-761-113
19	39.2	17.6	1941	14	US-10-156-761-2696
20	39	17.5	471	9	US-09-815-242-7717
21	39	17.5	3972	14	US-10-156-761-5427
22	38.8	17.4	393	14	US-10-077-381-1
23	38.8	17.4	393	14	US-10-077-381-1
24	38.6	17.3	1047	14	US-10-156-761-4357
25	38.6	17.3	1287	14	US-10-156-761-3515
26	38.6	17.3	1509	14	US-10-156-761-1992
27	38.6	17.3	9025568	14	US-10-156-761-1
28	38.4	17.2	1287	14	US-10-156-761-5314
29	38.2	17.1	1485	14	US-10-156-761-373
30	38.2	17.1	2610	12	US-10-246-330-1
31	38	17.0	175	9	US-09-923-876-5702
32	37.8	17.0	1629	14	US-10-156-761-3330
33	37.4	16.8	626	13	US-10-062-254-115
34	37.4	16.8	1449	14	US-10-156-761-6862
35	37.2	16.7	1044	14	US-10-156-761-566
36	37.2	16.7	1209	14	US-10-156-761-6008
37	37.2	16.7	1350	9	US-09-815-242-7965
38	37.2	16.7	1548	14	US-10-156-761-1248
39	37.2	16.7	63158	12	US-10-292-198-1
40	37	16.6	984	14	US-10-156-761-2093
41	37	16.6	1242	14	US-10-156-761-5818
42	37	16.6	2298	14	US-10-156-761-270
43	36.6	16.4	785	11	US-09-861-257-23
44	36.6	16.4	785	12	US-10-189-360-79
45	36.6	16.4	984	14	US-10-156-761-5986

ALIGNMENTS

RESULT 1

US-09-712-363-30
Sequence 30, Application US/09712363
Patent No. US20020164588A1
GENERAL INFORMATION:
APPLICANT: Eisenberg, David
APPLICANT: Rotstein, Sergio H.
APPLICANT: Marcotte, Edward M.
TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND
TITLE OF INVENTION: INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS
FILE REFERENCE: 07419-032001
CURRENT APPLICATION NUMBER: US/09/712,363
CURRENT FILING DATE: 2000-11-13
PRIOR APPLICATION NUMBER: PCT/US00/02246
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 60/179,531
PRIOR FILING DATE: 2000-02-01
PRIOR APPLICATION NUMBER: 60/117,844
PRIOR FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: 60/118,206,
PRIOR FILING DATE: 1999-02-01
PRIOR APPLICATION NUMBER: 60/126,593
PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: 60/134,093
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 60/134,092
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 60/165,124
PRIOR FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 60/165,086
PRIOR FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 292
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 30
LENGTH: 3519
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
US-09-712-363-30

Sequence 6689, Ap
Sequence 113, App
Sequence 2696, Ap
Sequence 7717, Ap
Sequence 5427, Ap
Sequence 1, Appli
Sequence 1, Appli
Sequence 4357, Ap
Sequence 3515, Ap
Sequence 1592, Ap
Sequence 1, Appli
Sequence 5314, Ap
Sequence 373, App
Sequence 1, Appli
Sequence 5702, Ap
Sequence 3330, Ap
Sequence 115, App
Sequence 6862, Ap
Sequence 566, App
Sequence 6008, Ap
Sequence 7965, Ap
Sequence 1248, Ap
Sequence 1, Appli
Sequence 2093, Ap
Sequence 5818, Ap
Sequence 270, App
Sequence 23, Appl
Sequence 79, Appl
Sequence 5986, Ap


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Query Match      55.5%; Score 123.8; DB 10; Length 3519;
Best Local Similarity 76.7%; Pred. No. 8.6e-27;
Matches 171; Conservative 0; Mismatches 37; Indels 15; Gaps 1;

QY 1 TCAAGAGAAGCGGTACAGCTGGCCCGGTCGGCGCTACAGGTCAACAAGAGCTGG 60
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DB 884 TCAAGAGAAGCGGTACAGCTGGCCCGGTCGGCGCTACAGGTCAACAAGAGCTGG 943
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 61 GCTGTACACCGGATCATCCGATCAACACGAGCTGACCGAAGAGAGCTGTCGCCA 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 944 GCTGTACGTCGGCGAGCCCATCATCGTCGTGACGCTGACCGAAGAGAGCTGTCGCCA 1003
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 121 CCATCGAGTACTGGTTCGCTGCACACCGCCCTCTCAGGTGGCCAGGCCCGCTATGA 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1004 CCATCGAATATCTGTCGCGCTTCACAGAGG-----GTCAGACCAAGATGA 1048
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 181 CTGTCCCGCGGGTGCAGGTCCCGGTGGAAACCGAGGACAT 223
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1049 CCGTTCGCGCGCGCTCGAGGTCCCGGTGGAAACCGAGGACAT 1091
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 2
US-10-156-761-4898
; Sequence 4898, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 4898
; LENGTH: 3543
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; NAME/KEY: CDS
; FEATURE:
; LOCATION: (1)..(3543)
US-10-156-761-4898

Query Match      29.4%; Score 65.6; DB 14; Length 3543;
Best Local Similarity 70.0%; Pred. No. 7.8e-10;
Matches 105; Conservative 0; Mismatches 39; Indels 6; Gaps 1;

QY 1 TCAAGAGAAGCGGTACAGCTGGCCCGGTCGGCGCTACAGGTCAACAAGAGCTGG 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 926 TCAACCGAAGCGGTACAGCTGGCGAAGTGGCGGCTACAGGTCAACAAGAGCTGG 985
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 61 GCTGTACACCGGATCATCCGATCAACACGAGCTGACCGAAGAGAGCTGTCGCCA 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 986 GCGG-----CGAGGCGCGCTGGACCGCGGATCCTGACCGTGGAGGACATCATCTCGT 1039
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 121 CCATCGAGTACTGGTTCGCTGCACACCG 150
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1040 CGATCAAGTACTGGTGAAGCTGCACGCG 1069
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 3
US-10-156-761-1
; Sequence 1, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
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; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
; LENGTH: 9025608
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1

Query Match      29.4%; Score 65.6; DB 14; Length 9025608;
Best Local Similarity 70.0%; Pred. No. 1.1e-09;
Matches 105; Conservative 0; Mismatches 39; Indels 6; Gaps 1;

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    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 5970494 TCAACCGAAGCGGTACAGCTGGCGAAGTGGCGGCTACAGGTCAACAAGAGCTGG 5970553
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 61 GCTGTACACCGGATCATCCGATCAACACGAGCTGACCGAAGAGAGCTGTCGCCA 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 5970554 GCGG-----CGAGGCGCGCTGGACCGCGGATCCTGACCGTGGAGGACATCATCTCGT 5970607
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 121 CCATCGAGTACTGGTTCGCTGCACACCG 150
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 5970608 CGATCAAGTACTGGTGAAGCTGCACGCG 5970637
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 4
US-09-738-626-547
; Sequence 547, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOL, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 547
; LENGTH: 3495
; TYPE: DNA
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; ORGANISM: Corynebacterium glutamicum
US-09-738-626-547

Query Match 28.2%; Score 62.8; DB 10; Length 3495;

Best Local Similarity 71.0%; Pred. No. 5.1e-09;

Matches 98; Conservative 0; Mismatches 37; Indels 3; Gaps 1;

QY 9 AAGCGCTAGCACTGGCGCGGCTGCGCGCTACAGGTCAACAAGAGCTGGCGCTGAAC 68

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 877 AAGCGCTAGCACTGGCTGCGGTTGCGTTACAGATCAACCGCAAGCTCGCGCTTGT 936

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 69 ACCGATCATCCGATCACCAACAGCAGCTGACCGAAGAGAGCTGCTGCCACCATCGAG 128

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 937 GCGACCAAGATGGTTGAT--GACTCTTACTGAGAGGACATCGCAACCATCGAG 993

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 129 TACCTGGTGGCTGCAC 146

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 994 TACCTGGTGGCTGCAC 1011

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 5

US-09-984-711-5

; Sequence 5, Application US/09884711

; Patent No. US20020119549A1

; GENERAL INFORMATION:

; APPLICANT: MOECKEL, Bettina

; APPLICANT: BATHE, Brigitte

; APPLICANT: STEPHAN, Hans

; APPLICANT: KREUTZER, Caroline

; APPLICANT: HERMANN, Thomas

; APPLICANT: PFEFFERLE, Walter

; APPLICANT: BINDER, Michael

; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE rpsL GENE

; FILE REFERENCE: 204209US0

; CURRENT APPLICATION NUMBER: US/09/984,711

; PRIOR FILING DATE: 2001-10-31

; PRIOR APPLICATION NUMBER: DE10108230.9

; PRIOR FILING DATE: 2001-02-16

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 5

; LENGTH: 5096

; TYPE: DNA

; ORGANISM: Corynebacterium glutamicum

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (702)..(4196)

; OTHER INFORMATION:

US-09-984-711-5

Query Match 28.2%; Score 62.8; DB 10; Length 5096;

Best Local Similarity 71.0%; Pred. No. 5.2e-09;

Matches 98; Conservative 0; Mismatches 37; Indels 3; Gaps 1;

QY 9 AAGCGCTAGCACTGGCGCGGCTGCGCGCTACAGGTCAACAAGAGCTGGCGCTGAAC 68

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 1578 AAGCGCTAGCACTGGCTGCGGTTGCGTTACAGATCAACCGCAAGCTCGCGCTTGT 1637

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 69 ACCGATCATCCGATCACCAACAGCAGCTGACCGAAGAGAGCTGCTGCCACCATCGAG 128

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 1638 GCGACCAAGATGGTTGAT--GACTCTTACTGAGAGGACATCGCAACCATCGAG 1694

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 129 TACCTGGTGGCTGCAC 146

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 1695 TACCTGGTGGCTGCAC 1712

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RESULT 6

US-09-887-052-1

; Sequence 1, Application US/09887052

; Patent No. US20020119537A1

; GENERAL INFORMATION:

; APPLICANT: MOECKEL, Bettina

; APPLICANT: BATHE, Brigitte

; APPLICANT: HERMANN, Thomas

; APPLICANT: PFEFFERLE, Walter

; APPLICANT: BINDER, Michael

; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE rpoB GENE

; FILE REFERENCE: 204212US0X

; CURRENT APPLICATION NUMBER: US/09/887,052

; CURRENT FILING DATE: 2001-06-25

; PRIOR APPLICATION NUMBER: DE10107229.5

; PRIOR FILING DATE: 2001-02-16

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 1

; LENGTH: 5099

; TYPE: DNA

; ORGANISM: Corynebacterium glutamicum

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (702)..(4196)

US-09-887-052-1

Query Match 28.2%; Score 62.8; DB 10; Length 5099;

Best Local Similarity 71.0%; Pred. No. 5.2e-09;

Matches 98; Conservative 0; Mismatches 37; Indels 3; Gaps 1;

QY 9 AAGCGCTAGCACTGGCGCGGCTGCGCGCTACAGGTCAACAAGAGCTGGCGCTGAAC 68

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Db 1578 AAGCGCTAGCACTGGCTGCGGTTGCGTTACAGATCAACCGCAAGCTCGCGCTTGT 1637

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QY 69 ACCGATCATCCGATCACCAACAGCAGCTGACCGAAGAGAGCTGCTGCCACCATCGAG 128

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 1638 GCGACCAAGATGGTTGAT--GACTCTTACTGAGAGGACATCGCAACCATCGAG 1694

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 129 TACCTGGTGGCTGCAC 146

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 1695 TACCTGGTGGCTGCAC 1712

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 7

US-09-887-052-3

; Sequence 3, Application US/09887052

; Patent No. US20020119537A1

; GENERAL INFORMATION:

; APPLICANT: MOECKEL, Bettina

; APPLICANT: BATHE, Brigitte

; APPLICANT: HERMANN, Thomas

; APPLICANT: PFEFFERLE, Walter

; APPLICANT: BINDER, Michael

; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE rpoB GENE

; FILE REFERENCE: 204212US0X

; CURRENT APPLICATION NUMBER: US/09/887,052

; CURRENT FILING DATE: 2001-06-25

; PRIOR APPLICATION NUMBER: DE10107229.5

; PRIOR FILING DATE: 2001-02-16

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 3

; LENGTH: 5099

; TYPE: DNA

; ORGANISM: Corynebacterium glutamicum

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (702)..(4196)

US-09-887-052-3

Query Match 28.2%; Score 62.8; DB 10; Length 5099;

Best Local Similarity 71.0%; Pred. No. 5.2e-09;

Matches 98; Conservative 0; Mismatches 37; Indels 3; Gaps 1;

QY 9 AAGCGCTAGCACTGGCGCGGCTGCGCGCTACAGGTCAACAAGAGCTGGCGCTGAAC 68

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 1578 AAGCGCTAGCACTGGCTGCGGTTGCGTTACAGATCAACCGCAAGCTCGCGCTTGT 1637

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY	69	ACCGATATCCGATCCACACACGACGCTGACCGGAAGAAGACGTCGTCGCCACCATCGAG	128
Db	1638	GGGACACAGATGGTTTGTAT--GACTCTTACTGAAGAGGACATCGCAACCCACCATCGAG	1694
QY	129	TACCTGSGTCGCCTGCAC	146
Db	1695	TACCTGSGTCGCTGCAC	1712

Query Match	28.2%;	Score 62.8;	DB 12;	Length 5099;
Best Local Similarity	71.0%;	Prod. No. 5.2e-09;		
Matches	98;	Conservative	0;	Mismatches 37; Indels 3; Gaps 1;
QY	9	AAGCGCTACGACTGGCCGGTCGGCCGCTACAGAGTCTCACAAGAGCTGGGCCCTGCAC	68	
Dd	1578	AAGCGCTACGACTGGCTGGCGTTGTGCTTACAGATCAACCCGCAAGCTTCGGCCCTTGCT	1637	
QY	69	ACCGCATCATCCGATCACCAACCACCGCTCAGCGAAGAAGACGCTGTCGCCACCATCGAG	128	
Dd	1638	GCGCAACACAGATTGTGAT--GACTCTTACTTAGAGAGGCATCGCAACCAACCATCGAG	1694	
QY	129	TACTGGTTTCGCTGCAC	146	
Dd	1695	TACCTGGTGGCTGTGCAC	1712	

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; FILE REFERENCE: 218472USOX
; CURRENT APPLICATION NUMBER: US/10/075,460
; CURRENT FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: DE 1010730.9
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: DE 10162386.0
; PRIOR FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 5099
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
; OTHER INFORMATION:
US-10-075-460-5

Query Match      28.2%; Score 62.8; DB 13; Length 5099;
Best Local Similarity 71.0%; Pred. No.5.2e-09;
Matches 98; Conservative 0; Mismatches 37; Indels 3; Gaps 1;

QY      9  AAGCGCTACGACCTGGCCGCGCTGGCGCCGCTACAGGCTCAACAAGAGCTGGCCCTGAC 68
        |||||
Db      1578  AAGCGCTACGACCTGGCTGGCGTGGTTCGCTTACAAGATCAACCGCAAGCTCGGCGCTTGGT 1637
        |||||

QY      69  ACCGATCATCCGATCAACCAACCAACGCTGACCGAAGAGACGTCGTCGCCACCATCGAG 128
        |||||
Db      1638  GCGACCAACGATGGTTTGGT--GACTCTTACTGAGAGGACATCGCAACCAACCATCGAG 1694
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QY      129  TACCTGGTTGCGCTGCAC 146
        |||||
Db      1695  TACCTGGTGGCTGCAC 1712
        |||||

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ATTORNEY: BENEDICT, MICHAEL
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE rpsL GENE

QY 9 AAGCGCTAGACCTGGCCGCGCTGCGCGCTACAAAGTCAACAAGAGCTGGCGCTGAAC 68
|||||
Db 513789 AAGCGCTAGACCTGGCTGCGCTTACAAAGTCAACAAGAGCTGGCGCTGGT 513848
QY 69 ACCGATCATCGATCACCACCGAGCTGACCGAAGACGCTGCTGCCACATCGAG 128
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Db 513849 GCGGACCAAGATGTTGAT--GACTCTTACTGAAGAGGACATCGCAACCACTCGAG 513905
QY 129 TACCTGGTTCGCTGCGAC 146
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Db 513906 TACCTGGTTCGCTGCGAC 513923

RESULT 14
US-10-062-254-109
; Sequence 109, Application US/10062254
; Publication No. US20020138882A1
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Edgar B
; APPLICANT: Cahoon, Rebecca E
; APPLICANT: Falcoo, Saverio Carl
; APPLICANT: Fang, Yiwen
; APPLICANT: Hantke, Sabine S.
; APPLICANT: Lee, Jian-Ming
; APPLICANT: Li, Zhongsen
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Morgante, Michele
; APPLICANT: Niu, Xiping
; APPLICANT: Odell, Joan
; APPLICANT: Rafalski, Antoni
; APPLICANT: Sakai, Hajime
; APPLICANT: Zheng, Peizhong
; APPLICANT: Zhu, Qun
; TITLE OF INVENTION: Polynucleotides Encoding Proteins Involved In Plant Metabolism
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/062,254
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 09/630,346
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/146511
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 60/156006
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/156899
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 60/157287
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/169767
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 60/171054
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: 60/172958
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 60/171515
; PRIOR FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 109
; LENGTH: 704
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (640)
; NAME/KEY: unsure
; LOCATION: (663)
; NAME/KEY: unsure
; LOCATION: (688)
; NAME/KEY: unsure
; LOCATION: (692)
; NAME/KEY: unsure

; LOCATION: (696)
US-10-062-254-109
Query Match 19.0%; Score 42.4; DB 13; Length 704;
Best Local Similarity 58.9%; Pred. No. 0.0042;
Matches 73; Conservative 0; Mismatches 51; Indels 0; Gaps 0;
QY 4 AGGAGAACGCTACGACCTGGCCGCGCTGCGCGCTACAAAGTCAACAAGAGCTGGGCC 63
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Db 275 AGCTGATGCGCCAGCAGCTGGCCACCAGTCCGGGAGGAGGTCACCAAGAGGTCGCC 334
QY 64 TGAACACCGATCATCGGATCACACACGACGCTGACCGAAGAGACGCTGTCGCCACCA 123
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Db 335 TCGTCTACCACTCAATCGCGCCGCCCAAGAGATCGCGCTTGATGAGGAGATCTTCGTGG 394
QY 124 TCGA 127
Db 395 TCGA 398
RESULT 15
US-10-062-254-111
; Sequence 111, Application US/10062254
; Publication No. US20020138882A1
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Edgar B
; APPLICANT: Cahoon, Rebecca E
; APPLICANT: Falcoo, Saverio Carl
; APPLICANT: Fang, Yiwen
; APPLICANT: Hantke, Sabine S.
; APPLICANT: Lee, Jian-Ming
; APPLICANT: Li, Zhongsen
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Morgante, Michele
; APPLICANT: Niu, Xiping
; APPLICANT: Odell, Joan
; APPLICANT: Rafalski, Antoni
; APPLICANT: Sakai, Hajime
; APPLICANT: Zheng, Peizhong
; APPLICANT: Zhu, Qun
; TITLE OF INVENTION: Polynucleotides Encoding Proteins Involved In Plant Metabolism
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/062,254
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 09/630,346
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/146511
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 60/156006
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/156899
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 60/157287
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/169767
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 60/171054
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: 60/172958
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 60/171515
; PRIOR FILING DATE: 1999-12-22
; PRIOR APPLICATION NUMBER: 60/173535
; PRIOR FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 111
; LENGTH: 752
; TYPE: DNA
; ORGANISM: Zea mays
US-10-062-254-111
Query Match 19.0%; Score 42.4; DB 13; Length 752;

Best Local Similarity 58.9%; Pred. No. 0.0042;
Matches 73; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

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Db	236	AGCTGATGCGCCAGCAGCTGGCCACCGATGCGCGCAAGAGGTACCAAGAAGTCTGGCC	295
QY	64	TGAACACCGATCATCCGATCAACCAACGACGCTGACCGAAGAGAGCTCTCGCCACA	123
Db	296	TGCTCTACAGCTCAACATCGCCCAAGAGATCGCGGTGATGAGGAGATCTTCGTGG	355
QY	124	TCGA	127
Db	356	TCGA	359

Search completed: September 17, 2003, 13:06:30
Job time : 136.066 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 17, 2003, 11:54:34 ; Search time 30.979 Seconds
(without alignments)
3049.028 Million cell updates/sec

Title: US-09-697-123B-14

Perfect score: 214

Sequence: 1 tcaaggagaagcgtacgac.....ccggtgagacgagacat 214

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	139.2	65.0	970	5	PCT-US95-06790-1
3	139.2	65.0	4403765	3	US-09-103-840A-2
4	139.2	65.0	4411529	3	US-09-103-840A-1
5	137.6	64.3	3447	2	US-08-313-185-57
6	137.6	64.3	3447	3	US-09-082-614A-57
7	42.2	19.7	1208	2	US-08-403-852D-4
8	42.2	19.7	1208	3	US-08-510-646B-4
9	42.2	19.7	1208	3	US-09-231-818-4
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14	41.4	19.3	11219	3	US-07-642-734C-1
15	41.4	19.3	11219	3	US-08-439-009A-1
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17	39.8	18.6	3282	4	US-09-252-991A-5256
18	39.8	18.6	4158	4	US-09-252-991A-5348
19	39.8	18.6	4953	4	US-09-252-991A-5227
20	39	18.2	597	4	US-09-252-991A-579
21	39	18.2	1047	4	US-09-252-991A-14678
22	39	18.2	1686	4	US-09-252-991A-14548
23	39	18.2	1815	4	US-09-252-991A-15077
24	38.8	18.1	1782	4	US-09-252-991A-8703
25	38.8	18.1	1830	4	US-09-252-991A-9916
26	38.6	18.0	780	4	US-09-252-991A-2544
27	38.6	18.0	1251	4	US-09-252-991A-2376

28 38.6 18.0 1445 4 US-09-252-991A-2461 Sequence 2461, Ap
29 38.6 18.0 2282 4 US-09-922-445-50 Sequence 50, Appl
30 38.2 17.9 1395 4 US-09-252-991A-12734 Sequence 12734, A
31 38.2 17.9 1434 4 US-09-252-991A-12585 Sequence 12585, A
32 38.2 17.9 4403765 3 US-09-103-840A-2 Sequence 2, Appli
33 37.8 17.7 1029 4 US-09-252-991A-8069 Sequence 8069, Ap
34 37.8 17.7 1167 4 US-09-252-991A-8122 Sequence 8122, Ap
35 37.8 17.7 1194 4 US-09-252-991A-8118 Sequence 8118, Ap
36 37.8 17.7 1845 4 US-09-252-991A-8187 Sequence 8187, Ap
37 37.3 930 4 US-09-252-991A-15663 Sequence 15663, A
38 37.3 1407 4 US-09-252-991A-11113 Sequence 11113, A
39 37.3 1416 4 US-09-252-991A-11168 Sequence 11168, A
40 37.3 1590 4 US-09-252-991A-11088 Sequence 11088, A
41 37.3 47981 4 US-09-679-279-1 Sequence 1, Appli
42 36.8 17.2 483 4 US-09-252-991A-5303 Sequence 5303, Ap
43 36.8 17.2 1608 4 US-09-252-991A-11665 Sequence 11665, A
44 36.8 17.2 1608 4 US-09-252-991A-11769 Sequence 11769, A
45 36.8 17.2 2304 4 US-09-252-991A-11691 Sequence 11691, A

ALIGNMENTS

RESULT 1
US-08-250-030-1
; Sequence 1, Application US/08250030
; Patent No. 5643723
; GENERAL INFORMATION:
; APPLICANT: Persing, David H.
; TITLE OF INVENTION: Detection of a Genetic Locus Encoding
; TITLE OF INVENTION: Resistance to Rifampin in Mycobacterial Cultures and in
; TITLE OF INVENTION: Clinical Specimens
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg & Woessner
; STREET: 3500 IDS Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/250,030
; FILING DATE: 26-MAY-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueeting, Ann M.
; REGISTRATION NUMBER: 33,977
; REFERENCE/DOCKET NUMBER: 150.105US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-339-0331
; TELEFAX: 612-339-3061
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 970 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-250-030-1

Query Match 65.0%; Score 139.2; DB 1; Length 970;
Best Local Similarity 81.8%; Pred. No. 2.9e-25;
Matches 175; Conservative 0; Mismatches 33; Indels 6; Gaps 1;

QY 1 TCAGGAGAGCGCTACACCTGGCCAGGGTTGGCCGTTCACAGGTCAACAGAGCTCG 60

26 TCAAGGAGAGCGCTACAGCTGGCCGCTGCTATAGGTCAACAGAGCTCG 85

QY 61 GCGTCGCGGCGCGGAGTGGCGGCTACCGCTCGACCGAGCTGACCGAGCGGATGTCG 120
 Db 86 GCGTCGATGTCGGGAGCC-----CATCAGCTGTCGAGCTGACCGAAGAGAGCTCG 139
 QY 121 TCGCCACCATCGAGTACCTGCTGCGCCCTGACAGGGCCAGCAGCATGATGCTCCCG 180
 Db 140 TGGCCACCATCGATATCTGCTGCGCTGTCACGAGGTCAGACGATGACCGTTCGG 199
 QY 181 GCGGCTCGAGGTGCGCGTGGAGACCGAGACAT 214
 Db 200 GCGGCTCGAGGTGCGCGTGGAAACCGAGACAT 233

RESULT 2

PCT-US95-06790-1

; Sequence 1, Application PC/TUS9506790
 ; GENERAL INFORMATION:
 ; APPLICANT: Mayo Foundation for Medical Education and Research
 ; APPLICANT: and Hoffmann-La Roche Inc.
 ; TITLE OF INVENTION: Detection of a Genetic Locus Encoding
 ; TITLE OF INVENTION: Resistance to Rifampin
 ; NUMBER OF SEQUENCES: 15
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Schwemmer, Lundberg & Woessner
 ; STREET: 3500 IDS Center
 ; CITY: Minneapolis
 ; STATE: MN
 ; COUNTRY: USA
 ; ZIP: 55402

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US95/06790
 ; FILING DATE: 26-MAY-1995

CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:
 ; NAME: Raasch, Kevin W.
 ; REGISTRATION NUMBER: 35,651
 ; REFERENCE/DOCKET NUMBER: 150.105W01
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 612-339-0331
 ; TELEFAX: 612-339-3061
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 970 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA
 PCT-US95-06790-1

Query Match 65.0%; Score 139.2; DB 5; Length 970;
 Best Local Similarity 81.8%; Pred. No. 2.9e-25;
 Matches 175; Conservative 0; Mismatches 33; Indels 6; Gaps 1;

QY 1 TCAAGGAGAGCGCTACGACTGGCGGAGGTTGCCGTTACAAAGTCAACAGAGAGCTCG 60
 Db 26 TCAAGGAGAGCGCTACGACTGGCGGAGGTTGCCGTTACAAAGTCAACAGAGAGCTCG 85
 QY 61 GCGTCGCGGCGCGGAGTGGCGGCTACCGCTGACACGCTGACCGAGCGGATGTCG 120
 Db 86 GCGTCGATGTCGGGAGCC-----CATCAGCTGTCGAGCTGACCGAAGAGAGCTCG 139
 QY 121 TCGCCACCATCGATCTGCTGCGCTGTCACGAGGCGCAGGCAAGATGAGCTTCGG 180
 Db 140 TGGCCACCATCGATATCTGCTGCGCTGTCACGAGGTCAGACGATGACCGTTCGG 199
 QY 181 GCGGCTCGAGGTGCGCGTGGAGACCGAGACAT 214
 Db 200 GCGGCTCGAGGTGCGCGTGGAAACCGAGACAT 233

RESULT 3

US-09-103-840A-2

; Sequence 2, Application US/09103840A
 ; Patent No. 6294328
 ; GENERAL INFORMATION:
 ; APPLICANT: FLEISCHMAN, Robert D.
 ; APPLICANT: WHITE, Owen R.
 ; APPLICANT: FRASER, Claire M.
 ; APPLICANT: VENTER, John C.

; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
 ; TITLE OF INVENTION: TUBERCULOSIS

FILE REFERENCE: 24366-20007.00

CURRENT APPLICATION NUMBER: US/09/103,840A

CURRENT FILING DATE: 1998-06-24

NUMBER OF SEQ ID NOS: 2

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 2

LENGTH: 4403765

TYPE: DNA

ORGANISM: Mycobacterium tuberculosis

FEATURE:

OTHER INFORMATION: CDC 1551

OTHER INFORMATION: "n" bases at various positions throughout the sequence

OTHER INFORMATION: represent a, t, c or g

US-09-103-840A-2

Query Match 65.0%; Score 139.2; DB 3; Length 4403765;

Best Local Similarity 81.8%; Pred. No. 5.7e-25;

Matches 175; Conservative 0; Mismatches 33; Indels 6; Gaps 1;

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 Db 762648 TCAAGGAGAGCGCTACGACTGGCGGAGGTTGCCGTTACAAAGTCAACAGAGAGCTCG 762707
 QY 61 GCGTCGCGGCGCGGAGTGGCGGCTACCGCTGACACGCTGACCGAGCGGATGTCG 120
 Db 762708 GCGTCGATGTCGGGAGCC-----CATCAGCTGTCGAGCTGACCGAAGAGAGCTCG 762761
 QY 121 TCGCCACCATCGAGTACCTGCTGCGCTGTCACGAGGCGCAGGCAAGATGAGCTTCGG 180
 Db 762762 TGGCCACCATCGATATCTGCTGCGCTGTCACGAGGTCAGACGATGACCGTTCGG 762821
 QY 181 GCGGCTCGAGGTGCGCGTGGAGACCGAGACAT 214
 Db 762822 GCGGCTCGAGGTGCGCGTGGAAACCGAGACAT 762855

RESULT 4

US-09-103-840A-1

; Sequence 1, Application US/09103840A

; Patent No. 6294328

; GENERAL INFORMATION:

; APPLICANT: FLEISCHMAN, Robert D.

; APPLICANT: WHITE, Owen R.

; APPLICANT: FRASER, Claire M.

; APPLICANT: VENTER, John C.

; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM

; TITLE OF INVENTION: TUBERCULOSIS

FILE REFERENCE: 24366-20007.00

CURRENT APPLICATION NUMBER: US/09/103,840A

CURRENT FILING DATE: 1998-06-24

NUMBER OF SEQ ID NOS: 2

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1

LENGTH: 4411529

TYPE: DNA

ORGANISM: Mycobacterium tuberculosis

OTHER INFORMATION: H37RV

US-09-103-840A-1

Query Match 65.0%; Score 139.2; DB 3; Length 4411529;

Best Local Similarity 81.8%; Pred. No. 5.7e-25;
Matches 175; Conservative 0; Mismatches 33; Indels 6; Gaps 1;

QY 1 TCAAGGAGAGCGCTAGCCTGGCCAGAGGTTGGCCGTTACAAAGGTCACAAAGAGCTCG 60
DB 760688 TCAAGGAGAGCGCTAGCCTGGCCAGAGGTTGGCCGTTACAAAGGTCACAAAGAGCTCG 760747
QY 61 GCTCCGCGCGCGAGCTGGCGGTACCGGCTGACACGCTGACCGAGCGGATGTCG 120
DB 760748 GCTCCGCGCGCGAGCTGGCGGTACCGGCTGACACGCTGACCGAGCGGATGTCG 760801
QY 121 TGCCACCATCGAGTACCTGCTGCGCTGCACGAGGCGCAGGCAAGATGACGGTTCCCG 180
DB 760802 TGCCACCATCGAGTACCTGCTGCGCTGCACGAGGCGCAGGCAAGATGACGGTTCCCG 760861
QY 181 GCGGCGTCGAGGTCCGCGGTGAGACCGAGGACAT 214
DB 760862 GCGGCGTCGAGGTCCGCGGTGAGACCGAGGACAT 760895

RESULT 5

US-08-313-185-57
; Sequence 57, Application US/08313185
; Patent No. 5851763

GENERAL INFORMATION:

APPLICANT: Heym, Beate
APPLICANT: Cole, Stewart
APPLICANT: Young, Douglas
APPLICANT: Zhang, Ying
APPLICANT: Honore, Nadine
APPLICANT: Telenti, Amalio
APPLICANT: Bodmer, Thomas
TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,185
FILING DATE: 12-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 02356.0068-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 3447 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

US-08-313-185-57

Query Match 64.3%; Score 137.6; DB 2; Length 3447;
Best Local Similarity 81.3%; Pred. No. 7.8e-25;
Matches 174; Conservative 0; Mismatches 34; Indels 6; Gaps 1;

QY 1 TCAAGGAGAGCGCTAGCCTGGCCAGAGGTTGGCCGTTACAAAGGTCACAAAGAGCTCG 60

DB 809 TCAAGGAGAGCGCTAGCCTGGCCAGAGGTTGGCCGTTACAAAGGTCACAAAGAGCTCG 868
QY 61 GCTCCGCGCGCGAGCTGGCGGTACCGGCTGACACGCTGACCGAGCGGATGTCG 120
DB 869 GCTCCGCGCGCGAGCTGGCGGTACCGGCTGACACGCTGACCGAGCGGATGTCG 922
QY 121 TGCCACCATCGAGTACCTGCTGCGCTGCACGAGGCGCAGGCAAGATGACGGTTCCCG 180
DB 923 TGCCACCATCGAGTACCTGCTGCGCTGCACGAGGCGCAGGCAAGATGACGGTTCCCG 982
QY 181 GCGGCGTCGAGGTCCGCGGTGAGACCGAGGACAT 214
DB 983 GCGGCGTCGAGGTCCGCGGTGAGACCGAGGACAT 1016

RESULT 6

US-09-082-614A-57
; Sequence 57, Application US/09082614A
; Patent No. 6124098

GENERAL INFORMATION:

APPLICANT: Heym, Beate
APPLICANT: Cole, Stewart
APPLICANT: Young, Douglas
APPLICANT: Zhang, Ying
APPLICANT: Honore, Nadine
APPLICANT: Telenti, Amalio
APPLICANT: Bodmer, Thomas
TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/082,614A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/313,185
FILING DATE: 12-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 02356.0068-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 3447 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

US-09-082-614A-57

Query Match 64.3%; Score 137.6; DB 3; Length 3447;
Best Local Similarity 81.3%; Pred. No. 7.8e-25;
Matches 174; Conservative 0; Mismatches 34; Indels 6; Gaps 1;

QY 1 TCAAGGAGAGCGCTAGCCTGGCCAGAGGTTGGCCGTTACAAAGGTCACAAAGAGCTCG 60

Db 809 TCAGGAGAAACGCTACGACCTGCGCCAGGCTGCTTACAAAGTCAACAAGAGCTCG 868
QY 61 GGCTGGCGGGCGCGAGTCGGCGCTACCGCTCGACACGCTGACGAGCGGATGTCG 120
Db 869 GTTTCACGCGCGGTGAGT-----TGATCAGCTGCTCCACGCTGACCGAAGAGATGTCG 922
QY 121 TCGCCACCAATCGAGTAGTACCTGCTGCGCTGCGACGAGGCGCAGCAACGATGACGGTCCCG 180
Db 923 TCGCCACCAATAGATGACTGCTGCTGCTGATGAGGCTCACTGCGACATGACTTCCAG 982
QY 181 CGCGCTGCGAGTCCGCTGCGACCGACGACAT 214
Db 983 GTGGGTTAGAAAGTGCAGTGGAAACTGACGATAT 1016

RESULT 7
US-08-403-852D-4
; Sequence 4, Application US/08403852D
; Patent No. 5891695
; GENERAL INFORMATION:
; APPLICANT: Blanc, Veronique
; APPLICANT: Blanche, Francis
; APPLICANT: Crouzet, Joel
; APPLICANT: Jacques, Nathalie
; APPLICANT: Lacroix, Patricia
; APPLICANT: Thibaut, Denis
; APPLICANT: Zagorec, Monique
; APPLICANT: Debussche, Laurent
; APPLICANT: De Crecy-Lagard, Valerie
; TITLE OF INVENTION: Polypeptides Involved In The
; TITLE OF INVENTION: Biosynthesis Of Streptogramins, Nucleotide Sequences
; TITLE OF INVENTION: Coding For These Polypeptides And Their Use
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,852D
; FILING DATE: 10-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR 93/00923
; FILING DATE: 25-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 92/11441
; FILING DATE: 25-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 03806.0054-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1208 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: S.pristinaespiralis
; FEATURE:

; NAME/KEY: CDS
; LOCATION: 1..1208
US-08-403-852D-4
Query Match 19.7%; Score 42.2; DB 2; Length 1208;
Best Local Similarity 54.1%; Pred. No. 0.062;
Matches 86; Conservative 0; Mismatches 73; Indels 0; Gaps 0;
QY 56 GCTGGGCTCGCGGGCGGAGTGGCGCTGACCGCTGACGACCGCTGACCGAGCGGA 115
Db 429 GCTGATCGCGCTGCCCATCGAGCTGCGCCACCGCTCTCGCGCGCTACCGAGGTCCG 488
QY 116 TGTGTCGCGCCACCATCGAGTACCTGCTGCGCTGCGACGAGGCGCAGGCAACGATGACGGT 175
Db 489 CAAGAGCGGACCGTCCCTACCTGCGCCCGGAGGAGCCAGGTCACCATCGAGTA 548
QY 176 TCCGCGCGCGTTCGAGGTGCGCGTGGAGACCGACGACAT 214
Db 549 CCAGGCGAGCGCGCGCTGCGCTGGACACCGTCTCGT 587

RESULT 8
US-08-510-646B-4
; Sequence 4, Application US/08510646B
; Patent No. 6077699
; GENERAL INFORMATION:
; APPLICANT: Blanc, Veronique
; APPLICANT: Blanche, Francis
; APPLICANT: Crouzet, Joel
; APPLICANT: Jacques, Nathalie
; APPLICANT: Lacroix, Patricia
; APPLICANT: Thibaut, Denis
; APPLICANT: Zagorec, Monique
; APPLICANT: Debussche, Laurent
; APPLICANT: De Crecy-Lagard, Valerie
; TITLE OF INVENTION: Polypeptides Involved In The
; TITLE OF INVENTION: Biosynthesis Of Streptogramins, Nucleotide Sequences
; TITLE OF INVENTION: Coding For These Polypeptides And Their Use
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/510,646B
; FILING DATE: 03-AUG-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/403,852
; FILING DATE: 10-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR 93/00923
; FILING DATE: 25-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 92/11441
; FILING DATE: 25-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 03806.0054-01000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:

LENGTH: 1208 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: S.pristinaeaspiralis
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1208
US-08-510-646B-4

Query Match 19.7%; Score 42.2; DB 3; Length 1208;
Best Local Similarity 54.1%; Pred. No. 0.062;
Matches 86; Conservative 0; Mismatches 73; Indels 0; Gaps 0;
QY 56 GCTCGGCTGCCGGCGCGGAGTGGCGCTGACCGCTGACCGAGCGGA 115
Db 429 GCTGATGGCGCTGCCCATCGAGCTGCCACCGCTCTCGCGGGTCAACGAGTCCG 488
QY 116 TGTGCTGGCCACCATCGAGTACCTGTGCGCTGACGAGGGCCAGGACGATGACGGT 175
Db 489 CAAGGACGGCAGCGTCCCTACCTGCGCCCGGACGAGACCCAGGTTCACCATCGAGTA 548
QY 176 TCCCGGGCGCTCGAGGTGCGGTGGAGACCGAGACAT 214
Db 549 CCAGGGCAGCGCGCGGTGCGCTGGACACCGTCTCGT 587

RESULT 9

US-09-231-818-4
Sequence 4, Application US/09231818
Patent No. 6171846

GENERAL INFORMATION:
APPLICANT: Blanc, Veronique
APPLICANT: Crouzet, Joel
APPLICANT: Crouzet, Joel
APPLICANT: Jacques, Nathalie
APPLICANT: Lacroix, Patricia
APPLICANT: Thibaut, Denis
APPLICANT: Zagorec, Monique
APPLICANT: Debussche, Laurent
TITLE OF INVENTION: Polypeptides Involved In The
TITLE OF INVENTION: Biosynthesis Of Streptogramins, Nucleotide Sequences
TITLE OF INVENTION: Coding For These Polypeptides And Their Use
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/231,818
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/403,852
FILING DATE: 10-MAY-1995
APPLICATION NUMBER: PCT/FR 93/00923
FILING DATE: 25-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 92/11441
FILING DATE: 25-SEP-1992
ATTORNEY/AGENT INFORMATION:

NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03806.0054-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1208 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: S.pristinaeaspiralis
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1208
US-09-231-818-4

Query Match 19.7%; Score 42.2; DB 3; Length 1208;
Best Local Similarity 54.1%; Pred. No. 0.062;
Matches 86; Conservative 0; Mismatches 73; Indels 0; Gaps 0;
QY 56 GCTCGGCTGCCGGCGCGGAGTGGCGCTGACCGCTGACCGAGCGGA 115
Db 429 GCTGATGGCGCTGCCCATCGAGCTGCCACCGCTCTCGCGGGTCAACGAGTCCG 488
QY 116 TGTGCTGGCCACCATCGAGTACCTGTGCGCTGACGAGGGCCAGGACGATGACGGT 175
Db 489 CAAGGACGGCAGCGTCCCTACCTGCGCCCGGACGAGACCCAGGTTCACCATCGAGTA 548
QY 176 TCCCGGGCGCTCGAGGTGCGGTGGAGACCGAGACAT 214
Db 549 CCAGGGCAGCGCGCGGTGCGCTGGACACCGTCTCGT 587

RESULT 10

US-08-403-852D-1
Sequence 1, Application US/08403852D
Patent No. 5891695
GENERAL INFORMATION:
APPLICANT: Blanc, Veronique
APPLICANT: Crouzet, Joel
APPLICANT: Crouzet, Joel
APPLICANT: Jacques, Nathalie
APPLICANT: Lacroix, Patricia
APPLICANT: Thibaut, Denis
APPLICANT: Zagorec, Monique
APPLICANT: Debussche, Laurent
APPLICANT: De Crecy-lagard, Valerie
TITLE OF INVENTION: Polypeptides Involved In The
TITLE OF INVENTION: Biosynthesis Of Streptogramins, Nucleotide Sequences
TITLE OF INVENTION: Coding For These Polypeptides And Their Use
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/403,852D
FILING DATE: 10-MAY-1995
PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: PCT/FR 93/00923
; FILING DATE: 25-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 92/11441
; FILING DATE: 25-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25.146
; REFERENCE/DOCKET NUMBER: 03806.0054-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5392 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: S.pristinaespiralis
;
US-08-403-852D-1

Query Match 19.7%; Score 42.2; DB 2; Length 5392;
Best Local Similarity 54.1%; Pred. No. 0.07;
Matches 86; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

QY 56 GCTCGGGTCCGGCGCGAGTCGCGCTACCGCTGACCGCTGACCGAGCGGGA 115
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3986 GCTGATCGCGCTGCCATCGCTGCCACCGCTCTGCGCGGCTCACCAGGTCOG 4045

QY 116 TGTGTCGCCACCATGAGTACCTGCTGCGCTGACAGAGGCGCAGCAACGATGACGGT 175
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 4046 CAGGACGGCAGCGTCCCTACTGCGCCCGCAGCGGAGACCCAGGTCACATCGAGTA 4105

QY 176 TCCCGGGCGGTCCAGGTCCGCTGAGACCGACGACAT 214
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Db 4106 CCAGGCGAGCGCGCGCTGCGCTGAGACCGTGGTGT 4144

RESULT 11
US-08-510-646B-1
; Sequence 1, Application US/08510646B
; Patent No. 6077699
; GENERAL INFORMATION:
; APPLICANT: Blanc, Veronique
; APPLICANT: Crouzet, Joel
; APPLICANT: Jacques, Nathalie
; APPLICANT: Lacroix, Patricia
; APPLICANT: Thibaut, Denis
; APPLICANT: Zagorec, Monique
; APPLICANT: Debussche, Laurent
; APPLICANT: De Crecy-Lagard, Valerie
; TITLE OF INVENTION: Polypeptides Involved In The
; TITLE OF INVENTION: Biosynthesis Of Streptogramins, Nucleotide Sequences
; TITLE OF INVENTION: Coding For These Polypeptides And Their Use
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/08/510.646B
; FILING DATE: 03-AUG-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/403,852
; FILING DATE: 10-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR 93/00923
; FILING DATE: 25-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 92/11441
; FILING DATE: 25-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25.146
; REFERENCE/DOCKET NUMBER: 03806.0054-01000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5392 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: S.pristinaespiralis
;
US-08-510-646B-1

Query Match 19.7%; Score 42.2; DB 3; Length 5392;
Best Local Similarity 54.1%; Pred. No. 0.07;
Matches 86; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

QY 56 GCTCGGGTCCGGCGCGAGTCGCGCTGACCGCTGACCGAGCGGGA 115
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3986 GCTGATCGCGCTGCCATCGCTGCCACCGCTCTGCGCGGCTCACCAGGTCOG 4045

QY 116 TGTGTCGCCACCATGAGTACCTGCTGCGCTGACAGAGGCGCAGCAACGATGACGGT 175
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 4046 CAGGACGGCAGCGTCCCTACTGCGCCCGCAGCGGAGACCCAGGTCACATCGAGTA 4105

QY 176 TCCCGGGCGGTCCAGGTCCGCTGAGACCGACGACAT 214
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 4106 CCAGGCGAGCGCGCGCTGCGCTGAGACCGTGGTGT 4144

RESULT 12
US-09-231-818-1
; Sequence 1, Application US/09231818
; Patent No. 6171846
; GENERAL INFORMATION:
; APPLICANT: Blanc, Veronique
; APPLICANT: Crouzet, Joel
; APPLICANT: Jacques, Nathalie
; APPLICANT: Lacroix, Patricia
; APPLICANT: Thibaut, Denis
; APPLICANT: Zagorec, Monique
; APPLICANT: Debussche, Laurent
; APPLICANT: De Crecy-Lagard, Valerie
; TITLE OF INVENTION: Polypeptides Involved In The
; TITLE OF INVENTION: Biosynthesis Of Streptogramins, Nucleotide Sequences
; TITLE OF INVENTION: Coding For These Polypeptides And Their Use
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
```



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;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/642,734C
; FILING DATE: 17-JAN-91
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dandekers, Andreas M
; REGISTRATION NUMBER: 32652
; REFERENCE/DOCKET NUMBER: 4952.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-9396
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11219 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Saccharopolyspora erythraea
; STRAIN: NRRL 2338
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 744..6659
; OTHER INFORMATION: /function= "APPROXIMATE SPAN OF
; OTHER INFORMATION: MODULE 1"
; OTHER INFORMATION: /label= FUNCTION
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 744..11219
; OTHER INFORMATION: /function= "gene= "eryA""
; OTHER INFORMATION: /product= "Ore1 encoding modules 1 & 2 for
; OTHER INFORMATION: 6-deoxyerythronolide B""
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 744..1868
; OTHER INFORMATION: /function= "approximate span of
; OTHER INFORMATION: acyltransferase domain 1 of module 1"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1988..2198
; OTHER INFORMATION: /function= "approximate span of
; OTHER INFORMATION: acyl carrier domain 1 of module 1"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2230..3626
; OTHER INFORMATION: /function= "approximate span of
; OTHER INFORMATION: beta-ketoacylACP synthase domain/module1"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 3831..4811
; OTHER INFORMATION: /function= "approximate span of
; OTHER INFORMATION: acyltransferase 2 domain of module 1"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 5574..6125
; OTHER INFORMATION: /function= "approximate span of
; OTHER INFORMATION: beta-ketoreductase domain of module 1"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 6369..6626
; OTHER INFORMATION: /function= "approximate span of
; OTHER INFORMATION: acyl carrier domain 2 of module 1"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 6678..11219
; OTHER INFORMATION: /function= "approximate span of
; OTHER INFORMATION: module 2"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 6678..8066
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;
; OTHER INFORMATION: /function= "approximate span of
; OTHER INFORMATION: beta-ketoacyl ACP synthase of module 2"
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; Best Local Similarity 50.8%; Pred. No. 0.12; 96; Indels 0; Gaps 0;
; Matches 99; Conservative 0; Mismatches 96; Indels 0; Gaps 0;
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; QY 73 CCGAGTCGGCCGTACCCGCTCGACCAAGTGTGCGGACCAAGCGATGTCTGCCACCATCG 132
; Db 247 TGTCCCGCGGAGCGCCGCGGTTCCGCGCGCGCGGAGGTCTGAGGACCTGCGCG 188
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; RESULT 15
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; Sequence 1, Application US/08439009A
; Patent No. 6004787
; GENERAL INFORMATION:
; APPLICANT: Donadio, S
; APPLICANT: Katz, L
; APPLICANT: Mcalpine, J B
; TITLE OF INVENTION: Method of Directing Biosynthesis of
; TITLE OF INVENTION: Specific Polyketides
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Steven F. Weinstein
; STREET: Abbott Laboratories D377/AP6D-2 One Abbott
; STREET: Park Rd
; CITY: Abbott Park
; STATE: IL
; COUNTRY: US
; ZIP: 60064-3500
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/439,009A
; FILING DATE: 11-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Casuto, Dianne
; REGISTRATION NUMBER: 40,943
; REFERENCE/DOCKET NUMBER: 4952.US.D1
; TELECOMMUNICATION INFORMATION:
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; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11219 base pairs
; TYPE: nucleic acid
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; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
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; OTHER INFORMATION: /function= "APPROXIMATE SPAN OF
; OTHER INFORMATION: MODULE 1"
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; FEATURE:
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; OTHER INFORMATION: /function= "approximate span of
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; LOCATION: 6678..11219
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; LOCATION: 9906..10454
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; OTHER INFORMATION: /function= "approximate span of
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; Query Match 19.3%; Score 41.4; DB 3; Length 11219;
; Best Local Similarity 50.8%; Pred. NO. 0.12; 96; Indels 0; Gaps 0;
; Matches 99; Conservative 0; Mismatches 0;
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; QY 13 GCTACGACCTGGCCAGGGTTGGCCGTTACAAAGGTCAACAAGAAGCTCGGCTCCCGGGCGG 72
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Title: US-09-697-123b-14

Perfect score: 214
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Gapop 10.0 , Gapext 1.0

Searched: 1660708 seqs, 1229959015 residues

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	80.4	37.6	3495	10	US-09-738-626-547
3	80.4	37.6	5096	10	US-09-884-711-5
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5	80.4	37.6	5099	10	US-09-887-052-3
6	80.4	37.6	5099	10	US-09-887-052-5
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19	41	19.2	402	14	US-10-156-761-3597	Sequence 3597, Ap
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21	40.4	18.9	2019	14	US-10-156-761-1314	Sequence 1314, Ap
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26	39.8	18.6	2331	14	US-10-156-761-3212	Sequence 3212, Ap
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29	39.2	18.3	11817	14	US-10-156-761-2884	Sequence 2884, Ap
30	39.2	18.3	125746	14	US-10-156-761-15102	Sequence 15102, A
31	39	18.2	1050	14	US-10-156-761-3473	Sequence 3473, Ap
32	38.8	18.1	630	14	US-10-156-761-3036	Sequence 3036, Ap
33	38.8	18.1	1698	9	US-09-815-243-7770	Sequence 7770, Ap
34	38.8	18.1	11238	14	US-10-205-032-15	Sequence 15, Appl
35	38.8	18.1	60196	14	US-10-205-032-1	Sequence 1, Appli
36	38.6	18.0	447	12	US-10-259-165-688	Sequence 688, App
37	38.6	18.0	855	14	US-10-156-761-3767	Sequence 3767, App
38	38.6	18.0	927	14	US-10-156-761-3926	Sequence 3926, Ap
39	38.6	18.0	1269	10	US-09-894-844-115	Sequence 115, App
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41	38.6	18.0	2282	10	US-09-739-754A-2	Sequence 2, Appli
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ALIGNMENTS

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; Sequence 30, Application US/09712363
; Patent No. US20020164588A1
; GENERAL INFORMATION:
; APPLICANT: Eisenberg, David
; APPLICANT: Rotstein, Sergio H.
; APPLICANT: Marcotte, Edward M.
; TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND
; INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS
; FILE REFERENCE: 07419-032001
; CURRENT APPLICATION NUMBER: US/09712,363
; CURRENT FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: PCT/US00/02246
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,531
; PRIOR FILING DATE: 2000-02-01
; PRIOR APPLICATION NUMBER: 60/117,844
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/118,206,
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: 60/126,593
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/134,093
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/134,092
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/165,124
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/165,086,
; PRIOR FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 3519
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-09-712-363-30

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QY 181 GCGGCTCGAGTGGCGGTTGGAGACCGAGACAT 214
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Db 1058 GCGGCTCGAGTGGCGGTTGGAGACCGAGACAT 1091

RESULT 2
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; Sequence 547, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 547
; LENGTH: 3495
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-547

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Best Local Similarity 66.0%; Pred. No. 8.3e-14;
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RESULT 3
US-09-984-711-5
; Sequence 5, Application US/09984711
; Patent No. US20020119549A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: STEPHAN, Hans
; APPLICANT: KREUTZER, Caroline
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE TPOL GENE
; FILE REFERENCE: 204209US0
; CURRENT APPLICATION NUMBER: US/09/984,711
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: DE10108230.9
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 5096
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
; OTHER INFORMATION:
US-09-984-711-5

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Best Local Similarity 66.0%; Pred. No. 8.2e-14;
Matches 136; Conservative 0; Mismatches 61; Indels 9; Gaps 1;

QY 9 AAGCGCTACGACCTGGCGGTTGCCGTTACAGGTTCAACAGAGCTCGGCTCGCG 68
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QY 69 GCGGCGGAGTGGCGGTTGCCGCTGCACAGGCTGACCGAGCGGATGTCGTCGCCACC 128
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QY 129 ATCGAGTACCTGGTGGCGCTGCACAGGCGCAGCAGATGACGTTCCCGGGCGGTC 188
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QY 189 GAGGTGCGGTTGGAGACCGAGACAT 214
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Db 1749 GAGATCCAGTCGAGACCGATGACAT 1774

RESULT 4
US-09-887-052-1
; Sequence 1, Application US/09887052
; Patent No. US20020119537A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE TPOL GENE
; FILE REFERENCE: 204212US0X
; CURRENT APPLICATION NUMBER: US/09/887,052
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: DE10107229.5
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 5099
US-09-887-052-1

;; TYPE: DNA
;; ORGANISM: Corynebacterium glutamicum
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: (702)..(4196)
US-09-887-052-1

Query Match 37.6%; Score 80.4; DB 10; Length 5099;
Best Local Similarity 66.0%; Pred. No. 8.2e-14;
Matches 136; Conservative 0; Mismatches 61; Indels 9; Gaps 1;

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QY 129 ATCGAGTACCTGGTGGCTGCGCTGACGAGGCGCCAGGACGATGCGGTTCCCGGCGGCTC 188
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DB 1749 GAGATCCAGTCGAGACCGGATGACAT 1774
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RESULT 5
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; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE rpoB GENE
; FILE REFERENCE: 204212USX
; CURRENT APPLICATION NUMBER: US/09/887,052
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: DE10107229.5
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 5099
; TYPE: DNA
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
US-09-887-052-3

Query Match 37.6%; Score 80.4; DB 10; Length 5099;
Best Local Similarity 66.0%; Pred. No. 8.2e-14;
Matches 136; Conservative 0; Mismatches 61; Indels 9; Gaps 1;

QY 9 AAGCGCTACGACCTGGCCGCTTACAGGTCAACAAGAGCTCGGGCTGCCG 68
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QY 189 GAGGTCCGGTGGAGACCGGACGACAT 214
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DB 1749 GAGATCCAGTCGAGACCGGATGACAT 1774

RESULT 6
US-09-887-052-5
; Sequence 5, Application US/09887052
; Patent No. US20020119537A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE rpoB GENE
; FILE REFERENCE: 204212USX
; CURRENT APPLICATION NUMBER: US/09/887,052
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: DE10107229.5
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 5099
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
US-09-887-052-5

Query Match 37.6%; Score 80.4; DB 10; Length 5099;
Best Local Similarity 66.0%; Pred. No. 8.2e-14;
Matches 136; Conservative 0; Mismatches 61; Indels 9; Gaps 1;

QY 9 AAGCGCTACGACCTGGCCGCTTACAGGTCAACAAGAGCTCGGGCTGCCG 68
|||||
DB 1578 AAGCGCTACGACCTGGCTGGCTTACAGGTCAACAAGAGCTCGGGCTGCCG 1637
|||||

QY 69 GCGGCCGAGTGGCCGCTTACCGCTCGACCGAGCGTGCAGCGGATGTCGCCACC 128
|||||
DB 1638 GCGGACCAAGATGTTT-----GATGACTCTTACTGAAGAGGACATCGCAACACC 1688
|||||

QY 129 ATCGAGTACCTGGTGGCTGCGCTGACGAGGCGCCAGGACGATGCGGTTCCCGGCGGCTC 188
|||||
DB 1689 ATCGAGTACCTGGTGGCTGCGCTGACGAGGCGCGTGCATGACTTCTCCAAATGGTGAA 1748
|||||

QY 189 GAGGTCCGGTGGAGACCGGACGACAT 214
|||||
DB 1749 GAGATCCAGTCGAGACCGGATGACAT 1774
|||||

RESULT 7
US-10-076-406-1
; Sequence 1, Application US/10076406
; Publication No. US20030166884A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: Nucleotide sequences coding for the rpoB gene
; FILE REFERENCE: 219774USOXCP
; CURRENT APPLICATION NUMBER: US/10/076,406
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: DE 10107229.5
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 09/887052
; PRIOR FILING DATE: 2001-06-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 5099

[illegible]

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RESULT 9
US-10-076-406-5
; Sequence 5, Application US/10076406
; Publication No. US20030166884A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: HERMANN, Thomas
; APPLICANT: PEPPERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: Nucleotide sequences coding for the rpoB gene
; FILE REFERENCE: 219774050XCIP
; CURRENT APPLICATION NUMBER: US/10/076,406

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; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: DE 10107229.5
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: US 09/887052
; PRIOR FILING DATE: 2001-06-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 5099
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
; OTHER INFORMATION:
; NAME/KEY: mutation
; LOCATION: (2016)..(2016)
; OTHER INFORMATION: Substitution of cytosine by thymine
; US-10-076-406-5
;

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DD I745 OASRIICCCAGIICONGRACONIGRCAI 1773

RESULT 10
US-10-075-460-5
; Sequence 5, Application US/10075460

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; Publication No. US2002015557A1
; GENERAL INFORMATION:
; APPLICANT: MCKEL, BETTINA
; APPLICANT: BATHE, BRIGITTE
; APPLICANT: HANS, STEFAN
; APPLICANT: KREUTZER, CAROLINE
; APPLICANT: HERMANN, THOMAS
; APPLICANT: PFEFFERLE, WALTER
; APPLICANT: BINDER, MICHAEL
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE rpsL GENE
; FILE REFERENCE: 218472USX
; CURRENT APPLICATION NUMBER: US/10/075,460
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: DE 10107230.9
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: DE 10162386.0
; PRIOR FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 5099
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
; OTHER INFORMATION:
US-10-075-460-5

Query Match 37.6%; Score 80.4; DB 13; Length 5099;
Best Local Similarity 66.0%; Pred. No. 8.2e-14;
Matches 136; Conservative 0; Mismatches 61; Indels 9; Gaps 1;

QY 9 AAGCGCTACGACCTGGCCAGGTTGGCCGTACAGGTTCACAGAGTCAACAGAGCTCGGGCTGCGG 68
DB 1578 AAGCGCTACGACCTGGCCAGGTTGGCCGTACAGGTTCACAGAGTCAACAGAGTCAACAGAGCTCGGGCTGCGG 1637
QY 69 GCGGCGGAGTGGCGCTACCGGCTCGACAGCGTGCACGAGGCGGATGTCGTCGCGCAC 128
DB 1638 GCGGACCACGATGGTT-----GATGACTCTTACTGAGAGGACATCGCAACACC 1698
QY 129 ATCGAGTACCTGGTGGCCCTGCACGAGGCGCCAGCAACGATGACGGTTCCCGGCGCGTC 188
DB 1689 ATCGAGTACCTGGTGGCCCTGCACGAGGCGGTCATGACTTCTCCAAATGGTGAA 1748
QY 189 GAGTCCGGTGGAGACCGACGACAT 214
DB 1749 GAGATCCAGTCGAGACCGATGACAT 1774

RESULT 11
US-09-738-626-1
; Sequence 1, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MUKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07

; Publication No. US2002015557A1
; GENERAL INFORMATION:
; APPLICANT: MCKEL, BETTINA
; APPLICANT: BATHE, BRIGITTE
; APPLICANT: HANS, STEFAN
; APPLICANT: KREUTZER, CAROLINE
; APPLICANT: HERMANN, THOMAS
; APPLICANT: PFEFFERLE, WALTER
; APPLICANT: BINDER, MICHAEL
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE rpsL GENE
; FILE REFERENCE: 218472USX
; CURRENT APPLICATION NUMBER: US/10/075,460
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: DE 10107230.9
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: DE 10162386.0
; PRIOR FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 5099
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
; OTHER INFORMATION:
US-10-075-460-5

Query Match 37.6%; Score 80.4; DB 10; Length 3309400;
Best Local Similarity 66.0%; Pred. No. 6.9e-14;
Matches 136; Conservative 0; Mismatches 61; Indels 9; Gaps 1;

QY 9 AAGCGCTACGACCTGGCCAGGTTGGCCGTACAGGTTCACAGAGTCAACAGAGCTCGGGCTGCGG 68
DB 513789 AAGCGCTACGACCTGGCCAGGTTGGCCGTACAGGTTCACAGAGTCAACAGAGCTCGGGCTGCGG 513848
QY 69 GCGGCGGAGTGGCGCTACCGGCTCGACAGCGTGCACGAGGCGGATGTCGTCGCGCAC 128
DB 513849 GCGGACCACGATGGTT-----GATGACTCTTACTGAGAGGACATCGCAACACC 513899
QY 129 ATCGAGTACCTGGTGGCCCTGCACGAGGCGCCAGCAACGATGACGGTTCCCGGCGCGTC 188
DB 513900 ATCGAGTACCTGGTGGCCCTGCACGAGGCGGTCATGACTTCTCCAAATGGTGAA 513959
QY 189 GAGTCCGGTGGAGACCGACGACAT 214
DB 513960 GAGATCCAGTCGAGACCGATGACAT 513985

RESULT 12
US-10-156-761-4898
; Sequence 4898, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 4898
; LENGTH: 3543
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3543)
US-10-156-761-4898

Query Match 32.5%; Score 69.6; DB 14; Length 3543;
Best Local Similarity 62.1%; Pred. No. 9.8e-11;
Matches 133; Conservative 0; Mismatches 69; Indels 12; Gaps 1;

QY 1 TCAAGGAGAGCGCTACGACCTGCCAGGTTGGCGGTTACAGGTCAACAGAGTCAACAGAGCTCG 60
DB 926 TCAACCCGAGCGCTACGACCTCGGAGGTCGGCGGCTACAGGTCAACAGAGTCAACAGAGCTCG 985
QY 61 GGTTCGCGGCGCGGAGTTCGCGGCTACCGCTCGACACCGCTGACCGAGAGCGGATGTCG 120
DB 986 GCGGCGAGGCGCGCTGACCGCGGATC-----CTGACCGTCGAGGACATCA 1033
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QY 121 TGGCAGACATCGAGTACCTCGGTGGCGCTGACAGAGGCGCAGCAACGATGACGGTTCGCG 180
    || || || || || || || || || || || || || || || || || || || || || ||
Db 1034 TCTGTCGATCAAGTACCTCGGTGGAAGCTGCACGCCGTGAGACCGAGCCGTGGCGACA 1093
    || || || || || || || || || || || || || || || || || || || || || ||
QY 181 GCGCGGTGAGGTCGCGGTGGAGCCGACGACAT 214
    || || || || || || || || || || || || || || || || || || || || || ||
Db 1094 ACGGCACCTCGATCGTCTGTCGAGACCGACGACAT 1127
    || || || || || || || || || || || || || || || || || || || || || ||

RESULT 13
US-10-156-761-1
; Sequence 1, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: HIRIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
; LENGTH: 9025608
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1

Query Match 32.5%; Score 69.6; DB 14; Length 9025608;
Best Local Similarity 62.1%; Pred. No. 7.9e-11;
Matches 133; Conservative 0; Mismatches 69; Indels 12; Gaps 1;

QY 1 TCAGGAGAGCGCTACGACCTGGCGAGGTGGCGCTTACAGGTCACAGAGAGCTCG 60
    || || || || || || || || || || || || || || || || || || || || || ||
Db 5970494 TCACCCGAGCGCTACGACCTGGCGAGGTGGCGCTTACAGGTCACAGAGAGCTGG 5970553
    || || || || || || || || || || || || || || || || || || || || || ||
QY 61 GCCTCCGCGCGCGAGTCGCGCTACCGGCTCGACACGCTGACCGAGCGGATGTCG 120
    || || || || || || || || || || || || || || || || || || || || || ||
Db 5970554 GCGGCGAGGCGCGCTGGAGCGCGGGATC-----CTGACCGCTCGAGGACATCA 5970601
    || || || || || || || || || || || || || || || || || || || || || ||
QY 121 TGGCCACCATCGATCTGCTGCGCTGCACAGAGGCGCAGCAACGATGACGGTTCGCG 180
    || || || || || || || || || || || || || || || || || || || || || ||
Db 5970602 TCTCGTCGATCAAGTACCTCGGTGAGCTGCACGCGGTGAGACCGAGCCGTGGCGACA 5970661
    || || || || || || || || || || || || || || || || || || || || || ||
QY 181 GCGCGGTGAGGTCGCGGTGGAGCCGACGACAT 214
    || || || || || || || || || || || || || || || || || || || || || ||
Db 5970662 ACGGCACCTCGATCGTCTGTCGAGACCGACGACAT 5970695
    || || || || || || || || || || || || || || || || || || || || || ||

RESULT 14
US-10-156-761-2559
; Sequence 2559, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: HIRIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
```

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; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 2559
; LENGTH: 2196
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2196)
US-10-156-761-2559

Query Match 20.3%; Score 43.4; DB 14; Length 2196;
Best Local Similarity 51.3%; Pred. No. 0.0027;
Matches 101; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

QY 14 CTACGACCTGCGCAGGTTGGCCGTTACAGGTCACAGAGAGCTCGGGCTGCCGGGGCG 73
    || || || || || || || || || || || || || || || || || || || || || ||
Db 1005 CTGGGACACCGCGTGGCGGGGCGCTTACACAGCGAGCGCAATGTCATCTGCAGAGCGC 1064
    || || || || || || || || || || || || || || || || || || || || || ||
QY 74 CGAGTGGCGGTACCGGCTCGACACGCTGACCGAGGAGGATGCTGTCGCCACCATCGA 133
    || || || || || || || || || || || || || || || || || || || || || ||
Db 1065 GTGCGCGCGCGAGCGCGCCCTCCCGAGGTCGAGGTCATGCCGCCCTGGTGCACGG 1124
    || || || || || || || || || || || || || || || || || || || || || ||
QY 134 GTACCTGGTGGCTCGACAGGCGCCAGGCAAGATGACGGTTCGCCGGCGCTCGAGGT 193
    || || || || || || || || || || || || || || || || || || || || || ||
Db 1125 CCAGTTGCGGCACTGGCGGACACAGCCCGGGCGATCTCGGTACCCGCTGGCTGCGC 1184
    || || || || || || || || || || || || || || || || || || || || || ||
QY 194 GCGGTGGAGCGGACG 210
    || || || || || || || || || || || || || || || || || || || || || ||
Db 1185 CCGCGCGACACCGAGC 1201
    || || || || || || || || || || || || || || || || || || || || || ||

RESULT 15
US-10-156-761-1/C
; Sequence 1, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: HIRIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
; LENGTH: 9025608
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1

Query Match 20.3%; Score 43.4; DB 14; Length 9025608;
Best Local Similarity 51.3%; Pred. No. 0.0022;
Matches 101; Conservative 0; Mismatches 96; Indels 0; Gaps 0;
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QY      14 CTACGACCTGGCCAGGCTTGGCCGTTACAGGTCAACAGAGAGCTGGGCTGCCGCGGC 73
Db      3156806 CTGGGACACCGCGTGGGGGGGCCCTTCACCAACGACCCCAATGTCATCTGCAGACGGC 3156747

QY      74 CGAGTCGGCCGTACCCCGCCTCGACACGCTGACCGAGCGGATGCTGCGCCACCATCGA 133
Db      3156746 GTCGGCCGCCGACGCGGCCCTCCCGGAGGTCTCCGAGGCTCATGCCGCCCTGGTGCACGG 3156687

QY      134 GTACCTGTGTGGCCCTGCACGAGGGCCAGGCAACGATGACGGTCCCGGCGGCGTGGAGGT 193
Db      3156686 CCAGTTGCCGCACTGGCGCGGACAAACGCCCGGGCGGATCTTCGGTACCGTGGGCTGCTGCGC 3156627

QY      194 GCGGTGGAGACCGACG 210
Db      3156626 CCCCAGCACACCGACG 3156610

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Search completed: September 17, 2003, 13:06:57
Job time : 138.382 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 17, 2003, 11:54:34 ; Search time 30.1105 Seconds
(without alignments)
3049.028 Million cell updates/sec

Title: US-09-697-123B-15
Perfect score: 208
Sequence: 1 tcaaggagaagcgtacgac.....ccgtgagaccgacacat 208

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*
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3: /cn2_6/ptodata/1/ina/6A_COMB.seq.*
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5: /cn2_6/ptodata/1/ina/PTUS_COMB.seq.*
6: /cn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	169.6	81.5	970	1 US-08-250-030-1	Sequence 1, Appli
2	169.6	81.5	970	5 PCT-US95-06790-1	Sequence 1, Appli
3	169.6	81.5	4403765	3 US-09-103-840A-2	Sequence 2, Appli
4	169.6	81.5	4411529	3 US-09-103-840A-1	Sequence 1, Appli
5	152	73.1	3447	2 US-08-313-185-57	Sequence 57, Appli
6	152	73.1	3447	3 US-09-082-614A-57	Sequence 57, Appli
7	45	21.6	6085	3 US-09-029-603-4	Sequence 4, Appli
8	43.8	21.1	4403765	3 US-09-103-840A-2	Sequence 2, Appli
9	41.2	19.8	702	4 US-09-252-991A-3145	Sequence 3145, A
10	41.2	19.8	1089	4 US-09-252-991A-14778	Sequence 14778, A
11	41.2	19.8	1347	4 US-09-252-991A-14972	Sequence 14972, A
12	41.2	19.8	1416	4 US-09-252-991A-3049	Sequence 3049, A
13	41.2	19.8	1432	4 US-09-252-991A-14656	Sequence 14656, A
14	41.2	19.8	1545	4 US-09-252-991A-2823	Sequence 2823, A
15	40.6	19.5	77536	4 US-09-410-551B-1	Sequence 1, Appli
16	40.2	19.3	816	4 US-09-252-991A-1108	Sequence 1108, A
17	40.2	19.3	1578	4 US-09-252-991A-935	Sequence 935, App
18	40.2	19.3	1553	4 US-09-252-991A-976	Sequence 976, App
19	40	19.2	540	4 US-09-252-991A-550	Sequence 550, App
20	40	19.2	945	4 US-09-252-991A-8027	Sequence 8027, App
21	40	19.2	1002	4 US-09-252-991A-542	Sequence 542, App
22	40	19.2	1173	4 US-09-252-991A-8287	Sequence 8287, App
23	40	19.2	1245	4 US-09-252-991A-594	Sequence 594, App
24	40	19.2	2067	4 US-09-252-991A-527	Sequence 527, App
25	39.8	19.1	1414	4 US-09-501-115-5	Sequence 5, Appli
26	39.6	19.0	4411529	3 US-09-103-840A-1	Sequence 1, Appli
27	39.4	18.9	1245	4 US-09-252-991A-4359	Sequence 4359, App

28 39.4 18.9 1305 4 US-09-252-991A-4477 Sequence 4477, Ap
29 39.4 18.9 1374 4 US-09-252-991A-4384 Sequence 4384, Ap
30 39 18.8 1518 1 US-08-660-765A-1 Sequence 1, Appli
31 38.4 18.5 1998 3 US-09-382-106-1 Sequence 1, Appli
32 38.4 18.5 2007 4 US-09-252-991A-3308 Sequence 3308, Ap
33 38.4 18.5 2229 4 US-09-252-991A-3240 Sequence 3240, Ap
34 38.4 18.5 2709 4 US-09-252-991A-3326 Sequence 3326, Ap
35 38.2 18.4 1029 4 US-09-252-991A-7456 Sequence 7456, Ap
36 38.2 18.4 1137 4 US-09-252-991A-7244 Sequence 7244, Ap
37 38.2 18.4 1593 4 US-09-252-991A-7381 Sequence 7381, Ap
38 38 18.3 822 4 US-09-252-991A-9029 Sequence 9029, Ap
39 38 18.3 1182 4 US-09-252-991A-200 Sequence 200, App
40 38 18.3 1485 4 US-09-252-991A-16168 Sequence 16168, A
41 38 18.3 1527 4 US-09-252-991A-8978 Sequence 8978, Ap
42 38 18.3 1548 4 US-09-252-991A-16059 Sequence 16059, A
43 38 18.3 1587 4 US-09-252-991A-16424 Sequence 16424, A
44 38 18.3 1698 4 US-09-252-991A-193 Sequence 193, App
45 38 18.3 1701 4 US-09-252-991A-219 Sequence 219, App

ALIGNMENTS

RESULT 1
US-08-250-030-1
; Sequence 1, Application US/08250030
; Patent No. 5643723
; GENERAL INFORMATION:
; APPLICANT: Persing, David H.
; TITLE OF INVENTION: Detection of a Genetic Locus Encoding
; TITLE OF INVENTION: Resistance to Rifampin in Mycobacterial Cultures and in
; TITLE OF INVENTION: Clinical Specimens
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg & Woessner
; STREET: 3500 IDS Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/250,030
; FILING DATE: 26-MAY-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueeting, Ann M.
; REGISTRATION NUMBER: 33,977
; REFERENCE/DOCKET NUMBER: 150.1050S1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-339-0331
; TELEFAX: 612-339-3061
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 970 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-250-030-1

Query Match 81.5%; Score 169.6; DB 1; Length 970;
Best Local Similarity 88.5%; Pred. No. 6.9e-31;
Matches 184; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1 TCAAGGAGAGCGCTACGACCTGGCCGGTGGCGGCTACAGGTCAACAGAACTCG 60
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Db 26 TCAAGGAGAGCGCTACGACCTGGCCGGTGGCGGCTACAGGTCAACAGAACTCG 85
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QY 61 GCGTCAGCGCGGTGAGCCGATCACAGCTGACGCTGACGAGGAGAGAGCTGCTGCGCA 120
Db 86 GCGTCAGCTGCGGAGCCGATCACAGCTGCTGACGCTGACGAGGAGAGAGCTGCTGCGCA 145
QY 121 CCATCGAGTACCTGCTGCGCTGACGAGGCTGACCCAGCATGACCTGCTGCGCGCGCA 180
Db 146 CCATCGATATCTGCTGCGCTGACGAGGCTGACCCAGCATGACCTGCTGCGCGCGCG 205
QY 181 TCGAGTCCGCTGAGAGCCGAGCAT 208
Db 206 TCGAGTCCGCTGAGAGCCGAGCAT 233

RESULT 2
PCT-US95-06790-1
; Sequence 1, Application PC/TUS9506790
; GENERAL INFORMATION:
; APPLICANT: Mayo Foundation for Medical Education and Research
; APPLICANT: and Hoffmann-La Roche Inc.
; TITLE OF INVENTION: Detection of a Genetic Locus Encoding
; TITLE OF INVENTION: Resistance to Rifampin
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Schwegman, Lundberg & Woessner
; STREET: 3500 IDS Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/06790
; FILING DATE: 26-MAY-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Raasch, Kevin W.
; REGISTRATION NUMBER: 35,651
; REFERENCE/DOCKET NUMBER: 150.105W01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-339-0331
; TELEFAX: 612-339-3061
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 970 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
PCT-US95-06790-1

Query Match 81.5%; Score 169.6; DB 5; Length 970;
Best Local Similarity 88.5%; Pred. No. 6.9e-31;
Matches 184; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1 TCAAGGAGAAGCGGTACGACCTGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 60
Db 26 TCAAGGAGAAGCGGTACGACCTGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 85
QY 61 GCGTCAGCGCGGTGAGCCGATCACAGCTGACGCTGACGAGGAGAGAGCTGCTGCGCA 120
Db 86 GCGTCAGCTGCGGAGCCGATCACAGCTGCTGACGCTGACGAGGAGAGAGCTGCTGCGCA 145
QY 121 CCATCGAGTACCTGCTGCGCTGACGAGGCTGACCCAGCATGACCTGCTGCGCGCGCA 180
Db 146 CCATCGATATCTGCTGCGCTGACGAGGCTGACCCAGCATGACCTGCTGCGCGCGCG 205
QY 181 TCGAGTCCGCTGAGAGCCGAGCAT 208
Db 206 TCGAGTCCGCTGAGAGCCGAGCAT 233

Query Match 81.5%; Score 169.6; DB 3; Length 4403765;
Best Local Similarity 88.5%; Pred. No. 1.1e-30;
Matches 184; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1 TCAAGGAGAAGCGGTACGACCTGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 60
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QY 61 GCGTCAGCGCGGTGAGCCGATCACAGCTGACGCTGACGAGGAGAGAGCTGCTGCGCA 120
Db 762708 GCGTCAGCTGCGGAGCCGATCACAGCTGCTGACGCTGACGAGGAGAGAGCTGCTGCGCA 762767
QY 121 CCATCGAGTACCTGCTGCGCTGACGAGGCTGACCCAGCATGACCTGCTGCGCGCGCA 180
Db 762768 CCATCGATATCTGCTGCGCTGACGAGGCTGACCCAGCATGACCTGCTGCGCGCGCG 762827
QY 181 TCGAGTCCGCTGAGAGCCGAGCAT 208
Db 762828 TCGAGTCCGCTGAGAGCCGAGCAT 762855

RESULT 4
US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match 81.5%; Score 169.6; DB 3; Length 4411529;
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Best Local Similarity 88.5%; Pred. No. 1.le-30;
Matches 184; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1 TCAGGAGAACCGCTAGCACTGGCCCGGTGGCCCTACAGAGTCAACAGAGCTCG 60
Db TCAGGAGAACCGCTAGCACTGGCCCGGTGGCCCTACAGAGTCAACAGAGCTCG 760747

QY 61 GCTCAGACCGCGGTGAGCCGATCACAGCTGACGCTGACCGAGGAGACGCTCGCGCA 120
Db GCTCAGACCGCGGTGAGCCGATCACAGCTGACGCTGACCGAGGAGACGCTCGCGCA 760748

QY 121 CCATCGAGTACCTGGTGGCGCTGCACGAGGCTGACCCAGATGACCTGCCGCGCGCA 180
Db CCATCGAGTACCTGGTGGCGCTGCACGAGGCTGACCCAGATGACCTGCCGCGCGCA 760807

QY 181 TCGAGTCCGCGGTGAGACCGAGACAT 208
Db TCGAGTCCGCGGTGAGACCGAGACAT 760895

RESULT 5
US-08-313-185-57
; Sequence 57, Application US/08313185
; Patent No. 5851763
; GENERAL INFORMATION:
; APPLICANT: Heym, Beate
; APPLICANT: Cole, Stewart
; APPLICANT: Young, Douglas
; APPLICANT: Zhang, Ying
; APPLICANT: Honore, Nadine
; APPLICANT: Telenti, Amalio
; APPLICANT: Bodmer, Thomas
; TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
; TITLE OF INVENTION: in Mycobacterium Tuberculosis
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 12-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 02356.0068-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3447 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-313-185-57

Query Match 73.1%; Score 152; DB 2; Length 3447;
Best Local Similarity 83.2%; Pred. No. 8.2e-27;
Matches 173; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 1 TCAGGAGAACCGCTAGCACTGGCCCGGTGGCCCTACAGAGTCAACAGAGCTCG 60

Db 809 TCAGGAGAACCGCTAGCACTGGCCCGGTGGCTTACAGGTCAACAGAGCTCG 868

QY 61 GCTCAGACCGCGGTGAGCCGATCACAGCTGACGCTGACCGAGGAGACGCTCGCGCA 120
Db GCTCAGACCGCGGTGAGCCGATCACAGCTGACGCTGACCGAGGAGACGCTCGCGCA 928

QY 121 CCATCGAGTACCTGGTGGCGCTGCACGAGGCTGACCCAGATGACCTGCCGCGCGCA 180
Db CCATCGAGTACCTGGTGGCGCTGCACGAGGCTGACCCAGATGACCTGCCGCGCGCA 988

QY 181 TCGAGTCCGCGGTGAGACCGAGACAT 208
Db TCGAGTCCGCGGTGAGACCGAGACAT 1016

RESULT 6
US-09-082-614A-57
; Sequence 57, Application US/09082614A
; Patent No. 6124098
; GENERAL INFORMATION:
; APPLICANT: Heym, Beate
; APPLICANT: Cole, Stewart
; APPLICANT: Young, Douglas
; APPLICANT: Zhang, Ying
; APPLICANT: Honore, Nadine
; APPLICANT: Telenti, Amalio
; APPLICANT: Bodmer, Thomas
; TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
; TITLE OF INVENTION: in Mycobacterium Tuberculosis
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 09/09/082, 614A
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/313,185
; FILING DATE: 12-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 02356.0068-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3447 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-082-614A-57

Query Match 73.1%; Score 152; DB 3; Length 3447;
Best Local Similarity 83.2%; Pred. No. 8.2e-27;
Matches 173; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 1 TCAGGAGAACCGCTAGCACTGGCCCGGTGGCCCTACAGAGTCAACAGAGCTCG 60

Db 172 CACCGTGTCTCGACCGCGTGGCGCGACGCCCGGATCACTACTCCGGCACCGCGCCTT 231

QY 182 CG 183

Db 232 CG 233

RESULT 13

US-09-252-991A-14656

; Sequence 14656, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 14656

; LENGTH: 1482

; TYPE: DNA

; ORGANISM: Pseudomonas aeruginosa

; FEATURE:

; NAME/KEY: unsure

; LOCATION: {63}

; OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.

US-09-252-991A-14656

Query Match 19.8%; Score 41.2; DB 4; Length 1482;

Best Local Similarity 51.6%; Pred. No. 0.22; Indels 0; Gaps 0;

Matches 94; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 24 GCCCGGTGGCGCGCTACAAAGTCAACAAAGTCTGGCTCGACGCGGTGAGCCGATC 83

Db 599 GCCTTCGTGGCGACTACTACCTGAGCGCGATACCTGCGAATCAACGAAAGCGGACG 658

QY 84 ACCAGCTCGCTGACCGGAGAGACGCTGTCGCCACCATCGAGTACTGTCGCGCTG 143

Db 659 ATGAGCTCGTGGCGCGCGGACGACGTCATTACCACTTGGCTACCGGGTCGGCCG 718

QY 144 CACGAGGGTCAGCCCGACGATGACCGTCCCGCGCGCATGAGTGTGCGGTGGAGACGAC 203

Db 719 TTCGATGAGAGCGCGCTGATCCGAACACCCGCGCATGATGAGCGCGGTGATCGGC 778

QY 204 GA 205

Db 779 AA 780

RESULT 14

US-09-252-991A-2823/c

; Sequence 2823, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 2823

; LENGTH: 1545

; TYPE: DNA

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-2823

Query Match 19.8%; Score 41.2; DB 4; Length 1545;

Best Local Similarity 51.6%; Pred. No. 0.22;

Matches 94; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 2 CAAGGAGAGCGCTAGCACTGGCCCGGGTGGCGCGTCAACAGGTCAACAGAGCTCGG 61

Db 285 CGAGGTGCTGCCCAAGCGCANCCTCTCGGTGGCGCGGAGAGTGGATGACCTGAAAC 206

QY 62 CCTGCAGCGCGGTGAGCGCATCACCAGCTGAGCGCTGACCGAGGAGACGTCGTCGCCAC 121

Db 205 CGCAAGAGACTGGTGGCATGCGCGCTGGTGGCGCGGAGATATCGCCACCGACAA 146

QY 122 CATGAGTACTGTCGCGCTGACGAGGAGTCAAGCGGACGATGACCGTCCCGCGGCGAT 181

Db 145 CACCGTGTCTCGACCGCGTGGCGCGACGCGCGATCACTACTCCGCGCACCGCGCCTT 86

QY 182 CG 183

Db 85 CG 84

RESULT 15

US-09-410-551B-1/c

; Sequence 1, Application US/09410551B

; Patent No. 6503737

; GENERAL INFORMATION:

; APPLICANT: KOSAN BIOSCIENCES, Inc.

; APPLICANT: REEVES, CHRISTOPHER

; APPLICANT: CHU, DANIEL

; APPLICANT: KHOSLA, CHAITAN

; APPLICANT: SANTU, DANIEL

; APPLICANT: WU, KAI

; TITLE OF INVENTION: POLYPEPTIDE SYNTHASE ENZYMES AND RECOMBINANT DNA

; TITLE OF INVENTION: CONSTRUCTS THEREFOR

; FILE REFERENCE: 30062-20026.00

; CURRENT APPLICATION NUMBER: US/09/410,551B

; CURRENT FILING DATE: 1999-10-01

; PRIOR APPLICATION NUMBER: US 60/139,650

; PRIOR FILING DATE: 1999-06-17

; PRIOR APPLICATION NUMBER: US 60/123,810

; PRIOR FILING DATE: 1999-03-11

; PRIOR APPLICATION NUMBER: US 60/102,748

; PRIOR FILING DATE: 1998-10-02

; NUMBER OF SEQ ID NOS: 72

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 77536

; TYPE: DNA

; ORGANISM: Streptomyces hygroscopicus

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (52275)...(71465)

US-09-410-551B-1

Query Match 19.5%; Score 40.6; DB 4; Length 77536;

Best Local Similarity 50.8%; Pred. No. 0.38;

Matches 97; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

QY 14 CTACGACTGGCCCGGGTGGCGCTACAAGGTCAACAAAGCTCGGCGCTGACGCGG 73

Db 23131 CTCGCGCGTCAACAGGAGCGCGCTCCACGCGCATCTCCGACCAACGCGCCCTCCCA 23072

QY 74 TGAGCGCATCACCAGCTCGACGCTGACCGAGGAGAGCTGTCGCCACCATCGAGTACCT 133

Db 23071 GCAGCGGTCTATCCCGCAGGCCCTCCAAAGGGGGGCTCGCCCGCGGCTGGAGCT 23012

QY 134 GGTGCGCTCAGCAGGGGTGACGCCACCATGATGACGCTCCCGCGCGCATCGAGGTCCGGT 193

Db 23011 GGTGGAGCGCACGGGACGCGGACGACGCTGGGCGATCCCATCGAGGCGCACGCGATTCT 22952

QY 194 GGAGACCGACG 204
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Db 22951 GCGACGTACG 22941

Search completed: September 17, 2003, 12:29:55
Job time : 49.1605 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 17, 2003, 11:54:34 ; Search time 108.259 Seconds
 (without alignments)
 4726.283 Million cell updates/sec

Title: US-09-697-123B-15
 Perfect score: 208
 Sequence: 1 tcaaggagaagcgtacgac.....ccggtgagacgagacat 208

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 1660708 seqs, 1229959015 residues

Total number of hits satisfying chosen parameters: 3321416

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published Applications NA:*

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 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	169.6	81.5	3519	10	US-09-712-363-30
2	88.4	42.5	3543	14	US-10-156-761-4898
3	88.4	42.5	9025608	14	US-10-156-761-1
4	86.4	41.5	3495	10	US-09-738-626-547
5	86.4	41.5	5096	10	US-09-984-711-5
6	86.4	41.5	5099	10	US-09-887-052-1
7	86.4	41.5	5099	10	US-09-887-052-3
8	86.4	41.5	5099	10	US-09-887-052-5
9	86.4	41.5	5099	12	US-10-076-406-1
10	86.4	41.5	5099	12	US-10-076-406-3
11	86.4	41.5	5099	12	US-10-076-406-5
12	86.4	41.5	5099	13	US-10-075-480-5
13	86.4	41.5	3309400	10	US-09-738-626-1
14	43	20.7	1389	14	US-10-156-761-5431
15	42.6	20.5	11058	14	US-10-156-761-3629
16	42.6	20.5	9025608	14	US-10-156-761-1

17 42.4 20.4 1535 12 US-10-199-672-545 Sequence 545, App
 18 42.4 20.4 1535 12 US-10-187-749-545 Sequence 545, App
 19 42.4 20.4 1535 12 US-10-194-457-545 Sequence 545, App
 20 42.4 20.4 1535 12 US-10-184-842-545 Sequence 545, App
 21 42.4 20.4 1535 12 US-10-196-747-545 Sequence 545, App
 22 42.4 20.4 1535 12 US-10-173-689-545 Sequence 545, App
 23 42.4 20.4 1535 12 US-10-173-690-545 Sequence 545, App
 24 42.4 20.4 1535 12 US-10-173-691-545 Sequence 545, App
 25 42.4 20.4 1535 12 US-10-173-692-545 Sequence 545, App
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 27 42.4 20.4 1535 12 US-10-173-698-545 Sequence 545, App
 28 42.4 20.4 1535 12 US-10-173-699-545 Sequence 545, App
 29 42.4 20.4 1535 12 US-10-173-707-545 Sequence 545, App
 30 42.4 20.4 1535 12 US-10-174-569-545 Sequence 545, App
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 33 42.4 20.4 1535 12 US-10-174-589-545 Sequence 545, App
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 35 42.4 20.4 1535 12 US-10-175-736-545 Sequence 545, App
 36 42.4 20.4 1535 12 US-10-175-742-545 Sequence 545, App
 37 42.4 20.4 1535 12 US-10-175-744-545 Sequence 545, App
 38 42.4 20.4 1535 12 US-10-175-745-545 Sequence 545, App
 39 42.4 20.4 1535 12 US-10-175-748-545 Sequence 545, App
 40 42.4 20.4 1535 12 US-10-175-751-545 Sequence 545, App
 41 42.4 20.4 1535 12 US-10-175-754-545 Sequence 545, App
 42 42.4 20.4 1535 12 US-10-176-480-545 Sequence 545, App
 43 42.4 20.4 1535 12 US-10-176-489-545 Sequence 545, App
 44 42.4 20.4 1535 12 US-10-176-754-545 Sequence 545, App
 45 42.4 20.4 1535 12 US-10-176-755-545 Sequence 545, App

ALIGNMENTS

RESULT 1
 US-09-712-363-30
 ; Sequence 30, Application US/09712363
 ; Patent No. US20020164588A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Eisenberg, David
 ; APPLICANT: Rotstein, Sergio H.
 ; APPLICANT: Marcotte, Edward M.
 ; TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND
 ; INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS
 ; FILE REFERENCE: 07419-032001
 ; CURRENT APPLICATION NUMBER: US/09/712,363
 ; CURRENT FILING DATE: 2000-11-13
 ; PRIOR APPLICATION NUMBER: PCT/US00/02246
 ; PRIOR FILING DATE: 2000-01-28
 ; PRIOR APPLICATION NUMBER: 60/179,531
 ; PRIOR FILING DATE: 2000-02-01
 ; PRIOR APPLICATION NUMBER: 60/117,844
 ; PRIOR FILING DATE: 1999-01-29
 ; PRIOR APPLICATION NUMBER: 60/118,206
 ; PRIOR FILING DATE: 1999-02-01
 ; PRIOR APPLICATION NUMBER: 60/126,593
 ; PRIOR FILING DATE: 1999-03-26
 ; PRIOR APPLICATION NUMBER: 60/134,093
 ; PRIOR FILING DATE: 1999-05-14
 ; PRIOR APPLICATION NUMBER: 60/134,092
 ; PRIOR FILING DATE: 1999-05-14
 ; PRIOR APPLICATION NUMBER: 60/165,124
 ; PRIOR FILING DATE: 1999-11-12
 ; PRIOR APPLICATION NUMBER: 60/165,086
 ; PRIOR FILING DATE: 1999-11-12
 ; NUMBER OF SEQ ID NOS: 292
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 30
 ; LENGTH: 3519
 ; TYPE: DNA
 ; ORGANISM: Mycobacterium tuberculosis
 US-09-712-363-30

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Query Match      81.5%; Score 169.6; DB 10; Length 3519;
Best Local Similarity 88.5%; Pred. No. 4e-39;
Matches 184; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1 TCAAGGAGAACGCTACGACCTGGCCCGGGTGGCGCTACAAAGTCAACAGAGAGCTCG 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 884 TCAAGGAGAACGCTACGACCTGGCCCGGGTGGCGCTACAAAGTCAACAGAGAGCTCG 943

QY 61 GCTTCGACGCGGCTGAGCGCGATCACCAGCTCGACGCTGACCGAGAGAGAGCTCGGCCA 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 944 GCGTGCATGTGCGCGAGCGCCATACGCTGCTGAGCGCTGACCGAGAGAGAGCTCGGCCA 1003

QY 121 CCATCGAGTACCTGGTGGCGCTGACGAGGCTGACGCCAGATGACCGTCCCGCGCGCA 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1004 CCATCGATATCTGGTCCGCTTGCACGAGGCTGACGACGATGACCGTCCCGCGCGCG 1063

QY 181 TCGAGGTGCCGCTGGAGACCGACGACAT 208
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1064 TCGAGGTGCCGCTGGAGAACCGACGACAT 1091

RESULT 2
US-10-156-761-4898
; Sequence 4898, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156.761
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
; LENGTH: 3543
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3543)
US-10-156-761-4898

Query Match      42.5%; Score 88.4; DB 14; Length 3543;
Best Local Similarity 67.8%; Pred. No. 4.3e-16;
Matches 141; Conservative 0; Mismatches 61; Indels 6; Gaps 1;

QY 1 TCAAGGAGAACGCTACGACCTGGCCCGGGTGGCGCTACAAAGTCAACAGAGAGCTCG 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 926 TCAACCGGAAGCGCTACGACCTGCGGAAGTGGCGCTACAAAGTCAACAGAGAGCTGG 985

QY 61 GCTTCGACGCGGCTGAGCGCGATCACCAGCTCGACGCTGACCGAGAGAGAGCTCGGCCA 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 986 G-----CGGCGAGCGCGCTGGACGCGCGGATCTTACCGCTCGAGGACATCATCTCGT 1039

QY 121 CCATCGAGTACCTGGTGGCGCTGACGAGGCTGACGCCAGATGACCGTCCCGCGCGCA 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1040 CCATCAAGTACCTGGTGAAGTGCACGCGCGGTGAGACCGGAGACCGTTCGCGACACGCA 1099

QY 181 TCGAGGTGCCGCTGGAGACCGACGACAT 208
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Db 1100 CCTGATCGTCTCGAGACCGACGACAT 1127

RESULT 3
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US-10-156-761-1
; Sequence 1, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156.761
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
; LENGTH: 9025608
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1

Query Match      42.5%; Score 88.4; DB 14; Length 9025608;
Best Local Similarity 67.8%; Pred. No. 3.1e-16;
Matches 141; Conservative 0; Mismatches 61; Indels 6; Gaps 1;

QY 1 TCAAGGAGAACGCTACGACCTGGCCCGGGTGGCGCTACAAAGTCAACAGAGAGCTCG 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 5970494 TCAACCGGAAGCGCTACGACCTGCGGAAGTGGCGCTACAAAGTCAACAGAGAGCTGG 5970553

QY 61 GCTTCGACGCGGCTGAGCGCGATCACCAGCTGACCGAGAGAGAGCTCGTCCGCCA 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 5970554 G-----CGGCGAGCGCGCTGGACGCGCGGATCTTACCGCTCGAGGACATCATCTCGT 5970607

QY 121 CCATCGAGTACCTGGTGGCGCTGACGAGGCTGACGCCAGATGACCGTCCCGCGCGCA 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 5970608 CGATCAAGTACCTGGTGAAGCTGCACGCGCGGTGAGACCGGAGACCGTTCGCGACACGCA 5970667

QY 181 TCGAGGTGCCGCTGGAGACCGACGACAT 208
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 5970668 CCTGATCGTCTCGAGACCGACGACAT 5970695

RESULT 4
US-09-738-626-547
; Sequence 547, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OKAZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
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Query Match	41.5%;	Score 86.4;	DB 12;	Length 5099;
Best Local Similarity	68.0%;	Prod. No. 1.6e-15;		
Matches 136;	Conservative	0;	Mismatches 61;	Indels 3; Gaps 1;
QY	9	AAGCGGTACGACTGGCCGCGGTGGGCGGCTCAAGGTCACAAAGAGAGCTGCGCGCTGCAC	68	
Db	1578	AAGCGGTACGACTGGCTCGGCTGGTCTGTACAGATCAACCGCAGCTGGCGCT---	1634	
QY	69	CGCGGTGAGCCGATCACAGCTGCACGAGGAGACGTCGTCGCGCACCATCGAG	128	
Db	1635	GGTGGGACACCGATGGTTTGATGACTCTTACTGAAGAGGACATCGCAACACCATCGAG	1694	
QY	129	TACCTGTGTGGCTTCGACGAGGGTCACCCACGAGTACCGTCGCCGCGCATCGAGGTG	188	
Db	1695	TACCTGTGTGGCTTCGACCGCAGGTGACCGGCTCATGACTTCTCCAAATGGTGAAGATC	1754	
QY	189	CCGGTGGAGACCGACGACAT	208	
Db	1755	CCAGTTCGAGACCGATGACAT	1774	

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? ERROR AFFILIATION NUMBER: 2001-12-19
? PRIOR FILING DATE: 2001-12-19
? NUMBER OF SEQ ID NOS: 14
? SOFTWARE: PatentIn version 3.1
? SEQ ID NO 5
? LENGTH: 5099
? TYPE: DNA
? ORGANISM: Corynebacterium glutamicum
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (702)..(4196)
? OTHER INFORMATION:
US-10-075-460-5

Query Match          41.5%; Score 86.4; DB 13; Length 5099;
Best Local Similarity 68.0%; Pred. No. 1.6e-15;
Matches 136; Conservative 0; Mismatches 61; Indels 3; Gaps 1;

Qy      9  AAGCGCTACGACCTGCCCGGGTGGCGCGCTACAAGTCTCAACAGAGAGCTCGCGCTGCAC 68
Db      1578  AAGCGCTACGACCTGGCTGCTGGCTGGCTTACAAAGTCAACCGCAAGCTCGCGCTT--- 1634
Qy      69  GCGGCTGAGCCGATCACCAGCTTCGACGCTGACCGAGGAAGAGCTGCTGCCACCATCGAG 128
Db      1635  GTGGCGACCAACAGATGGTTTGTATGACTCTTACTGAAGAGGACATCGCAACCATCATCGAG 1694
Qy      129  TACCTGGTGGCGCTGTCAGCAGGAGGTACGCCACGATGACCGTCCCGCGGCGCATCGAGTG 188
Db      129  TACCTGGTGGCGCTGTCAGCAGGAGGTACGCCACGATGACCGTCCCGCGGCGCATCGAGTG 188

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Db 1695 TACCTGGTGGCTGTGCACGAGGTGAGCGCGTCACTTCTCCAAATGGTGAAGAGATC 1754
QY 189 CCGGTGAGACCCGACGACAT 208
    || || ||||| |||||
Db 1755 CCAGTCGAGACCGATGACAT 1774

RESULT 13
US-09-738-626-1
; Sequence 1, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENO, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 1
; LENGTH: 3309400
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-1

Query Match 41.5%; Score 86.4; DB 10; Length 3309400;
Best Local Similarity 68.0%; Pred. No. 1.2e-15;
Matches 136; Conservative 0; Mismatches 61; Indels 3; Gaps 1;

QY 9 AAGCGCTACGACCTGGCGCGGTGAGCGGCTACAGGTCAACAAGAGCTCGGCGTGCAC 68
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 513789 AAGCGCTACGACCTGGCTGCGTGTGCTTACAGATCAACCGCAAGCTCGGCGTT--- 513845

QY 69 GCGGTGAGCGGATFACACAGCTCGAGCGTGCAGCGGAGGAGAGCTGCTGCCACCATCGAG 128
    | || | | || | | || | | || | | || | | || | | || | | || | |
Db 513846 GGTGCGGACCAAGATGTTGATCTTCTTACGAGGAGACATCGCAACCATCGAG 513905

QY 129 TACCTGGTGGCTGTGCACGAGGTGAGCGGCTGAGCGGATGACCGTCCCGCGGCGATCGAGTG 188
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 513906 TACCTGGTGGCTGTGCACGAGGTGAGCGGCTGAGCGGCTGATCTTCCAAATGGTGAAGAGATC 513965

QY 189 CCGGTGAGACCCGACGACAT 208
    || || ||||| |||||
Db 513966 CCAGTCGAGACCGATGACAT 513985

RESULT 14
US-10-156-761-5431
; Sequence 5431, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
```

```
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 5431
; LENGTH: 1389
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1389)
US-10-156-761-5431

Query Match 20.7%; Score 43; DB 14; Length 1389;
Best Local Similarity 54.2%; Pred. No. 0.0034;
Matches 110; Conservative 0; Mismatches 90; Indels 3; Gaps 1;

QY 3 AAGGAGAAGCGCTACGACCTGGCGCGGTGGCGCGCTACAAGGTCAACAAGAGCTCGGC 62
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 814 AACATGAAGCAGTACGACCAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTG 873
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 63 CTGACGCGCGGTGAGCGGATCACCAAGCTGCGAGCTGACCGGAGGAGAGAGCTGCTGCCACC 122
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 874 GAGCTGCGCGGAGTGGCGGCTGCG---CGAGAGAGTGTGCGGAGCGAGATCAACACCGC 930

QY 123 ATCGAGTACCTGTGCGCGTGCACGAGGTGACGCCACGATGACCGTCCCGGCGGCGATC 182
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 931 AAGCACAACTGGAGCACCACCAAGCTCGGCCAGATGGGCGCTCGAAGAGTACCTC 990

QY 183 GAGTGGCGGTGGAGACCGACGA 205
    ||||| ||||| ||||| |||||
Db 991 GAGATCCAGGCAAGACGTCGA 1013

RESULT 15
US-10-156-761-3629
; Sequence 3629, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 3629
; LENGTH: 11058
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(11058)
US-10-156-761-3629

Query Match 20.5%; Score 42.6; DB 14; Length 11058;
Best Local Similarity 51.3%; Pred. No. 0.004;
Matches 99; Conservative 0; Mismatches 94; Indels 0; Gaps 0;
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QY	11	CGCTAGCAGCCTGGCCGGGTGGCGCGCTACAAGTCTACAAGAGAGCTCGGCCCTGCACGC	70
Db	225	CGCGGGCGCCTCGACCCAGAGGCCCTCGACAAGGCGCTGGCACCAACTGCTGGAGCGGCA	284
QY	71	CGGTGACCGATCACCAGCTCGACGCTGACCGAGGAGAGCTCTCGCCCACTCATCGAGTA	130
Db	285	CGAGATCCTCGCACCCGCTAGCCCTGGACGGCAGAGCCGCTCCAGATCATCGACGC	344
QY	131	CTGTGTGGCTGCACGAGGGTACGCCACAGATGACCGTCCCGCGCGCATCGAGGTGC	190
Db	345	CGCGGCCCTCGCCCTGGACCGTCCGGGGCCGGACGACGACGGGTCCGCGCCT	404
QY	191	GGTGGAGACCGAC	203
Db	405	GGTCGAGGCGGAC	417

Search completed: September 17, 2003, 13:07:16
Job time : 127.259 secs

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OM nucleic - nucleic search, using sw model

Run on: September 17, 2003, 11:54:34 ; Search time 30.1105 Seconds
(without alignments)
3049.028 Million cell updates/sec

Title: US-09-697-123B-16
Perfect score: 208
Sequence: 1 tcaaggagaagcgctacgac.....ccggtgaacgcgacacat 208

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA: *
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5: /cgn2_6/ptodata/1/ina/PTCOMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	208	100.0	970	1	US-08-250-030-1
2	208	100.0	970	5	US-08-250-030-1
3	208	100.0	4403765	3	US-09-103-840A-2
4	208	100.0	4411529	3	US-09-103-840A-1
5	148.8	71.5	3447	2	US-08-313-185-57
6	148.8	71.5	3447	3	US-08-313-185-57
7	38.6	18.6	924	4	US-09-082-614A-57
8	38.6	18.6	939	4	US-09-252-991A-969
9	38.2	18.4	768	4	US-09-252-991A-925
10	37.2	17.9	1412	1	US-08-097-831-1
11	37.2	17.9	1452	4	US-09-252-991A-13650
12	37.2	17.9	1980	4	US-09-252-991A-13782
13	37.2	17.9	6085	3	US-09-029-603-4
14	36.4	17.5	258	4	US-09-252-991A-13457
15	36.4	17.5	615	4	US-09-252-991A-13899
16	36.4	17.5	1695	4	US-09-252-991A-13695
17	36	17.3	870	4	US-09-252-991A-7157
18	36	17.3	2415	4	US-09-252-991A-7480
19	36	17.3	2667	4	US-09-252-991A-7216
20	35.2	16.9	1326	4	US-09-252-991A-10931
21	35.2	16.9	2211	4	US-09-252-991A-11256
22	35.2	16.9	2289	4	US-09-252-991A-10995
23	34.6	16.6	1621	1	US-08-722-001-13
24	34.6	16.6	1776	1	US-08-722-001-29
25	34.6	16.6	2002	4	US-09-016-434-1172
26	34.6	16.6	2140	1	US-08-334-698-1
27	34.6	16.6	2140	1	US-08-228-932-1

28 34.6 16.6 2140 1 US-08-468-939-1 Sequence 1, Appli
29 34.6 16.6 2140 2 US-08-406-855A-1 Sequence 1, Appli
30 34.6 16.6 2140 3 US-08-722-190-1 Sequence 1, Appli
31 34.6 16.6 2140 3 US-08-244-384-1 Sequence 1, Appli
32 34.6 16.6 2140 3 US-09-206-899-1 Sequence 1, Appli
33 34.6 16.6 2140 4 US-09-444-783-1 Sequence 1, Appli
34 34.6 16.6 2140 4 US-09-688-415-1 Sequence 1, Appli
35 34.6 16.6 2140 5 PCT-US95-04203-1 Sequence 1, Appli
36 34.4 16.5 1894 3 US-09-329-350-32 Sequence 32, Appli
37 34.4 16.5 30001 1 US-08-125-488-1 Sequence 1, Appli
38 34.4 16.5 30001 2 US-08-474-933-1 Sequence 1, Appli
39 34 16.3 680 4 US-09-556-877-267 Sequence 267, App
40 34 16.3 680 4 US-09-620-412C-267 Sequence 267, App
41 34 16.3 680 4 US-09-598-419-267 Sequence 267, App
42 34 16.3 1716 4 US-09-252-991A-1306 Sequence 1306, Ap
43 34 16.3 1788 4 US-09-252-991A-1395 Sequence 1395, Ap
44 34 16.3 1980 4 US-09-252-991A-1160 Sequence 1160, Ap
45 33.8 16.2 894 4 US-09-252-991A-10907 Sequence 10907, A

ALIGNMENTS

RESULT 1
US-08-250-030-1
; Sequence 1, Application US/08250030
; Patent No. 5643723
; GENERAL INFORMATION:
; APPLICANT: Persing, David H.
; TITLE OF INVENTION: Detection of a Genetic Locus Encoding
; TITLE OF INVENTION: Resistance to Rifampin in Mycobacterial Cultures and in
; TITLE OF INVENTION: Clinical Specimens
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Schwegman, Lundberg & Woessner
; STREET: 3500 IDS Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/250,030
; FILING DATE: 26-MAY-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Muetting, Ann M.
; REGISTRATION NUMBER: 33,977
; REFERENCE/DOCKET NUMBER: 150.105US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-339-0331
; TELEFAX: 612-339-3061
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 970 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-250-030-1

Query Match 100.0%; Score 208; DB 1; Length 970;
Best Local Similarity 100.0%; Pred. No. 3.6e-48;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAGGAGAGCGCTACGACCTGCGCTCGCTATAGGTCACACAGAGCTCG 60
|||||
DB 26 TCAAGGAGAGCGCTACGACCTGCGCTCGCTATAGGTCACACAGAGCTCG 85

QY 61 GGCTGATGTCGGCGAGCCCATCAGCTCGCTGACGCTGACCAAGAGAGAGCTGCTGGCCA 120
Db 86 GGCTGATGTCGGCGAGCCCATCAGCTCGCTGACGCTGACCAAGAGAGAGCTGCTGGCCA 145
QY 121 CCATCGAATATCTGTCGGTTCGACGAGGTCAGACCAAGATGACCGTTCCGGGCGGCG 180
Db 146 CCATCGAATATCTGTCGGTTCGACGAGGTCAGACCAAGATGACCGTTCCGGGCGGCG 205
QY 181 TCGAGTCCGCTGGAACCGACGACAT 208
Db 206 TCGAGTCCGCTGGAACCGACGACAT 233

RESULT 2

PCT-US95-06790-1
; Sequence 1, Application PC/TUS9506790
; GENERAL INFORMATION:
; APPLICANT: Mayo Foundation for Medical Education and Research
; APPLICANT: and Hoffmann-La Roche Inc.
; TITLE OF INVENTION: Detection of a Genetic Locus Encoding
; TITLE OF INVENTION: Resistance to Rifampin
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg & Woessner
; STREET: 3500 IDS Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/06790
; FILING DATE: 26-MAY-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Raasch, Kevin W.
; REGISTRATION NUMBER: 35,651
; REFERENCE/DOCKET NUMBER: 150.105W01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-339-0331
; TELEFAX: 612-339-3061
; INFORMATION FOR SEQ. ID NO. 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 970 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
PCT-US95-06790-1

Query Match 100.0%; Score 208; DB 5; Length 970;
Best Local Similarity 100.0%; Pred. No. 3.6e-48;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCAGGAGAGCCCTACGACCTGGCCCGCTGCTGCTATAGCTACAGAGAGCTCG 60
Db 26 TCAAGGAGAGCCCTACGACCTGGCCCGCTGCTGCTATAGCTACAGAGAGCTCG 85
QY 61 GGCTGATGTCGGCGAGCCCATCAGCTCGCTGACGCTGACCAAGAGAGCTGCTGGCCA 120
Db 86 GGCTGATGTCGGCGAGCCCATCAGCTCGCTGACGCTGACCAAGAGAGCTGCTGGCCA 145
QY 121 CCATCGAATATCTGTCGGTTCGACGAGGTCAGACCAAGATGACCGTTCCGGGCGGCG 180
Db 146 CCATCGAATATCTGTCGGTTCGACGAGGTCAGACCAAGATGACCGTTCCGGGCGGCG 205
QY 181 TCGAGTCCGCTGGAACCGACGACAT 208
Db 206 TCGAGTCCGCTGGAACCGACGACAT 233

RESULT 3

US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match 100.0%; Score 208; DB 3; Length 4403765;
Best Local Similarity 100.0%; Pred. No. 1.5e-47;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCAGGAGAGAGCCCTACGACCTGGCCCGCTGCTGCTATAGCTACAGAGAGCTCG 60
Db 762648 TCAGGAGAGAGCCCTACGACCTGGCCCGCTGCTGCTATAGCTACAGAGAGCTCG 762707
QY 61 GGCTGATGTCGGCGAGCCCATCAGCTCGCTGACGCTGACCAAGAGAGCTGCTGGCCA 120
Db 762708 GGCTGATGTCGGCGAGCCCATCAGCTCGCTGACGCTGACCAAGAGAGCTGCTGGCCA 762767
QY 121 CCATCGAATATCTGTCGGTTCGACGAGGTCAGACCAAGATGACCGTTCCGGGCGGCG 180
Db 762768 CCATCGAATATCTGTCGGTTCGACGAGGTCAGACCAAGATGACCGTTCCGGGCGGCG 762827
QY 181 TCGAGTCCGCTGGAACCGACGACAT 208
Db 762828 TCGAGTCCGCTGGAACCGACGACAT 762855

RESULT 4

US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match 100.0%; Score 208; DB 3; Length 4411529;

Best Local Similarity 100.0%; Pred. No. 1.5e-47;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAGGAGAGCGCTACGACCTGGCCCGCTCGCTGCTATAGGTCAACAGAGCTCG 60
760688 TCAAGGAGAGCGCTACGACCTGGCCCGCTCGCTGCTATAGGTCAACAGAGCTCG 760747

QY 61 GCTCATATCTGCTGAGCCCATCAGTGTGCTGAGCCGAGAGAGAGCTGCGCCA 120
760748 GCTCATATCTGCTGAGCCCATCAGTGTGCTGAGCCGAGAGAGAGCTGCGCCA 760807

QY 121 CCATCGATATCTGCTGAGCCCATCAGTGTGCTGAGCCGAGAGAGAGCTGCGGCCG 180
760808 CCATCGATATCTGCTGAGCCCATCAGTGTGCTGAGCCGAGAGAGAGCTGCGGCCG 760867

QY 181 TCGAGGTCCGGTGGAAACCGACGACAT 208
760868 TCGAGGTCCGGTGGAAACCGACGACAT 760895

RESULT 5
US-08-313-185-57
; Sequence 57, Application US/08313185
; Patent No. 5851763
; GENERAL INFORMATION:
; APPLICANT: Heym, Beate
; APPLICANT: Cole, Stewart
; APPLICANT: Young, Douglas
; APPLICANT: Zhang, Ying
; APPLICANT: Honore, Nadine
; APPLICANT: Telenti, Amalio
; APPLICANT: Bodmer, Thomas
; TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
; TITLE OF INVENTION: in Mycobacterium Tuberculosis
; NUMBER OF SEQUENCES: 66
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/313,185
; FILING DATE: 12-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 02356.0068-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3447 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-313-185-57

Query Match 71.5%; Score 148.8; DB 2; Length 3447;
Best Local Similarity 82.2%; Pred. No. 6.4e-32;
Matches 171; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 1 TCAAGGAGAGCGCTACGACCTGGCCCGCTCGCTGCTATAGGTCAACAGAGCTCG 60

Db 809 TCAAGGAGAGCGCTACGACCTGGCCCGCTCGCTGCTATAGGTCAACAGAGCTCG 868

QY 61 GCTCATATCTGCTGAGCCCATCAGTGTGCTGAGCCGAGAGAGAGCTGCGCCA 120

Db 869 GCTTCAGCGCGCTGAGTTGATACGTGCTCCAGCTGACCGAAGAGGATGCTGCGCCA 928

QY 121 CCATCGATATCTGCTGAGCCCATCAGTGTGCTGAGCCGAGAGAGAGCTGCGGCCG 180

Db 929 CCATAGAGTACCTGGTTCGCTGCTGAGGAGGTGAGTCAACATGACTGTCCCGAGGTGGG 988

QY 181 TCGAGGTCCGGTGGAAACCGACGACAT 208

Db 989 TAGAGTGGCACTGGAACTGACGATAT 1016

RESULT 6
US-09-082-614A-57
; Sequence 57, Application US/09082614A
; Patent No. 6124098
; GENERAL INFORMATION:
; APPLICANT: Heym, Beate
; APPLICANT: Cole, Stewart
; APPLICANT: Young, Douglas
; APPLICANT: Zhang, Ying
; APPLICANT: Honore, Nadine
; APPLICANT: Telenti, Amalio
; APPLICANT: Bodmer, Thomas
; TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
; TITLE OF INVENTION: in Mycobacterium Tuberculosis
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/082,614A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/313,185
; FILING DATE: 12-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 02356.0068-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3447 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-082-614A-57

Query Match 71.5%; Score 148.8; DB 3; Length 3447;
Best Local Similarity 82.2%; Pred. No. 6.4e-32;
Matches 171; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 1 TCAAGGAGAGCGCTACGACCTGGCCCGCTCGCTGCTATAGGTCAACAGAGCTCG 60

Db 809 TCAAGGAGAAACGCTAGACCTGGCCAGGTTGGTCTTACAAAGGTCACAAAGAAAGCTCG 868
QY 61 GGTGTCATGTGGCGAGCCCATACGTGTCGACGCTGACCGAGAGAGAGAGCTGCTGGCCA 120
Db 869 GGTTCACCGCGGTGAGTTGATCAGCTGCTCCACGCTGACCGAGAGAGATGCTGTCGCCA 928
QY 121 CCATCGAATATCTGCTCGCTGTCACGAGGGTCAGACACCATGACCGTTCGCGGGGGG 180
Db 929 CCAAGAGTACTGTTGCTGCTGATGAGGTCAGTCGACATGACTGTCCAGGTGGGG 988
QY 181 TCGAGTGGCGGTGGAACGAGACAT 208
Db 989 TAGAAGTGGCAGTGAAGAACTGACGATAT 1016

RESULT 7

US-09-252-991A-969
; Sequence 969, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 969
; LENGTH: 924
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-969

Query Match 18.6%; Score 38.6; DB 4; Length 924;
Best Local Similarity 51.4%; Pred. No. 0.061;
Matches 89; Conservative 0; Mismatches 84; Indels 0; Gaps 0;
QY 17 CGACCTGGCCGCGTCTGCTATTAAGTCAACAAAGAGCTCGGGCTGCTATCGCGCA 76
Db 597 CGACCGCTGCGCGTCTGCTCGACCCGCGAGGCGGTGCGCGCGACCTGCTGAG 656
QY 77 GCCATCAGCTGCTGACGCTGACCGAGAGAGAGCTGCTGCGCCACCATCGAATATCTGTT 136
Db 657 CACGAGCTGTGGCTCGATGGCGCAGGAGAGAGCGCCGCGGCATCGCCCTGTT 716
QY 137 CCGTTGCAAGGGTCAACACCATGACCGTTCGCGCGCGCTCGAGGTGC 189
Db 717 CCGTCCCTACAGGTGAACGCGCGTTCGATGGGGCGCGCGACGATGTAC 769

RESULT 8

US-09-252-991A-925
; Sequence 925, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 925
; LENGTH: 939
; TYPE: DNA

; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-925
Query Match 18.6%; Score 38.6; DB 4; Length 939;
Best Local Similarity 51.4%; Pred. No. 0.061;
Matches 89; Conservative 0; Mismatches 84; Indels 0; Gaps 0;
QY 17 CGACCTGGCCGCGTCTGCTATTAAGTCAACAAAGAGCTCGGGCTGCTATCGCGCA 76
Db 604 CGACCGCTGCGCGTCTGCTCGACCCGCGAGGCGGTGCGCGCGACCTGTTGAG 663
QY 77 GCCATCAGCTGCTGACGCTGACCGAGAGAGAGCTGCTGCGCCACCATCGAATATCTGTT 136
Db 664 CACGAGCTGTGGCTCGATGGCGCAGGAAGAGAGCGCGCGCATCGCCCTGTT 723
QY 137 CCGTTGCAAGGGTCAACACCATGACCGTTCGCGCGCGCTCGAGGTGC 189
Db 724 CCGTCCCTACAGGTGAACGCGCGTTCGATGGGGCGCGCGACGATGTAC 776

RESULT 9

US-09-252-991A-1114/3
; Sequence 1114, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 1114
; LENGTH: 768
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1114

Query Match 18.4%; Score 38.2; DB 4; Length 768;
Best Local Similarity 51.5%; Pred. No. 0.076;
Matches 88; Conservative 0; Mismatches 83; Indels 0; Gaps 0;
QY 17 CGACCTGGCCGCGTCTGCTATTAAGTCAACAAAGAGCTCGGGCTGCTATCGCGCA 76
Db 172 CGACCGCTGCGCGTCTGCTCGGACCCGCGAGGCGGTGCGCGCGACCTGTTGAG 113
QY 77 GCCATCAGCTGCTGACGCTGACCGAGAGAGAGCTGCTGCGCCACCATCGAATATCTGTT 136
Db 112 CACGAGCTGTGGCTCGATGGCGCAGGAAGAGCGCGCGCATCGCCCTGTT 53
QY 137 CCGTTGCAAGGGTCAACACCATGACCGTTCGCGCGCGCTCGAGGT 187
Db 52 CCGTCCCTACAGGTGAACGCGCGTTCGATGGGGCGCGCGACGATGT 2

RESULT 10

US-08-097-831-1
; Sequence 1, Application US/08097831.
; Patent No. 5510473
; GENERAL INFORMATION:
; APPLICANT: Camerini-Otero, Rafael D.
; APPLICANT: Angov, Evangelina
; TITLE OF INVENTION: Cloning and Expression of Taq reca
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KNOBBE, MARTENS, OLSON AND BEAR
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA

COUNTRY: USA
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/097,831
FILING DATE: 19930726
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E.
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: NIH066.001A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
TELEFAX: 714-760-9502
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1412 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOPHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: Taq reca
FEATURE:
NAME/KEY: CDS
LOCATION: 62..1082
US-08-097-831-1

Query Match 17.9%; Score 37.2; DB 1; Length 1412;
Best Local Similarity 53.4%; Pred. No. 0.16;
Matches 78; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY 50 CAGAGAGCTCGGGCTGATCGGGAGCGCCATCAGCTCGACGCTGACCGAGAGA 109
|||||
DB 370 CAGAGAGCTCGGGGTGACGTCTGCTGCTCCCGACCGGACCGGGAGCA 429
|||||
QY 110 CTTGCTGGCCACCATCGAATATCTGGTTCGACGAGGTCAGACCATGACCGT 169
|||||
DB 430 GCGTTGGAGATCGTGAGCTTCTGCGCGCTCGGGGGCGGTGAGCTGATGTTGA 489
|||||
QY 170 TCGGGCGCGCTCGAGTGCCTGGTGG 195
|||||
DB 490 TTCGTGGCGCTTGTGTTGCCAAGG 515
|||||

RESULT 11
US-09-252-991A-13650/C
; Sequence 13650, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; LENGTH: 1452
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13650

Query Match 17.9%; Score 37.2; DB 4; Length 1452;
Best Local Similarity 56.8%; Pred. No. 0.16;
Matches 69; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 13 GCTACGACCTGGCCCGCTGCTGCTATAGGTCAACAAGAGCTCGGGCTGCATGCG 72
|||||
DB 806 GCGCTACCTGCTGCTTCGAGAGCTTCGAGAGATCGCCCAATAACCTGCCCATGACG 747
|||||
QY 73 GCGAGCCCATCAGCTGCTGCGAGCTGACCGGAGAGAGCTGCTGGCCACCATGCAATATC 132
|||||
DB 746 ACGAGCAGCGCGAGGAGCGCTGGCGGCAATGTCGACGCTGGCGCCCTGGAAGC 687
|||||
QY 133 TG 134
|
DB 686 AG 685
|

RESULT 12
US-09-252-991A-13782
; Sequence 13782, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 13782
; LENGTH: 1980
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13782

Query Match 17.9%; Score 37.2; DB 4; Length 1980;
Best Local Similarity 56.8%; Pred. No. 0.17;
Matches 69; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 13 GCTACGACCTGGCCCGCTGCTGCTATAGGTCAACAAGAGCTCGGGCTGCATGCG 72
|||||
DB 1340 GCGCTACCTGCTGCTTCGAGAGCTTCGAGAGATCGCCCAATAACCTGCCCATGACG 1399
|||||
QY 73 GCGAGCCCATCAGCTGCTGCGAGCTGACCGGAGAGAGCTGCTGGCCACCATGCAATATC 132
|||||
DB 1400 ACGAGCAGCGCGAGGAGCGCTGGCGGCAATGTCGACGCTGGCGCCCTGGAAGC 1459
|||||
QY 133 TG 134
|
DB 1460 AG 1461
|

RESULT 13
US-09-029-603-4
; Sequence 4, Application US/09029603
; Patent No. 6210935
; GENERAL INFORMATION:
; APPLICANT: Schupp, Thomas
; APPLICANT: Engel, Natalie
; APPLICANT: Bietenhader, Jurg
; APPLICANT: Toupet, Christine
; APPLICANT: Pospelch, Andreas
; TITLE OF INVENTION: Staurosporin Biosynthesis Gene Clusters
; FILE REFERENCE: 4-20555/A/PCT
; CURRENT APPLICATION NUMBER: US/09/029,603
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: PCT/EP96/03643
; PRIOR FILING DATE: 1996-08-19
; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 6085
; TYPE: DNA
; ORGANISM: Streptomyces longisporoflavus
; FEATURE:
; NAME/KEY: misc_RNA
; LOCATION: (378)..(1665)
; OTHER INFORMATION: ORF
; FEATURE:
; NAME/KEY: misc_RNA
; LOCATION: (1747)..(2553)
; OTHER INFORMATION: ORF
; FEATURE:
; NAME/KEY: misc_RNA
; LOCATION: (2593)..(4011)
; OTHER INFORMATION: ORF
; FEATURE:
; NAME/KEY: misc_RNA
; LOCATION: (4013)..(4999)
; OTHER INFORMATION: ORF
; FEATURE:
; NAME/KEY: misc_RNA
; LOCATION: (5071)..(6085)
; OTHER INFORMATION: ORF
US-09-029-603-4

Query Match 17.8%; Score 37; DB 3; Length 6085;
Best Local Similarity 51.5%; Pred. No. 0.23; Indels 0; Gaps 0;
Matches 85; Conservative 0; Mismatches 80; Indels 0; Gaps 0;
QY 18 GACCTGGCCGGCTCGCTGCTATAGGTCAACAAGAGCTCGGGCTGCTATGTCGGCGAG 77
DB 1017 GAGTGGACCGCGCGCGGCGGACCGACGAGATGCTCACCTCTCTGTCGCGGCC 1076
QY 78 CCATCATGCTGCTGACCTGACCGAAGAGAGCTGCTGGCCACCATCGAATATCTGGTC 137
DB 1077 CGGGACACGGATCACCTGCTAGCGTGGAGCGGATCGTCGGCACCTCGTCCATCTGCTC 1136
QY 138 CGCTTCGACGAGGCTCAGACCATGACCGTTCGGGGCGGCTC 182
DB 1137 ACCGCGGCGCAGAGACCAACCACTGCTCGCCAGGGCGGTC 1181

RESULT 14
US-09-252-991A-13457/c
; Sequence 13457, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 13457
; LENGTH: 258
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13457

Query Match 17.5%; Score 36.4; DB 4; Length 258;
Best Local Similarity 56.8%; Pred. No. 0.2;
Matches 67; Conservative 0; Mismatches 51; Indels 0; Gaps 0;
QY 17 CGACCTGGCCGGCTCGCTGCTATAGGTCAACAAGAGCTCGGGCTGCTATGTCGGCGA 76
DB 258 CTACCTGTGCTTGAAGGCTTCGAGAAGATCGCCCAAAATACCTGCCCCCATGACGACGA 199

QY 77 GCCATCAGCTCGCTGAGCGTGCACGAGAGAGAGCTGTGGCCACCATGAATATCTG 134
DB 198 GCACGCCGACGAGGAGCGCTGGCGCCATGTCAGCTGGCCGCTGAAAGCAG 141
RESULT 15
US-09-252-991A-13899
; Sequence 13899, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 13899
; LENGTH: 615
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13899

Query Match 17.5%; Score 36.4; DB 4; Length 615;
Best Local Similarity 51.9%; Pred. No. 0.23; Indels 0; Gaps 0;
Matches 82; Conservative 0; Mismatches 76; Indels 0; Gaps 0;
QY 6 GAGAAGCGTACGACCTGGCCGCGCTCGCTGCTATAGGTCAACAAGAGCTCGGGCTG 65
DB 311 GCGAGTTCCTACAGGTCTCCTCGCGGCGAGCTCGGCGCGGACGCCCTCGGGCAG 370
QY 66 CATGTGGGAGCCCATCATCATGCTGTCAGCTGACCGAGAGAGAGCTGTCGTGGCCCATC 125
DB 371 ATCCTCGGCCCTCTCTTCCGCCAGAGAGATGGCCGACGTGATCGACAAGATCATCCAG 430
QY 126 GAATATCTGTCTCGCTTGCACGAGGGTTCAGACCATGAT 163
DB 431 GTCTAGCTGAACGCGGACCGAGAGAACCTTCAT 468

Search completed: September 17, 2003, 12:30:07
Job time : 42.1605 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 17, 2003, 11:54:34 : Search time 108.259 Seconds
(without alignments)
4726.283 Million cell updates/sec

Title: US-09-697-123B-16

Perfect score: 208

Sequence: 1 tcaagagaagcgtacgac.....ccgtggaacacgagacat 208

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1660708 seqs, 1229959015 residues

Total number of hits satisfying chosen parameters: 3321416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

- 1: /cgn2.6/ptodata/1/pubpna/us07_PUBCOMB.seq:*
- 2: /cgn2.6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2.6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2.6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2.6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2.6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2.6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2.6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2.6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2.6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2.6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2.6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2.6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2.6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2.6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 16: /cgn2.6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 17: /cgn2.6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	208	100.0	3519	10	US-09-712-363-30	Sequence 30, Appl
2	89.6	43.1	3495	10	US-09-738-626-547	Sequence 547, App
3	89.6	43.1	5096	10	US-09-984-711-5	Sequence 5, Appli
4	89.6	43.1	5099	10	US-09-887-052-1	Sequence 1, Appli
5	89.6	43.1	5099	10	US-09-887-052-3	Sequence 3, Appli
6	89.6	43.1	5099	10	US-09-887-052-5	Sequence 5, Appli
7	89.6	43.1	5099	12	US-10-076-406-1	Sequence 1, Appli
8	89.6	43.1	5099	12	US-10-076-406-3	Sequence 3, Appli
9	89.6	43.1	5099	12	US-10-076-406-5	Sequence 5, Appli
10	89.6	43.1	5099	13	US-10-075-460-5	Sequence 5, Appli
11	89.6	43.1	3309400	10	US-09-738-626-1	Sequence 1, Appli
12	67.6	32.5	3543	14	US-10-156-761-4898	Sequence 4898, Ap
13	67.6	32.5	9025608	14	US-10-156-761-1	Sequence 1, Appli
14	40.4	19.4	1215	14	US-10-156-761-2811	Sequence 2811, Ap
15	38.6	18.6	1131	14	US-10-156-761-2479	Sequence 2479, Ap
16	38.6	18.6	9025608	14	US-10-156-761-1	Sequence 1, Appli

c

17	38.2	18.4	1395	14	US-10-205-032-21	Sequence 21, Appl
18	38.2	18.4	60196	14	US-10-205-032-1	Sequence 1, Appl
19	36.4	17.5	588	14	US-10-156-761-5853	Sequence 5853, Ap
20	35.8	17.2	1509	12	US-09-967-484-84	Sequence 64, Appl
21	35.8	17.2	1509	12	US-09-967-484-88	Sequence 68, Appl
22	35.6	17.1	3756	9	US-09-841-132-425	Sequence 425, App
23	35.4	17.0	1461	14	US-10-156-761-2120	Sequence 2120, Ap
24	35	16.8	3774	14	US-10-156-761-2845	Sequence 2845, Ap
25	34.6	16.6	1458	14	US-10-156-761-4634	Sequence 4634, Ap
26	34.6	16.6	2130	14	US-10-225-587A-33	Sequence 33, Appl
27	34.6	16.6	2140	14	US-10-183-991-1	Sequence 1, Appl
28	34.6	16.6	2140	14	US-10-238-139-1	Sequence 1, Appl
29	34.6	16.6	2140	14	US-10-238-667-1	Sequence 32, Appl
30	34.4	16.5	1894	8	US-08-841-636A-32	Sequence 32, Appl
31	34.4	16.5	5721	14	US-10-156-761-2880	Sequence 2880, Ap
32	34.4	16.5	125746	14	US-10-156-761-15102	Sequence 15102, A
33	34.2	16.4	1191	14	US-10-156-761-1671	Sequence 1671, Ap
34	34.2	16.4	1398	14	US-10-156-761-2212	Sequence 2212, Ap
35	34.2	16.4	2334	14	US-10-156-761-5079	Sequence 5079, Ap
36	34	16.3	680	9	US-09-841-132-267	Sequence 267, App
37	34	16.3	993	14	US-10-156-761-4673	Sequence 4673, Ap
38	34	16.3	1509	14	US-10-156-761-1592	Sequence 1592, Ap
39	34	16.3	1596	14	US-10-156-761-4136	Sequence 4136, Ap
40	33.8	16.2	723	14	US-10-156-761-6797	Sequence 6797, Ap
41	33.8	16.2	1029	14	US-10-156-761-5440	Sequence 5440, Ap
42	33.8	16.2	1284	14	US-10-156-761-5434	Sequence 5434, Ap
43	33.8	16.2	2715	14	US-10-156-761-2245	Sequence 2245, Ap
44	33.8	16.2	5418	14	US-10-156-761-5959	Sequence 5959, Ap
45	33.6	16.2	825	14	US-10-156-761-2303	Sequence 2303, Ap

ALIGNMENTS

RESULT 1
US-09-712-363-30
; Sequence 30, Application US/09712363
; Patent No. US20020164588A1
; GENERAL INFORMATION:
; APPLICANT: Eisenberg, David
; APPLICANT: Rotstein, Sergio H.
; APPLICANT: Marcotte, Edward M.
; TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND
; TITLE OF INVENTION: INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS
; FILE REFERENCE: 07419-032001
; CURRENT APPLICATION NUMBER: US/09/712,363
; CURRENT FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: PCT/US00/02246
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,531
; PRIOR FILING DATE: 2000-02-01
; PRIOR APPLICATION NUMBER: 60/117,844
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/118,206,
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: 60/126,593
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/134,093
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/134,092
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/165,124
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/165,086
; PRIOR FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 3519
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-09-712-363-30

Query Match 100.0%; Score 208; DB 10; Length 3519;
Best Local Similarity 100.0%; Pred. No. 4e-58;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAGGAGAGCGGTACGACCTGGCCCGCGTGGCTATAGGTCAACAAGAGCTCG 60
DB 884 TCAGGAGAGCGGTACGACCTGGCCCGCGTGGCTATAGGTCAACAAGAGCTCG 943

QY 61 GCTCATCTCGGCGAGCCCATACGCTCGTCCAGCGTACCGAAGAGCGTCTGGCCA 120
DB 944 GCTCATCTCGGCGAGCCCATACGCTCGTCCAGCGTACCGAAGAGCGTCTGGCCA 1003

QY 121 CCATCGAATATCTGCTCCGCTTGCACGAGGFTCAACACGATGACCGTTCGGCGGCG 180
DB 1004 CCATCGAATATCTGCTCCGCTTGCACGAGGFTCAACACGATGACCGTTCGGCGGCG 1063

QY 181 TCGAGTGCCTGGTGGAAACCGAGCAT 208
DB 1064 TCGAGTGCCTGGTGGAAACCGAGCAT 1091

RESULT 2
US-09-738-626-547
; Sequence 547, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENO, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: Patent in ver. 3.0
; SEQ ID NO 547
; LENGTH: 3495
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-547

Query Match 43.1%; Score 89.6; DB 10; Length 3495;
Best Local Similarity 69.0%; Pred. No. 1.6e-19;
Matches 138; Conservative 0; Mismatches 59; Indels 3; Gaps 1;

QY 9 AAGCGTACGACCTGGCCCGCGTGGCTATAGGTCAACAAGAGCTCGGCTGCAT 68
DB 877 AAGCGTACGACCTGGCCCGCGTGGCTATAGGTCAACAAGAGCTCGGCTGCAT 933

QY 69 GTGGGAGAGCCCATCAGCTCGTCCAGCGTACCGAAGAGAGCGTGGGCCACCATCGAA 128
DB 934 GTGGGAGAGCCCATCAGCTCGTCCAGCGTACCGAAGAGAGCGTGGGCCACCATCGAG 993

QY 129 TATCTGCTCGGCTTCAGAGGFTCAACAAGAGCGTTCGGCGGCGCTCGAGGTG 188
DB 994 TATCTGCTCGGCTTCAGAGGFTCAACAAGAGCGTTCGGCGGCGCTCGAGGTG 1053

QY 189 CCGGTGGAACCGAGCAT 208
DB 1054 CCGGTGGAACCGAGCAT 1073

RESULT 3
US-09-984-711-5
; Sequence 5, Application US/09984711
; Patent No. US20020119549A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: STEPHAN, Hans
; APPLICANT: KREUTZER, Caroline
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE rpsL GENE
; FILE REFERENCE: 204209US0
; CURRENT APPLICATION NUMBER: US/09/984,711
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: DE10108230.9
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 5
; LENGTH: 5096
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
; OTHER INFORMATION:
US-09-984-711-5

Query Match 43.1%; Score 89.6; DB 10; Length 5096;
Best Local Similarity 69.0%; Pred. No. 1.6e-19;
Matches 138; Conservative 0; Mismatches 59; Indels 3; Gaps 1;

QY 9 AAGCGTACGACCTGGCCCGCGTGGCTATAGGTCAACAAGAGCTCGGCTGCAT 68
DB 1578 AAGCGTACGACCTGGCCCGCGTGGCTATAGGTCAACAAGAGCTCGGCTGCAT 1634

QY 69 GTGGGAGAGCCCATCAGCTCGTCCAGCGTACCGAAGAGAGCGTGGGCCACCATCGAA 128
DB 1635 GTGGGAGAGCCCATCAGCTCGTCCAGCGTACCGAAGAGAGCGTGGGCCACCATCGAG 1694

QY 129 TATCTGCTCGGCTTCAGAGGFTCAACAAGAGCGTTCGGCGGCGCTCGAGGTG 188
DB 1695 TATCTGCTCGGCTTCAGAGGFTCAACAAGAGCGTTCGGCGGCGCTCGAGGTG 1754

QY 189 CCGGTGGAACCGAGCAT 208
DB 1755 CCGGTGGAACCGAGCAT 1774

RESULT 4
US-09-887-052-1
; Sequence 1, Application US/09887052
; Patent No. US20020119537A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE rpoB GENE
; FILE REFERENCE: 204212US0X
; CURRENT APPLICATION NUMBER: US/09/887,052
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: DE10107229.5
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 1
; LENGTH: 5099

; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
US-09-887-052-1

Query Match 43.1%; Score 89.6; DB 10; Length 5099;
Best Local Similarity 69.0%; Pred. No. 1.6e-19;
Matches 138; Conservative 0; Mismatches 59; Indels 3; Gaps 1;

QY 9 AAGCGCTACGACTGGCCGGCTGCGTCTATAGGTCACCAAGAGCTCGGGCTGCAT 68
DB 1578 AAGCGCTACGACTGGCTGGCTGCTACAGTCAACCCAGCTCGGCT---T 1634

QY 69 GTCGGGAGCCCATCAGCTGCTGACGCTGACGAGAGAGAGCTGCTGGCCACCATCGAA 128
DB 1635 GGTGGGACACGATGGTTGATGACTCTTACTGAAGAGGACATCGCAACCATCGAG 1694

QY 129 TATCTGCTCGCTTCACGAGGTCAGACACGATCCGCTTCGGGGCGCTCGAGTG 188
DB 1695 TACCTGGTGGCTCGACGAGTGAGCGGCTCATGACTTCTCCAAATGGTGAAGATC 1754

QY 189 CCGGTGGAACCGACGACAT 208
DB 1755 CCAGTCGAGACCGATGACAT 1774

RESULT 5
US-09-887-052-3
; Sequence 3, Application US/09887052
; Patent No. US20020119537A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE rpoB GENE
; FILE REFERENCE: 204212USOX
; CURRENT APPLICATION NUMBER: US/09/887,052
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: DE10107229.5
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 5099
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
US-09-887-052-3

Query Match 43.1%; Score 89.6; DB 10; Length 5099;
Best Local Similarity 69.0%; Pred. No. 1.6e-19;
Matches 138; Conservative 0; Mismatches 59; Indels 3; Gaps 1;

QY 9 AAGCGCTACGACTGGCCGGCTGCGTCTATAGGTCACCAAGAGCTCGGGCTGCAT 68
DB 1578 AAGCGCTACGACTGGCTGGCTGCTACAGTCAACCCAGCTCGGCT---T 1634

QY 69 GTCGGGAGCCCATCAGCTGCTGACGCTGACGAGAGAGAGCTGCTGGCCACCATCGAA 128
DB 1635 GGTGGGACACGATGGTTGATGACTCTTACTGAAGAGGACATCGCAACCATCGAG 1694

QY 129 TATCTGCTCGCTTCACGAGGTCAGACACGATCCGCTTCGGGGCGCTCGAGTG 188
DB 1695 TACCTGGTGGCTCGACGAGTGAGCGGCTCATGACTTCTCCAAATGGTGAAGATC 1754

QY 189 CCGGTGGAACCGACGACAT 208
DB 1755 CCAGTCGAGACCGATGACAT 1774

DB 1755 CCAGTCGAGACCGATGACAT 1774

RESULT 6
US-09-887-052-5
; Sequence 5, Application US/09887052
; Patent No. US20020119537A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE rpoB GENE
; FILE REFERENCE: 204212USOX
; CURRENT APPLICATION NUMBER: US/09/887,052
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: DE10107229.5
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 5099
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
US-09-887-052-5

Query Match 43.1%; Score 89.6; DB 10; Length 5099;
Best Local Similarity 69.0%; Pred. No. 1.6e-19;
Matches 138; Conservative 0; Mismatches 59; Indels 3; Gaps 1;

QY 9 AAGCGCTACGACTGGCCGGCTGCGTCTATAGGTCACCAAGAGCTCGGGCTGCAT 68
DB 1578 AAGCGCTACGACTGGCTGGCTGCTTACAGTCAACCCAGCTCGGCT---T 1634

QY 69 GTCGGGAGCCCATCAGCTGCTGACGCTGACGAGAGAGAGCTGCTGGCCACCATCGAA 128
DB 1635 GGTGGGAGCCCATGAGTTGATGACTCTTACTGAAGAGGACATCGCAACCATCGAG 1694

QY 129 TATCTGCTCGCTTCACGAGGTCAGACACGATCCGCTTCGGGGCGCTCGAGTG 188
DB 1695 TACCTGGTGGCTCGACGAGTGAGCGGCTCATGACTTCTCCAAATGGTGAAGATC 1754

QY 189 CCGGTGGAACCGACGACAT 208
DB 1755 CCAGTCGAGACCGATGACAT 1774

RESULT 7
US-10-076-406-1
; Sequence 1, Application US/10076406
; Publication No. US20030166884A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: Nucleotide sequences coding for the rpoB gene
; FILE REFERENCE: 219774USOXIP
; CURRENT APPLICATION NUMBER: US/10/076,406
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: DE 10107229.5
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 09/887052
; PRIOR FILING DATE: 2001-06-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 5099

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; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
; OTHER INFORMATION:
US-10-076-406-1

Query Match          43.1%; Score 89.6; DB 12; Length 5099;
Best Local Similarity 69.0%; Pred. No. 1.6e-19;
Matches 138; Conservative 0; Mismatches 59; Indels 3; Gaps 1;

QY 9 AACGCTACGACCTGGCCGCGTGCCTATAGCTCAACAAGAGCTCGGGCTGCAT 68
    |||||
DB 1578 AACGCTACGACCTGGCTGGCTTTGATGACTCTTACTGAGAGGACATCGAACCTCGGCT--T 1634
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QY 69 GTCCGCGAGCCATCAGCTCGTCGACGCTGACCGAAGAGAGCTGTCGCCACCATCGAA 128
    |||||
DB 1635 GGTGGCGACCAACGATGGTTGATGACTCTTACTGAGAGGACATCGAACCATCGAG 1694
    |||||
QY 129 TATCTGGTCCGCTTGCACGAGGTCAGACCATGATGACCTCCGGGGCGGCTCGAGTG 188
    |||||
DB 1695 TACCTGGTGGCTGTCACCGAGGTGAGCGCTCATGACTTCTCCAAATGGTGAAGAGATC 1754
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QY 189 CCGGTGGAACCGACGACAT 208
    |||||
DB 1755 CCAGTCGAGACCGATGACAT 1774
    |||||

RESULT 8
US-10-076-406-3
; Sequence 3, Application US/10076406
; Publication No. US20030166884A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: Nucleotide sequences coding for the rpoB gene
; FILE REFERENCE: 219774USOXCIP
; CURRENT APPLICATION NUMBER: US/10/076,406
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: DE 10107229.5
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 09/887052
; PRIOR FILING DATE: 2001-06-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 5099
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
; OTHER INFORMATION:
; NAME/KEY: mutation
; LOCATION: (1987)..(1987)
; OTHER INFORMATION: Substitution of adenine by thymine
; NAME/KEY: mutation
; LOCATION: (1288)..(1288)
; OTHER INFORMATION: Substitution of cytosine by thymine
; NAME/KEY: mutation
; LOCATION: (715)..(715)
; OTHER INFORMATION: Substitution of cytosine by thymine
US-10-076-406-3

Query Match          43.1%; Score 89.6; DB 12; Length 5099;
Best Local Similarity 69.0%; Pred. No. 1.6e-19;
Matches 138; Conservative 0; Mismatches 59; Indels 3; Gaps 1;

QY 9 AACGCTACGACCTGGCCGCGTGCCTATAGCTCAACAAGAGCTCGGGCTGCAT 68
    |||||
DB 1578 AACGCTACGACCTGGCTGGCTTTGATGACTCTTACTGAGAGGACATCGAACCTCGGCT--T 1634
    |||||
QY 69 GTCCGCGAGCCATCAGCTCGTCGACGCTGACCGAAGAGAGCTGTCGCCACCATCGAA 128
    |||||
DB 1635 GGTGGCGACCAACGATGGTTGATGACTCTTACTGAGAGGACATCGAACCATCGAG 1694
    |||||
QY 129 TATCTGGTCCGCTTGCACGAGGTCAGACCATGATGACCTCCGGGGCGGCTCGAGTG 188
    |||||
DB 1695 TACCTGGTGGCTGTCACCGAGGTGAGCGCTCATGACTTCTCCAAATGGTGAAGAGATC 1754
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QY 189 CCGGTGGAACCGACGACAT 208
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DB 1755 CCAGTCGAGACCGATGACAT 1774
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RESULT 9
US-10-076-406-5
; Sequence 5, Application US/10076406
; Publication No. US20030166884A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: Nucleotide sequences coding for the rpoB gene
; FILE REFERENCE: 219774USOXCIP
; CURRENT APPLICATION NUMBER: US/10/076,406
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: DE 10107229.5
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 09/887052
; PRIOR FILING DATE: 2001-06-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 5099
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
; OTHER INFORMATION:
; NAME/KEY: mutation
; LOCATION: (2016)..(2016)
; OTHER INFORMATION: Substitution of cytosine by thymine
US-10-076-406-5

Query Match          43.1%; Score 89.6; DB 12; Length 5099;
Best Local Similarity 69.0%; Pred. No. 1.6e-19;
Matches 138; Conservative 0; Mismatches 59; Indels 3; Gaps 1;

QY 9 AACGCTACGACCTGGCCGCGTGCCTATAGCTCAACAAGAGCTCGGGCTGCAT 68
    |||||
DB 1578 AACGCTACGACCTGGCTGGCTTTGATGACTCTTACTGAGAGGACATCGAACCTCGGCT--T 1634
    |||||
QY 69 GTCCGCGAGCCATCAGCTCGTCGACGCTGACCGAAGAGAGCTGTCGCCACCATCGAA 128
    |||||
DB 1635 GGTGGCGACCAACGATGGTTGATGACTCTTACTGAGAGGACATCGAACCATCGAG 1694
    |||||
QY 129 TATCTGGTCCGCTTGCACGAGGTCAGACCATGATGACCTCCGGGGCGGCTCGAGTG 188
    |||||
DB 1695 TACCTGGTGGCTGTCACCGAGGTGAGCGCTCATGACTTCTCCAAATGGTGAAGAGATC 1754
    |||||
QY 189 CCGGTGGAACCGACGACAT 208
    |||||
DB 1755 CCAGTCGAGACCGATGACAT 1774
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RESULT 10
US-10-075-460-5
; Sequence 5, Application US/10075460
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; Publication No. US2002015557A1
; GENERAL INFORMATION:
; APPLICANT: MCKEL, BETTINA
; APPLICANT: BATHE, BRIGITTE
; APPLICANT: HANS, STEFAN
; APPLICANT: KREUTZER, CAROLINE
; APPLICANT: HERMANN, THOMAS
; APPLICANT: PFEFFERLE, WALTER
; APPLICANT: BINDER, MICHAEL
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE rpsL GENE
; FILE REFERENCE: 218472USOX
; CURRENT FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: DE 10107230.9
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: DE 10162386.0
; PRIOR FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 5099
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
; OTHER INFORMATION:
US-10-075-460-5

Query Match 43.1%; Score 89.6; DB 13; Length 5099;
Best Local Similarity 69.0%; Pred. No. 1.6e-19;
Matches 138; Conservative 0; Mismatches 59; Indels 3; Gaps 1;

QY 9 AAGCCTACGACCTGGCCCGCGTCGCTATAGGTCAACAGAGCTCGGCTGCAT 68
DB 1578 AAGCCTACGACCTGGCCCGCGTCGCTATAGGTCAACAGAGCTCGGCTGCAT 1634
QY 69 GTCGGCGAGCCATCAGCTGCTGACCGAGAGACGCTGCGCCACCATCGAA 128
DB 1635 GTGGCGGACCATGCTGTTGATGACTCTTACTGAGAGGACATCGCAACCATCGAG 1694
QY 129 TATCTGGTCCGCTGACAGAGGTGACACGATGACCGTTCGGGGCGGCTCGAGTG 188
DB 1695 TACCTGGTGGCTGCTGACGAGGTGAGCGCTCATGACTTCTCCAAATGGTGAAGATC 1754
QY 189 CCGGTGGAACCGACGACAT 208
DB 1755 CCAGTCGAGACCGATGACAT 1774

RESULT 11
US-09-738-626-1
; Sequence 1, Application US/09738626
; Publication No. US20020197603A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOL, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07

; Publication No. US2002015557A1
; GENERAL INFORMATION:
; APPLICANT: MCKEL, BETTINA
; APPLICANT: BATHE, BRIGITTE
; APPLICANT: HANS, STEFAN
; APPLICANT: KREUTZER, CAROLINE
; APPLICANT: HERMANN, THOMAS
; APPLICANT: PFEFFERLE, WALTER
; APPLICANT: BINDER, MICHAEL
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE rpsL GENE
; FILE REFERENCE: 218472USOX
; CURRENT FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: DE 10107230.9
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: DE 10162386.0
; PRIOR FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 5099
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
; OTHER INFORMATION:
US-10-075-460-5

Query Match 43.1%; Score 89.6; DB 13; Length 5099;
Best Local Similarity 69.0%; Pred. No. 1.6e-19;
Matches 138; Conservative 0; Mismatches 59; Indels 3; Gaps 1;

QY 9 AAGCCTACGACCTGGCCCGCGTCGCTATAGGTCAACAGAGCTCGGCTGCAT 68
DB 1578 AAGCCTACGACCTGGCCCGCGTCGCTATAGGTCAACAGAGCTCGGCTGCAT 1634
QY 69 GTCGGCGAGCCATCAGCTGCTGACCGAGAGACGCTGCGCCACCATCGAA 128
DB 1635 GTGGCGGACCATGCTGTTGATGACTCTTACTGAGAGGACATCGCAACCATCGAG 1694
QY 129 TATCTGGTCCGCTGACAGAGGTGACACGATGACCGTTCGGGGCGGCTCGAGTG 188
DB 1695 TACCTGGTGGCTGCTGACGAGGTGAGCGCTCATGACTTCTCCAAATGGTGAAGATC 1754
QY 189 CCGGTGGAACCGACGACAT 208
DB 1755 CCAGTCGAGACCGATGACAT 1774

RESULT 12
US-10-156-761-4898
; Sequence 4898, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 4898
; LENGTH: 3543
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3543)
US-10-156-761-4898

Query Match 32.5%; Score 67.6; DB 14; Length 3543;
Best Local Similarity 61.5%; Pred. No. 2.3e-12;
Matches 128; Conservative 0; Mismatches 74; Indels 6; Gaps 1;

QY 1 TCAGGAGAAGCGCTACGACCTGGCCCGCGTCGCTATAGGTCAACAGAGCTCG 60
DB 926 TCAGCCGAGCGCTACGACCTGGCCCGCGTCGCTATAGGTCAACAGAGCTCG 985
QY 61 GCGTGCATGTCGGGAGCCCATCAGCTGCTGACGCTGACCGAGAGAGAGCTGGGCA 120
DB 986 GC-----GGCGAGGCGCCCGCTGAGCGCCGGATCTTCCACCTGCGAGGACATCTCGT 1039

; Publication No. US2002015557A1
; GENERAL INFORMATION:
; APPLICANT: MCKEL, BETTINA
; APPLICANT: BATHE, BRIGITTE
; APPLICANT: HANS, STEFAN
; APPLICANT: KREUTZER, CAROLINE
; APPLICANT: HERMANN, THOMAS
; APPLICANT: PFEFFERLE, WALTER
; APPLICANT: BINDER, MICHAEL
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE rpsL GENE
; FILE REFERENCE: 218472USOX
; CURRENT FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: DE 10107230.9
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: DE 10162386.0
; PRIOR FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 5099
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
; OTHER INFORMATION:
US-10-075-460-5

Query Match 43.1%; Score 89.6; DB 13; Length 5099;
Best Local Similarity 69.0%; Pred. No. 1.6e-19;
Matches 138; Conservative 0; Mismatches 59; Indels 3; Gaps 1;

QY 9 AAGCCTACGACCTGGCCCGCGTCGCTATAGGTCAACAGAGCTCGGCTGCAT 68
DB 1578 AAGCCTACGACCTGGCCCGCGTCGCTATAGGTCAACAGAGCTCGGCTGCAT 1634
QY 69 GTCGGCGAGCCATCAGCTGCTGACCGAGAGACGCTGCGCCACCATCGAA 128
DB 1635 GTGGCGGACCATGCTGTTGATGACTCTTACTGAGAGGACATCGCAACCATCGAG 1694
QY 129 TATCTGGTCCGCTGACAGAGGTGACACGATGACCGTTCGGGGCGGCTCGAGTG 188
DB 1695 TACCTGGTGGCTGCTGACGAGGTGAGCGCTCATGACTTCTCCAAATGGTGAAGATC 1754
QY 189 CCGGTGGAACCGACGACAT 208
DB 1755 CCAGTCGAGACCGATGACAT 1774

RESULT 11
US-09-738-626-1
; Sequence 1, Application US/09738626
; Publication No. US20020197603A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOL, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
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QY	111	GTCTGTGCCACCATCGATATCTGTCGCTTGCACGAGGTCTCAGACCAACGATGACCGTT	170
Db	373	GCTCTGGAGATCTGGACATGCTGTCGCTCCGCGCGCTCGACCTGATCGTCATCGAC	432
QY	171	CCGGCGCGCGCTCGAGGTGCCG	191
Db	433	TCCGTCGCGCGCCCTGCTGCCG	453

Search completed: September 17, 2003, 13:07:36
Job time : 128.259 secs

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OM nucleic - nucleic search, using sw model

Run on: September 17, 2003, 11:54:34 ; Search time 30.1105 Seconds
(without alignments)
3049.028 Million cell updates/sec

Title: US-09-697-123B-17
Perfect score: 208
Sequence: 1 tcaaggaagcgtacgac.....cgggtgaaacccagacat 208

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents.NA.*
1: /cgn2.6/ptodata/1/ina/5A.COMB.seq.*
2: /cgn2.6/ptodata/1/ina/5B.COMB.seq.*
3: /cgn2.6/ptodata/1/ina/6A.COMB.seq.*
4: /cgn2.6/ptodata/1/ina/6B.COMB.seq.*
5: /cgn2.6/ptodata/1/ina/PCRUS.COMB.seq.*
6: /cgn2.6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	160	76.9	970	1 US-08-250-030-1	Sequence 1, Appli
2	160	76.9	970	5 PCR-US95-06790-1	Sequence 1, Appli
3	160	76.9	4403765	3 US-09-103-840A-2	Sequence 2, Appli
4	160	76.9	4411529	3 US-09-103-840A-1	Sequence 1, Appli
5	144	69.2	3447	2 US-08-313-185-57	Sequence 57, Appli
6	144	69.2	3447	3 US-09-082-614A-57	Sequence 57, Appli
7	43.4	20.9	924	4 US-09-252-991A-969	Sequence 969, App
8	43.4	20.9	939	4 US-09-252-991A-925	Sequence 925, App
c 9	43	20.7	768	4 US-09-252-991A-1114	Sequence 1114, Ap
10	41.2	19.8	1485	4 US-09-252-991A-16168	Sequence 16168, A
11	41.2	19.8	1548	4 US-09-252-991A-16059	Sequence 16059, A
12	41.2	19.8	1587	4 US-09-252-991A-16424	Sequence 16424, A
c 13	40.4	19.4	77536	4 US-09-410-551B-1	Sequence 1, Appli
14	39	18.8	937	4 US-09-252-991A-14451	Sequence 14451, A
15	39	18.8	1338	4 US-09-252-991A-16571	Sequence 16571, A
c 16	39	18.8	1404	4 US-09-252-991A-16031	Sequence 16031, A
17	39	18.8	2157	4 US-09-252-991A-16462	Sequence 16462, A
c 18	38.8	18.7	4403765	3 US-09-103-840A-2	Sequence 2, Appli
c 19	38.8	18.7	4411529	3 US-09-103-840A-1	Sequence 1, Appli
c 20	38.6	18.6	903	4 US-09-252-991A-12465	Sequence 12465, A
21	38.6	18.6	1575	1 US-07-988-260B-2	Sequence 2, Appli
22	38.4	18.5	1781	1 US-09-675-018B-7	Sequence 7, Appli
23	38.4	18.5	1889	4 US-09-675-018B-9	Sequence 9, Appli
24	38.2	18.4	750	4 US-09-252-991A-13005	Sequence 13005, A
c 25	38.2	18.4	1021	4 US-09-598-747-24	Sequence 24, Appli
26	38.2	18.4	2122	4 US-09-029-603-1	Sequence 1, Appli
27	38.2	18.4	44377	2 US-08-804-227C-7	Sequence 7, Appli

28	38.2	18.4	44377	2 US-08-804-198-1	Sequence 1, Appli
29	38	18.3	717	4 US-09-513-783A-49	Sequence 49, Appli
30	38	18.3	720	3 US-09-094-359-7	Sequence 7, Appli
31	38	18.3	720	3 US-09-172-063-13	Sequence 13, Appli
32	38	18.3	720	4 US-09-316-919-14	Sequence 14, Appli
33	38	18.3	768	3 US-09-094-359-11	Sequence 11, Appli
34	38	18.3	972	3 US-09-172-063-27	Sequence 27, Appli
35	38	18.3	1623	4 US-09-513-783A-33	Sequence 33, Appli
36	38	18.3	2742	3 US-09-232-468A-1	Sequence 1, Appli
37	38	18.3	2742	3 US-09-232-468A-1	Sequence 1, Appli
38	38	18.3	4897	6 5196516-7	Patent No. 5196516
c 39	37.6	18.1	888	4 US-09-252-991A-12914	Sequence 12914, A
c 40	37.6	18.1	1386	4 US-09-252-991A-9044	Sequence 9044, Ap
41	37.6	18.1	1395	4 US-09-252-991A-12878	Sequence 12878, A
42	37.6	18.1	1608	4 US-09-252-991A-8961	Sequence 8961, Ap
43	37.6	18.1	1749	4 US-09-252-991A-8742	Sequence 8742, Ap
44	37.6	18.1	1824	4 US-09-252-991A-12570	Sequence 12570, A
45	37.4	18.0	981	4 US-09-252-991A-5092	Sequence 5092, Ap

ALIGNMENTS

RESULT 1
US-08-250-030-1
; Sequence 1, Application US/08250030
; Patent No. 5643723
; GENERAL INFORMATION:
; APPLICANT: Persing, David H.
; TITLE OF INVENTION: Detection of a Genetic Locus Encoding
; TITLE OF INVENTION: Resistance to Rifampin in Mycobacterial Cultures and in
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg & Woessner
; STREET: 3500 IDS Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/250,030
; FILING DATE: 26-MAY-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Muetting, Ann M.
; REGISTRATION NUMBER: 33,977
; REFERENCE/DOCKET NUMBER: 150.105US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-339-0331
; TELEFAX: 612-339-3061
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 970 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-250-030-1

Query Match 76.9%; Score 160; DB 1; Length 970;
Best Local Similarity 85.6%; Pred. No. 1.le-28;
Matches 178; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 1 TCAAGGAAGCGCTACGACCTCGCGCGGTCGCGGTCGCTATAGCTCAGCAGAGCTCG 60
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Db 26 TCAAGGAAGCGCTACGACCTCGCGCGGTCGCGGTCGCTATAGCTCAGCAGAGCTCG 85
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[illegible]

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RESULT 2
PCT-US95-06790-1
; Sequence 1, Application PC/TUS9506790
; GENERAL INFORMATION:
; APPLICANT: Mayo Foundation for Medical Education and Research
; APPLICANT: and Hoffmann-La Roche Inc.
; TITLE OF INVENTION: Detection of a Genetic Locus Encoding
; TITLE OF INVENTION: Resistance to Rifampin
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg & Woessner
; STREET: 3500 IDS Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402

```

Query Match	76.9%;	Score 160;	DB 5;	Length 970;
Best Local Similarity	85.6%;	Pred.No.1.le-28;		
Matches 178; Conservative	0;	Mismatches 30;	Indels 0;	Gaps 0;
QY	1	TCAAGGAGAAGCGCTACGACTTCGGCGGTGGCGCGTACAAAGTCAACAAGAAGCTCG	60	
Db	26	TCAAGGAGAAGCGTAAGNCCCTGCCCGCGTGCTATTAAGTCAACAAGAAGCTCG	85	
QY	61	GCCTGAACACCGCGTCCCAGATACAGACACCACCTCTGACGAGAGAGAGCTCGTCGCCA	120	
Db	86	GSCTGCATGTCTGGCGAGCCCCATACGTCGTCGACGTGACCGGAAGAAGAGCTCGTGCCA	145	
QY	121	CCATCGAGTAGTACCTGTGTCGCTGACGAGGGGCCACACACGATCACCGTCCGGGGGGAG	180	
Db	146	CCATCGATATCTGGTTCGCTTCACGAGGGTCAGACACAGCATGCCGGTTCGGGGGGCG	205	
QY	181	TCGAGGTCCCGGTGGAAACCGACGACAT	208	
Db	206	TCGAGGTCCCGGTGGAAACCGACGACAT	233	

RESULT 3
 US-09-103-840A-2
 ; Sequence 2, Application US/09103840A
 ; Patent No. 6294328
 ; GENERAL INFORMATION:
 ; APPLICANT: FLEISCHMAN, Robert D.
 ; APPLICANT: WHITE, Owen R.
 ; APPLICANT: FRASER, Claire M.
 ; APPLICANT: VENTER, John C.
 ; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
 ; TITLE OF INVENTION: TUBERCULOSIS
 ; FILE REFERENCE: 24366-20007.00
 ; CURRENT APPLICATION NUMBER: US/09/103,840A
 ; CURRENT FILING DATE: 1998-06-24
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 2
 ; LENGTH: 4403765
 ; TYPE: DNA
 ; ORGANISM: Mycobacterium tuberculosis
 ; FEATURE:
 ; OTHER INFORMATION: CDC 1551
 ; OTHER INFORMATION: "n" bases at various positions throughout the sequence
 ; OTHER INFORMATION: represent a, t, c or g
 US-09-103-840A-2

Query Match	76.9%;	Score 150;	DB 3;	Length 4403765;
Best Local Similarity	& 85.6%;	Prod. No. 1.7e-28;		
Matches 178;	Conservative	0;	Mismatches 30;	Indels 0; Gaps 0;
QY	1	TCAGAGAGAGCGTACGACCTCGCGCGGGTGGCGCGCTCAAGGTCACACAGAGACTCG	60	
Db	762648	TCAGGAGAGAGCGTACGACCTGCGCCGCTGCTATANGTCAACAGAGACTCG	762707	
QY	61	GCGTGAACACCGGTCCCGGATCAGACGACCATCTGACCGAGAGAGACTCTCGCCCA	120	
Db	762708	GGCTGCATGTGCGGAGAGCCCATACGTCGTGAGCGTGAACGAGAGACGTCGTGGCCA	762767	
QY	121	CCATCGAGTACCTGGTCCGCTGCACGAGGGCCACACACGATGACCGTCCCGGGCGGAG	180	
Db	762768	CCATCGAATATCTGGTCCGCTTGCACAGAGGTGACACACGATGACCGTCCGGGGCGGCG	762827	
QY	181	TCGAGGTCCCGGTGAAACCGACGACAT	208	
Db	762828	TCGAGGTCCCGGTGAAACCGACGACAT	762855	

RESULT 4
 US-09-103-840A-1
 ; Sequence 1, Application US/09103840A
 ; Patent No. 6294328
 ; GENERAL INFORMATION:
 ; APPLICANT: FLEISCHMAN, Robert D.
 ; APPLICANT: WHITE, Owen R.
 ; APPLICANT: FRASER, Claire M.
 ; APPLICANT: VENTER, John C.
 ; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
 ; TITLE OF INVENTION: TUBERCULOSIS
 ; FILE REFERENCE: 24366-20007.00
 ; CURRENT APPLICATION NUMBER: US/09/103,840A
 ; CURRENT FILING DATE: 1998-06-24
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 4411529
 ; TYPE: DNA
 ; ORGANISM: Mycobacterium tuberculosis
 ; OTHER INFORMATION: H37Rv
 US-09-103-840A-1

Query Match 76.98; Score 160; DB 3; Length 4411529;

Best Local Similarity 85.6%; Pred. No. 1.7e-28;
Matches 176; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 1 TCAAGGAGAGCGCTACGACCTCCGCGGGTGGCGGCTACAGGTCAACAAGAGCTCG 60
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DB 760688 TCAAGGAGAGCGCTACGACCTCCGCGGGTGGCGGCTACAGGTCAACAAGAGCTCG 760747
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QY 61 GCTGTGAACACCGCGTCCCGGATCACGAGCACCACCTCTGACCGAGAGAGCGTGTGGCCA 120
|||||
DB 760748 GCTGTGATGTGGCGAGGCCATCACGTCGTCGACGCTGACCGAGAGAGCGTGTGGCCA 760807
|||||
QY 121 CCATCGAGTACCTGTTCGCGCTGTCACGAGGCGCCACACGACGATGACCGTCCCGGGGGAG 180
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DB 760808 CCATCGAATATCTGTGTCGCTTGCACGAGGTCAGACACGATGACCGTTCGCGGGCGG 760867
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QY 181 TCGAGGTGCGGTGGGAACCGACGACAT 208
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DB 760868 TCGAGGTGCGGTGGGAACCGACGACAT 760895
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RESULT 5

US-08-313-185-57
; Sequence 57, Application US/08313185
; Patent No. 5851763
; GENERAL INFORMATION:
; APPLICANT: Heym, Beate
; APPLICANT: Cole, Stewart
; APPLICANT: Young, Douglas
; APPLICANT: Zhang, Ying
; APPLICANT: Honore, Nadine
; APPLICANT: Telenti, Amalio
; APPLICANT: Bodmer, Thomas
; TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
; TITLE OF INVENTION: in Mycobacterium tuberculosis
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/313,185
; FILING DATE: 12-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 02356.0068-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3447 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-313-185-57

Query Match 69.2%; Score 144; DB 2; Length 3447;
Best Local Similarity 80.8%; Pred. No. 5.6e-25;
Matches 168; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
QY 1 TCAAGGAGAGCGCTACGACCTCCGCGGGTGGCGGCTACAGGTCAACAAGAGCTCG 60
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DB 809 TCAAGGAGAGCGCTACGACCTCCGCGGGTGGCGGCTACAGGTCAACAAGAGCTCG 868
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QY 61 GCTGTGAACACCGCGTCCCGGATCACGAGCACCACCTCTGACCGAGAGAGCGTGTGGCCA 120
|||||
DB 869 GGTGTGACGCGGTGAGTTGATCACGTCGTCACCGCTGACCGAGAGAGTGTGTGTGGCCA 928
|||||
QY 121 CCATCGAGTACCTGTTCGCGCTGTCACGAGGCGCCACACGACGATGACCGTCCCGGGGGAG 180
|||||
DB 929 CCATGAGTACCTGTGTCGTCGATGAGGGTCAGTCGACATGACTGTCCAGGTGGGG 988
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QY 181 TCGAGGTGCGGTGGGAACCGACGACAT 208
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DB 989 TAGAGTGCCACTGGAACTGACGATAT 1016
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RESULT 6

US-09-082-614A-57
; Sequence 57, Application US/09082614A
; Patent No. 6124098
; GENERAL INFORMATION:
; APPLICANT: Heym, Beate
; APPLICANT: Cole, Stewart
; APPLICANT: Young, Douglas
; APPLICANT: Zhang, Ying
; APPLICANT: Honore, Nadine
; APPLICANT: Telenti, Amalio
; APPLICANT: Bodmer, Thomas
; TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
; TITLE OF INVENTION: in Mycobacterium tuberculosis
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/082,614A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/313,185
; FILING DATE: 12-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 02356.0068-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3447 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-082-614A-57

Query Match 69.2%; Score 144; DB 3; Length 3447;
Best Local Similarity 80.8%; Pred. No. 5.6e-25;
Matches 168; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
QY 1 TCAAGGAGAGCGCTACGACCTCCGCGGGTGGCGGCTACAGGTCAACAAGAGCTCG 60
|||||

Db 809 TCAGGAGAGAGCGTACGACCTGGCCAGGGTTGGTCTTCAAGAGTCAACAGAGCTCG 868
QY 61 GCGTGAACACCGCGTCCCGGACATCAGACGACCACTCTGACCGAAGAGGAGCTGTCGCGCA 120
Db 869 GGTTCACACCGCGGTGAGTGTATGATCAGCTCTCCACGCTGACCGAAGAGGATGTCGTGCGCA 928
QY 121 CCATCGAGTACCTGTCGCTGCGCTCAGAGGCGCCACACGATGACCGTCCCGGGCGGAG 180
Db 929 CCATAGAGTACCTGTCGCTGCTGATGAGGGTCACTGACAACTGATGTCCTCCAGGTGGGG 988
QY 181 TCGAGGTGCGGTGGAAACGACGACAT 208
Db 989 TAGAAGTGCACGTGGAAGTCAAGCAT 1016

RESULT 7
US-09-252-991A-969
; Sequence 969, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 969
; LENGTH: 924
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-969

Query Match 20.9%; Score 43.4; DB 4; Length 924;
Best Local Similarity 53.2%; Pred. No. 0.067;
Matches 92; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

QY 17 CGACCTCGCGGGTGGCCGCTACAGGTCAACAGAGTCTCGGCTGACACCGCTC 76
Db 537 CGACCGCTGCGCGTGGTCCGCGACCCGCGAGCGGTGGCGCGCGCACCTGTGTAG 656
QY 77 CCGGATCAGACGACCACTCTGACCGAAGAGGAGCTGCTGCGCCACCATCGAGTACCTGTT 136
Db 657 CACCGAGTGTGGCTCGATGGGCGCAGGAGAGAGCGCGCGCGCATCGCCCTGTT 716
QY 137 CCGGCTGCAGAGGGCCACACGATGACCGTCCCGGGCGGAGTGCAGGTGC 189
Db 717 CCGTCCCTACAGGTGAACGCGCGGTGCTCGATGGGGCGCGCGCATGTATAC 769

RESULT 8
US-09-252-991A-925
; Sequence 925, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 925
; LENGTH: 939
; TYPE: DNA

Db 809 TCAGGAGAGAGCGTACGACCTGGCCAGGGTTGGTCTTCAAGAGTCAACAGAGCTCG 868
QY 61 GCGTGAACACCGCGTCCCGGACATCAGACGACCACTCTGACCGAAGAGGAGCTGTCGCGCA 120
Db 869 GGTTCACACCGCGGTGAGTGTATGATCAGCTCTCCACGCTGACCGAAGAGGATGTCGTGCGCA 928
QY 121 CCATCGAGTACCTGTCGCTGCGCTCAGAGGCGCCACACGATGACCGTCCCGGGCGGAG 180
Db 929 CCATAGAGTACCTGTCGCTGCTGATGAGGGTCACTGACAACTGATGTCCTCCAGGTGGGG 988
QY 181 TCGAGGTGCGGTGGAAACGACGACAT 208
Db 989 TAGAAGTGCACGTGGAAGTCAAGCAT 1016

RESULT 9
US-09-252-991A-1114/c
; Sequence 1114, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 1114
; LENGTH: 768
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1114

Query Match 20.7%; Score 43; DB 4; Length 768;
Best Local Similarity 53.2%; Pred. No. 0.082;
Matches 91; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

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Db 172 CGACCGCTGCGCGTGGTCCGCGACCCGCGAGCGGTGGCGCGCGCATCGTGTGAG 113
QY 77 CCGGATCAGACGACCACTCTGACCGAAGAGGAGCTGCTGCGCCACCATCGAGTACCTGTT 136
Db 112 CACCGAGTGTGGGCTCGATGGGCGCAGGAAGACGCGCGCGCATCGCCCTGTT 53
QY 137 CCGGCTGCAGAGGGCCACACGATGACCGTCCCGGGCGGAGTGCAGGT 187
Db 52 CCGTCCCTACAGGTGAACGCGCGGTGCTCGATGGGGCGCGCGCATGT 2

RESULT 10
US-09-252-991A-16168
; Sequence 16168, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 939
; LENGTH: 939
; TYPE: DNA

; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-925

Query Match 20.9%; Score 43.4; DB 4; Length 939;
Best Local Similarity 53.2%; Pred. No. 0.067;
Matches 92; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

QY 17 CGACCTCGCGGGTGGCCGCTACAGGTCAACAGAGTCTCGGCTGACACCGCTC 76
Db 604 CGACCGCTGCGCGTGGTCCGCGACCCGCGAGCGGTGGCGCGCGCATCGTGTGAG 663
QY 77 CCGGATCAGACGACCACTCTGACCGAAGAGGAGCTGCTGCGCCACCATCGAGTACCTGTT 136
Db 664 CACCGAGTGTGGGCTCGATGGGCGCAGGAAGACGCGCGCGCATCGCCCTGTT 723
QY 137 CCGGCTGCAGAGGGCCACACGATGACCGTCCCGGGCGGAGTGCAGGTGC 189
Db 724 CCGTCCCTACAGGTGAACGCGCGGTGCTCGATGGGGCGCGCGCATGTAC 776

RESULT 9
US-09-252-991A-1114/c
; Sequence 1114, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 1114
; LENGTH: 768
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1114

Query Match 20.7%; Score 43; DB 4; Length 768;
Best Local Similarity 53.2%; Pred. No. 0.082;
Matches 91; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

QY 17 CGACCTCGCGGGTGGCCGCTACAGGTCAACAGAGTCTCGGCTGACACCGCTC 76
Db 172 CGACCGCTGCGCGTGGTCCGCGACCCGCGAGCGGTGGCGCGCGCATCGTGTGAG 113
QY 77 CCGGATCAGACGACCACTCTGACCGAAGAGGAGCTGCTGCGCCACCATCGAGTACCTGTT 136
Db 112 CACCGAGTGTGGGCTCGATGGGCGCAGGAAGACGCGCGCGCATCGCCCTGTT 53
QY 137 CCGGCTGCAGAGGGCCACACGATGACCGTCCCGGGCGGAGTGCAGGT 187
Db 52 CCGTCCCTACAGGTGAACGCGCGGTGCTCGATGGGGCGCGCGCATGT 2

RESULT 10
US-09-252-991A-16168
; Sequence 16168, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 939
; LENGTH: 939
; TYPE: DNA

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1 APPLICANT:  KRUSLEY, CHARLIE
2 APPLICANT:  SANTIL, DANIEL
3
4 APPLICANT:  WU, KAI
5
6 TITLE OF INVENTION:  POLYKETIDE SYNTHASE ENZYMES AND RECOMBINANT DNA
7
8 TITLE OF INVENTION:  CONSTRUCTS THEREFOR
9
10 FILE OF INVENTION:  30062-20026.00
11
12 FILE REFERENCE:  30062-20026.00
13
14 CURRENT APPLICATION NUMBER:  US/09/410,551B
15
16 CURRENT FILING DATE:  1999-10-01
17
18 PRIOR APPLICATION NUMBER:  US 60/139,650
19
20 PRIOR FILING DATE:  1999-06-17
21
22 PRIOR APPLICATION NUMBER:  US 60/123,810
23
24 PRIOR FILING DATE:  1999-03-11
25
26 PRIOR APPLICATION NUMBER:  US 60/102,748
27
28 PRIOR FILING DATE:  1998-10-02
29
30 NUMBER OF SEQ ID NOS:  72
31
32 SOFTWARE:  FastSEQ for Windows Version 4.0
33
34 SEQ ID NO 1
35
36 LENGTH:  77536
37
38 TYPE:  DNA
39
40 ORGANISM:  Streptomyces hygroscopicus
41
42 FEATURE:
43
44 NAME/KEY:  CDS
45
46 LOCATION:  (522/75)...(714/65)

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RESULT 15
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: Patent No. 6551795
: GENERAL INFORMATION:
: APPLICANT: Marc J. Rubenfield et al.
: TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
: TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
: FILE REFERENCE: 107196.136
: CURRENT APPLICATION NUMBER: US/09/252,991A
: CURRENT FILING DATE: 1999-02-18
: PRIOR APPLICATION NUMBER: US 60/074,788
: PRIOR FILING DATE: 1998-02-18
: PRIOR APPLICATION NUMBER: US 60/094,190
: PRIOR FILING DATE: 1998-07-27
: NUMBER OF SEQ ID NOS: 33142
: SEQ ID NO 16571
: LENGTH: 1338
: TYPE: DNA

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GenCore version 5.1.6
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Gapop 10.0 , Gapext 1.0

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Database : Published Applications NA:

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- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq*
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- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq*
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- 10: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq*
- 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq*
- 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq*
- 15: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq*
- 16: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq*
- 17: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	81.6	39.2	3495	10	US-09-738-626-547
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4	81.6	39.2	5099	10	US-09-887-052-1
5	81.6	39.2	5099	10	US-09-887-052-3
6	81.6	39.2	5099	10	US-09-887-052-5
7	81.6	39.2	5099	12	US-10-076-406-1
8	81.6	39.2	5099	12	US-10-076-406-3
9	81.6	39.2	5099	12	US-10-076-406-5
10	81.6	39.2	5099	13	US-10-075-460-5
11	81.6	39.2	3309400	10	US-09-738-626-1
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13	78.8	37.9	9025608	14	US-10-156-761-1
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c 15	41.4	19.9	9025608	14	US-10-156-761-1
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17	40.8	19.6	936	14	US-10-156-761-6260
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19	39.6	19.0	6811	11	US-09-883-573-2
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22	39.4	18.9	11058	14	US-10-156-761-3629
23	39	18.8	1071	14	US-10-156-761-5911
24	39	18.8	6798	11	US-09-918-740-57
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26	39	18.8	8077	11	US-09-918-740-63
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29	38.8	18.7	2304	14	US-10-156-761-5121
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43	38	18.3	720	11	US-09-866-538-5
44	38	18.3	720	12	US-09-794-308-5
45	38	18.3	720	14	US-10-221-461-25

ALIGNMENTS

RESULT 1

US-09-712-363-30
; Sequence 30, Application US/09712363
; Patent No. US20020164588A1
; GENERAL INFORMATION:
; APPLICANT: Eisenberg, David
; APPLICANT: Rotstein, Sergio H.
; APPLICANT: Marcotte, Edward M.
; TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND
; FILE REFERENCE: 07419-032001
; CURRENT APPLICATION NUMBER: US/09/712,363
; CURRENT FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: PCT/US00/02246
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,531
; PRIOR FILING DATE: 2000-02-01
; PRIOR APPLICATION NUMBER: 60/117,844
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/118,206,
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: 60/126,593
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/134,093
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/134,092
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/165,124
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/165,086
; PRIOR FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 3519
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-09-712-363-30

Sequence 6260, Ap
Sequence 57, Appl
Sequence 2, Appl
Sequence 4, Appl
Sequence 1, Appl
Sequence 3629, Ap
Sequence 5911, Ap
Sequence 57, Appl
Sequence 13, Appl
Sequence 63, Appl
Sequence 10512, A
Sequence 4984, Ap
Sequence 5121, Ap
Sequence 646, App
Sequence 45, Appl
Sequence 47, Appl
Sequence 2607, Ap
Sequence 3537, Ap
Sequence 5154, Ap
Sequence 5600, Ap
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Sequence 3952, Ap
Sequence 7755, Ap
Sequence 49, Appl
Sequence 14, Appl
Sequence 5, Appl
Sequence 5, Appl
Sequence 25, Appl

Query Match 76.9%; Score 160; DB 10; Length 3519;
Best Local Similarity 85.68; Pred. No. 7.3e-37;
Matches 178; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 1 TCAAGGAGAAGCGCTACGACTCGCGGGTGGCGGCTACAGGTCAACAAGAGCTCG 60
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 884 TCAAGGAGAAGCGCTACGACTCGCGGGTGGCGGCTACAGGTCAACAAGAGCTCG 943
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 61 GCGTGACACCGCTCCCGATCACAGCAACCACTCTGACCGAGAGAGCGCTCGTCCGA 120
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 944 GCGTGATGTCGGGAGCGCCATCACGTCGTCGACCTGACCGAAGAAGAGCGTCGTGGCCA 1003
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 121 CCATCGAGTACCTGCTCGGCTCGACGAGGGCCACACCAATGACCGTCCCGGGCGGAG 180
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1004 CCATCGAATATCTGCTCGGCTTGACAGAGGTCAGACCAATGACCGTTCGGGGCGG 1063
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 181 TCGAGTGGCGGTGAACCGAGACAT 208
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1064 TCGAGTGGCGGTGAACCGAGACAT 1091
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 2
US-09-738-626-547
; Sequence 547, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENO, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; CURRENT APPLICATION NUMBER: US/09738,626
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 547
; LENGTH: 3495
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-547

Query Match 39.2%; Score 81.6; DB 10; Length 3495;
Best Local Similarity 66.5%; Pred. No. 2.4e-14;
Matches 133; Conservative 0; Mismatches 64; Indels 3; Gaps 1;

QY 9 AAGCGTACGACTCGCGGGTGGCGGCTACAGGTCAACAAGCTCAACAAGCTCGCTGAAC 68
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 877 AAGCGTACGACTCGCGGGTGGCGGCTACAGGTCAACAAGCTCAACAAGCTCGCTGGT 936
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 69 ACCGCGTCCCGATCACGACCACTGACGCGAAGAGAGCGTGGCGCCACCATCGAG 128
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 937 GCGACACCATGTTGATG---ACCTTACTGAGAGGACATCGCAACCATCATCGAG 993
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 129 TACCTGTGCGCTCGACAGGGCCACACCAATGACCGTCCCGGGCGGAGTGGAGGTG 188
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 994 TACCTGTGCGCTCGACAGGGTGGCGGCTGATGACTTCTCCAAATGTTGAAGAGATC 1053
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 189 CCGGTGAACCGACGACAT 208
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1054 CCAGTCGACCGATGACAT 1073
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 3
US-09-984-711-5
; Sequence 5, Application US/09984711
; Patent No. US20020119549A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: STEPHAN, Hans
; APPLICANT: KREUTZER, Caroline
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE rpsL GENE
; FILE REFERENCE: 204209US0
; CURRENT APPLICATION NUMBER: US/09/984,711
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: DE10108230.9
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 5096
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
; OTHER INFORMATION:
US-09-984-711-5

Query Match 39.2%; Score 81.6; DB 10; Length 5096;
Best Local Similarity 66.5%; Pred. No. 2.4e-14;
Matches 133; Conservative 0; Mismatches 64; Indels 3; Gaps 1;

QY 9 AAGCGTACGACTCGCGGGTGGCGGCTACAGGTCAACAAGCTCGCGCTGAAC 68
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1578 AAGCGTACGACTCGCGGGTGGCGGCTACAGGTCAACAAGCTCGCGCTGGT 1637
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 69 ACSCGTCCCGATCACGACGACCACTGACGGAAGAGAGCGTGGCGCCACCATCGAG 128
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1638 GCGACACCATGATGTTGATG---ACCTTACTGAGAGGACATCGCAACCATCGAG 1694
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 129 TACCTGTGCGCTCGACAGGGCCACACCAATGACCGTCCCGGGCGGAGTGGAGGTG 188
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1695 TACCTGTGCGCTCGACGCGAGTGGCGGCTCATGACTTCTCCAAATGTTGAAGAGATC 1754
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 189 CCGGTGAACCGACGACAT 208
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1755 CCAGTCGACCGATGACAT 1774
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 4
US-09-887-052-1
; Sequence 1, Application US/09887052
; Patent No. US20020119537A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE rpoB GENE
; FILE REFERENCE: 204212US0X
; CURRENT APPLICATION NUMBER: US/09/887,052
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: DE10107229.5
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 5099

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; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
US-09-887-052-1

Query Match          39.2%; Score 81.6; DB 10; Length 5099;
Best Local Similarity 66.5%; Pred. No. 2.4e-14;
Matches 133; Conservative 0; Mismatches 64; Indels 3; Gaps 1;

QY 9 AAGCGCTACGACCTCGCGGGTGGCGGTACAAAGGTCAACAAGAGCTCGGCTGAAC 68
Db 1578 AAGCGCTACGACCTCGCTGGTGGTGTTCACAGATCAACCGAAGCTGGCTTGGT 1637

QY 69 ACCGCGTCCCGATCAGCAGACCACTCTGACCGAAGAGAGCTGTGCGCCACCATCGAG 128
Db 1638 GCGCAGCACCAGATGGTTTGATG---ACTCTTACTGAAGAGGACATCGCAACCATCGAG 1694

QY 129 TACCTGTGCTGCTGCACGAGGGCCACACCAAGATGACCGTCCCGGGGGAGTCGAGTG 188
Db 1695 TACCTGTGCTGCTGCACGAGGTCGACGAGGTCGAGCGGCTCATGACTCTCCAAATGGTGAAGAGATC 1754

QY 189 CCGGTGGAACCGACGACAT 208
Db 1755 CCAGTCGAGACCGATGACAT 1774

RESULT 5
US-09-887-052-3
; Sequence 3, Application US/09887052
; Patent No. US20020119537A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE rpoB GENE
; FILE REFERENCE: 204212USOX
; CURRENT APPLICATION NUMBER: US/09/887,052
; PRIOR FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: DE10107229.5
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 5099
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
US-09-887-052-5

Query Match          39.2%; Score 81.6; DB 10; Length 5099;
Best Local Similarity 66.5%; Pred. No. 2.4e-14;
Matches 133; Conservative 0; Mismatches 64; Indels 3; Gaps 1;

QY 9 AAGCGCTACGACCTCGCGGGTGGCGGTACAAAGGTCAACAAGAGCTCGGCTGAAC 68
Db 1578 AAGCGCTACGACCTCGCTGGTGGTGTTCACAGATCAACCGAAGCTGGCTTGGT 1637

QY 69 ACCGCGTCCCGATCAGCAGACCACTCTGACCGAAGAGAGCTGTGCGCCACCATCGAG 128
Db 1638 GCGCAGCACCAGATGGTTTGATG---ACTCTTACTGAAGAGGACATCGCAACCATCGAG 1694

QY 129 TACCTGTGCTGCTGCACGAGGGCCACACCAAGATGACCGTCCCGGGGGAGTCGAGTG 188
Db 1695 TACCTGTGCTGCTGCACGAGGTCGACGAGGTCGAGCGGCTCATGACTCTCCAAATGGTGAAGAGATC 1754

QY 189 CCGGTGGAACCGACGACAT 208
Db 1755 CCAGTCGAGACCGATGACAT 1774

RESULT 6
US-09-887-052-5
; Sequence 5, Application US/09887052
; Patent No. US20020119537A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE rpoB GENE
; FILE REFERENCE: 204212USOX
; CURRENT APPLICATION NUMBER: US/09/887,052
; PRIOR FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: DE10107229.5
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 5099
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
US-09-887-052-5

Query Match          39.2%; Score 81.6; DB 10; Length 5099;
Best Local Similarity 66.5%; Pred. No. 2.4e-14;
Matches 133; Conservative 0; Mismatches 64; Indels 3; Gaps 1;

QY 9 AAGCGCTACGACCTCGCGGGTGGCGGTACAAAGGTCAACAAGAGCTCGGCTGAAC 68
Db 1578 AAGCGCTACGACCTCGCTGGTGGTGTTCACAGATCAACCGAAGCTGGCTTGGT 1637

QY 69 ACCGCGTCCCGATCAGCAGACCACTCTGACCGAAGAGAGCTGTGCGCCACCATCGAG 128
Db 1638 GCGCAGCACCAGATGGTTTGATG---ACTCTTACTGAAGAGGACATCGCAACCATCGAG 1694

QY 129 TACCTGTGCTGCTGCACGAGGGCCACACCAAGATGACCGTCCCGGGGGAGTCGAGTG 188
Db 1695 TACCTGTGCTGCTGCACGAGGTCGACGAGGTCGAGCGGCTCATGACTCTCCAAATGGTGAAGAGATC 1754

QY 189 CCGGTGGAACCGACGACAT 208
Db 1755 CCAGTCGAGACCGATGACAT 1774

RESULT 7
US-10-076-406-1
; Sequence 1, Application US/10076406
; Publication No. US2003016684A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: Nucleotide sequences coding for the rpoB gene
; FILE REFERENCE: 219774USOXIP
; CURRENT APPLICATION NUMBER: US/10/076,406
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: DE 10107229.5
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 09/887052
; PRIOR FILING DATE: 2001-06-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 5099

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Db 1755 CCAGTCGAGACCGATGACAT 1774

RESULT 6
US-09-887-052-5
; Sequence 5, Application US/09887052
; Patent No. US20020119537A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE rpoB GENE
; FILE REFERENCE: 204212USOX
; CURRENT APPLICATION NUMBER: US/09/887,052
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: DE10107229.5
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 5099
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
US-09-887-052-5

Query Match          39.2%; Score 81.6; DB 10; Length 5099;
Best Local Similarity 66.5%; Pred. No. 2.4e-14;
Matches 133; Conservative 0; Mismatches 64; Indels 3; Gaps 1;

QY 9 AAGCGCTACGACCTCGCGGGTGGCGGTACAAAGGTCAACAAGAGCTCGGCTGAAC 68
Db 1578 AAGCGCTACGACCTCGCTGGTGGTGTTCACAGATCAACCGAAGCTGGCTTGGT 1637

QY 69 ACCGCGTCCCGATCAGCAGACCACTCTGACCGAAGAGAGCTGTGCGCCACCATCGAG 128
Db 1638 GCGCAGCACCAGATGGTTTGATG---ACTCTTACTGAAGAGGACATCGCAACCATCGAG 1694

QY 129 TACCTGTGCTGCTGCACGAGGGCCACACCAAGATGACCGTCCCGGGGGAGTCGAGTG 188
Db 1695 TACCTGTGCTGCTGCACGAGGTCGACGAGGTCGAGCGGCTCATGACTCTCCAAATGGTGAAGAGATC 1754

QY 189 CCGGTGGAACCGACGACAT 208
Db 1755 CCAGTCGAGACCGATGACAT 1774

RESULT 7
US-10-076-406-1
; Sequence 1, Application US/10076406
; Publication No. US2003016684A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: Nucleotide sequences coding for the rpoB gene
; FILE REFERENCE: 219774USOXIP
; CURRENT APPLICATION NUMBER: US/10/076,406
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: DE 10107229.5
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 09/887052
; PRIOR FILING DATE: 2001-06-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 5099

```



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; Publication No. US2002015557A1
; GENERAL INFORMATION:
; APPLICANT: MCKEL, BETTINA
; APPLICANT: BATHE, BRIGITTE
; APPLICANT: HANS, STEFAN
; APPLICANT: KREUTZER, CAROLINE
; APPLICANT: HERMANN, THOMAS
; APPLICANT: PEPPERLE, WALTER
; APPLICANT: BINDER, MICHAEL
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE rpsL GENE
; FILE REFERENCE: 21847205X
; CURRENT APPLICATION NUMBER: US/10/075,460
; CURRENT FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: DE 10107230.9
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: DE 10162386.0
; PRIOR FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 5099
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
; OTHER INFORMATION:
; US-10-075-460-5

Query Match      39.2%; Score 81.6; DB 13; Length 5099;
Best Local Similarity 66.5%; Pred. No. 2.4e-14;
Matches 133; Conservative 0; Mismatches 64; Indels 3; Gaps 1;

QY      9 AACGCTAGACCTCGCGGGTGGCGGCTACAGGTCACACAGAAGCTCGCGCTGAAC 68
Db      1578 AACGCTAGACCTCGCGGTTGGTTCGTTTACAAAGATCAACCGCAAGCTCGCGCTTGGT 1637
QY      69 ACCGCTCCCGATCACGACGACCATCTGACGAGGAGGAGGAGGCTGTCGCCACCATCGAG 128
Db      1638 GCGACACAGATGGTTGATG---ACTCTTACTGAGAGGAGCATCGCAACCATCGAG 1694
QY      129 TACCTGGTCCGCTCGACGAGGCGCCACACACAGATGACCGTCCCGGGGAGTCGAGGTG 188
Db      1695 TACCTGGTCCGCTCGACGAGGAGGAGGAGGCTGTCGCTTCTTCCAAATGGTGAAGATC 1754
QY      189 CCGGTGGAACCGACGACAT 208
Db      1755 CCACTCGAGACCGATGACAT 1774

RESULT 11
US-09-738-626-1
; Sequence 1, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIRO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07

; Publication No. US2002015557A1
; GENERAL INFORMATION:
; APPLICANT: MCKEL, BETTINA
; APPLICANT: BATHE, BRIGITTE
; APPLICANT: HANS, STEFAN
; APPLICANT: KREUTZER, CAROLINE
; APPLICANT: HERMANN, THOMAS
; APPLICANT: PEPPERLE, WALTER
; APPLICANT: BINDER, MICHAEL
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE rpsL GENE
; FILE REFERENCE: 21847205X
; CURRENT APPLICATION NUMBER: US/10/075,460
; CURRENT FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: DE 10107230.9
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: DE 10162386.0
; PRIOR FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 1
; LENGTH: 3309400
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; US-09-738-626-1

Query Match      39.2%; Score 81.6; DB 10; Length 3309400;
Best Local Similarity 66.5%; Pred. No. 2.3e-14;
Matches 133; Conservative 0; Mismatches 64; Indels 3; Gaps 1;

QY      9 AACGCTAGACCTCGCGGGTGGCGGCTACAGGTCACACAGAAGCTCGCGCTGAAC 68
Db      513789 AACGCTAGACCTCGCGGTTGGTTCGTTTACAAAGATCAACCGCAAGCTCGCGCTTGGT 513848
QY      69 ACCGCTCCCGATCACGACGACCATCTGACGAGGAGGAGGAGGCTGTCGCCACCATCGAG 128
Db      513849 GCGACACAGATGGTTGATG---ACTCTTACTGAGAGGAGCATCGCAACCATCGAG 513905
QY      129 TACCTGGTCCGCTCGACGAGGCGCCACACACAGATGACCGTCCCGGGGAGTCGAGGTG 188
Db      513906 TACCTGGTCCGCTCGACGAGGAGGAGGAGGCTGTCGCTTCTTCCAAATGGTGAAGATC 513965
QY      189 CCGGTGGAACCGACGACAT 208
Db      513966 CCACTCGAGACCGATGACAT 513985

RESULT 12
US-10-156-761-4898
; Sequence 4898, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 4898
; LENGTH: 3543
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3543)
; US-10-156-761-4898

Query Match      37.9%; Score 78.8; DB 14; Length 3543;
Best Local Similarity 64.9%; Pred. No. 1.5e-13;
Matches 135; Conservative 0; Mismatches 67; Indels 6; Gaps 1;

QY      1 TCAGGAGAGCGCTACGACCTCGCGGGTGGCGGCTACAGGTCACACAGAAGCTCG 60
Db      926 TCACCCGAGCGCTACGACCTCGCGAGGTCGCGGCTACAGGTCACACAGAAGCTCG 985
QY      61 GCTTGACACCGCGTCCCGGATCAGACGACCACTCTGACCGAGAGAGAGCTGTCGCCA 120
Db      986 G-----CGCGAGGCGCGCTGGAGCCGCGGATCTCTGACCTCGAGGACATCATCTCGT 1039
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QY 121 CCATCGAGTACCTGGTCCGCTGACGAGGCGCACACAGAGTACCGTCCGCGCGGAG 180
DB 1040 CGATCAAGTACTGTTGAAGCTGCACGCGGTGAGACGAGAGCGTTGGCGACACGCGCA 1099
QY 181 TCGAGTGCCTGCTGGAACCGAGACAT 208
DB 1100 CCTCGATGCTGCTGAGACCGAGACAT 1127

RESULT 13
US-10-156-761-1
; Sequence 1, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
; LENGTH: 9025608
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1

Query Match 37.9%; Score 78.8; DB 14; Length 9025608;
Best Local Similarity 64.9%; Pred. No. 1.4e-13;
Matches 135; Conservative 0; Mismatches 67; Indels 6; Gaps 1;

QY 1 TCAAGAGAGAGCGCTACGACCTCGCGGGTGGCGGTACAGGTCACAGTCAACAAGAGCTCG 60
DB 5970494 TCAACCGAGAGCGCTACGACCTCGCGAGGTGGCGGTACAGGTCACAGGAGCTGG 5970553
QY 61 GCTGTAACACCGCTCCCGGATCAGCAGACCACTCTGACGAGAGAGAGCTGCTGCGCA 120
DB 5970554 G-----CGCGAGGCGCGGTGGAGCGCGGGATCTGACCGTGGAGGACATCATCTGT 5970607
QY 121 CCATCGAGTACCTGGTCCGCTGACGAGGCGCACACAGTACCGTCCGCGCGGAG 180
DB 5970608 CGATCAAGTACTGTTGAAGCTGCACGCGGTGAGACCGAGACCGCTGGCGGCAACGCGCA 5970667
QY 181 TCGAGTGCCTGCTGGAACCGAGACAT 208
DB 5970668 CCTCGATGCTGCTGAGACCGAGACAT 5970695

RESULT 14
US-10-156-761-6278/c
; Sequence 6278, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
```

```
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 6278
; LENGTH: 1368
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1368)
US-10-156-761-6278

Query Match 19.9%; Score 41.4; DB 14; Length 1368;
Best Local Similarity 52.6%; Pred. No. 0.0085;
Matches 90; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

QY 4 AGAGAAGCGCTACGACCTCGCGGGTGGCGGTACAGGTCACAGGTCACAGAGCTCGGCC 63
DB 490 AGCGCTTGTGAGAGAGCGTCTGGAGGTGTGTCAGCGAAGCGCGACGACGACGCG 431
QY 64 TGAACACCGCGTCCCGATCAAGACGACCACTCTGACGAGAGGAGGAGCTGTCGCGCA 123
DB 430 GGATGACGCGTGTCCGAGCCCGCGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGG 371
QY 124 TCGAGTACTGTGTCGCTGACGAGGCGCACACAGGATGACCGTCCCG 174
DB 370 CGGTGTCCAGCGCCACATGCGCGCGTGTGTCCACCGCGTCCGCGAGCGG 320

RESULT 15
US-10-156-761-1/c
; Sequence 1, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
; LENGTH: 9025608
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1

Query Match 19.9%; Score 41.4; DB 14; Length 9025608;
Best Local Similarity 52.6%; Pred. No. 0.008;
Matches 90; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

QY 4 AGAGAAGCGCTACGACCTCGCGGGTGGCGGTACAGGTCACAGGTCACAGAGCTCGGCC 63
DB 490 AGCGCTTGTGAGAGAGCGTCTGGAGGTGTGTCAGCGAAGCGCGACGACGACGCG 431
QY 64 TGAACACCGCGTCCCGATCAAGACGACCACTCTGACGAGAGGAGGAGCTGTCGCGCA 123
DB 430 GGATGACGCGTGTCCGAGCCCGCGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGG 371
QY 124 TCGAGTACTGTGTCGCTGACGAGGCGCACACAGGATGACCGTCCCG 174
DB 370 CGGTGTCCAGCGCCACATGCGCGCGTGTGTCCACCGCGTCCGCGAGCGG 320
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US-10-156-761-1
; Sequence 1, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
```

QY	64	TGAACACCGCGTCCCGGATCACGACGACCACTCTGTACCGAAGAGGAGCGTGTGCGCACCA	123
Db	7564221	GGATCGACGCGGTGTCCGAGCCCGGACGCGGAGCGCGGAGGACGCCACCAAGTGTCCCGCGTA	7564162
QY	124	TCGAGTACCTGTGCTCCGCTGTGACGAGGCGCACACCAAGATGACCGTCCCGG	174
Db	7564161	CCGTGTCCACGCGCCACATGCGCGCGGCTGTGTCCACCGCGTCCCGGACGG	7564111

Search completed: September 17, 2003, 13:08:03
 Job time : 135.259 secs

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OM nucleic - nucleic search, using sw model

Run on: September 17, 2003, 11:54:34 ; Search time 30.5448 Seconds
(without alignments)
3049.028 Million cell updates/sec

Title: US-09-697-123B-18

Perfect score: 211

Sequence: 1 tcaagagaagcgtacgac.....cccgctcgaggtcgacgacat 211

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents.NA.*

- 1: /cgn2_6/ptodata/1/ina/5A.COMB.seq.*
- 2: /cgn2_6/ptodata/1/ina/5B.COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A.COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B.COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/PTCUTS.COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	126.2	59.8	970	1	US-08-250-030-1
2	126.2	59.8	970	5	PCR-US95-06790-1
3	126.2	59.8	4403765	3	US-09-103-840A-2
4	126.2	59.8	4411529	3	US-09-103-840A-1
5	119.8	56.8	3447	2	US-08-313-185-57
6	119.8	56.8	3447	3	US-09-082-614A-57
7	42.2	20.0	1026	4	US-09-252-991A-16085
8	42.2	20.0	1437	4	US-09-252-991A-15986
9	41.2	19.5	1723	4	US-09-199-637A-135
10	40.4	19.1	915	4	US-09-252-991A-15231
11	40.4	19.1	948	4	US-09-252-991A-480
12	40.4	19.1	2058	4	US-09-252-991A-15243
13	40.4	19.1	7449	4	US-09-252-991A-396
14	40.2	19.1	573	4	US-09-252-991A-5674
15	40.2	19.1	804	4	US-09-252-991A-10427
16	40.2	19.1	882	4	US-09-252-991A-5644
17	40.2	19.1	1020	4	US-09-252-991A-5550
18	40.2	19.1	1776	4	US-09-252-991A-10519
19	40.2	19.1	2079	4	US-09-252-991A-5584
20	40	19.0	911	2	US-08-924-759-9
21	40	19.0	911	3	US-09-248-335-9
22	39.6	18.8	402	3	US-09-060-756-673
23	39.6	18.8	1208	2	US-09-670-314-673
24	39.6	18.8	1208	3	US-08-403-852D-4
25	39.6	18.8	1208	3	US-08-510-646B-4
26	39.6	18.8	1208	3	US-09-231-818-4
27	39.6	18.8	5392	2	US-08-403-852D-1

28 39.6 18.8 5392 3 US-08-510-646B-1 Sequence 1, Appli
29 39.6 18.8 5392 3 US-09-231-818-1 Sequence 1, Appli
30 39.4 18.7 680 4 US-09-556-877-267 Sequence 267, App
31 39.4 18.7 680 4 US-09-620-412C-267 Sequence 267, App
32 39.4 18.7 680 4 US-09-598-419-267 Sequence 267, App
33 39.4 18.7 2302 4 US-09-620-312D-915 Sequence 915, App
34 39.4 18.7 4897 6 5196516-7 Patent No. 5196516
35 39.2 18.6 77536 4 US-09-410-551B-1 Sequence 1, Appli
36 39 18.5 531 4 US-09-252-991A-5042 Sequence 5042, Ap
37 39 18.5 540 4 US-09-252-991A-5073 Sequence 5073, Ap
38 39 18.5 978 4 US-09-252-991A-5172 Sequence 5172, Ap
39 39 18.5 1197 4 US-09-252-991A-5115 Sequence 5115, Ap
40 39 18.5 1371 4 US-09-252-991A-5005 Sequence 5005, Ap
41 39 18.5 47981 4 US-09-679-379-1 Sequence 1, Appli
42 38.8 18.4 1278 4 US-09-252-991A-442 Sequence 442, App
43 38.8 18.4 1473 4 US-09-252-991A-420 Sequence 420, App
44 38.8 18.4 1488 4 US-09-252-991A-421 Sequence 421, App
45 38.6 18.3 77536 4 US-09-410-551B-1 Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-08-250-030-1

; Sequence 1, Application US/08250030

; Patent No. 5643723

; GENERAL INFORMATION:

; APPLICANT: Persing, David H.

; TITLE OF INVENTION: Detection of a Genetic Locus Encoding

; TITLE OF INVENTION: Resistance to Rifampin in Mycobacterial Cultures and in

; NUMBER OF SEQUENCES: 15

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Schwegman, Lundberg & Woessner

; STREET: 3500 IDS Center

; CITY: Minneapolis

; STATE: MN

; COUNTRY: USA

; ZIP: 55402

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/250,030

; FILING DATE: 26-MAY-1994

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Muegling, Ann M.

; REGISTRATION NUMBER: 33,977

; REFERENCE/DOCKET NUMBER: 150.105U51

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 612-339-0331

; TELEFAX: 612-339-3061

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 970 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA

US-08-250-030-1

Query Match

Best Local Similarity 59.8%; Score 126.2; DB 1; Length 970;

Matches 165; Conservative 0; Mismatches 43; Indels 3; Gaps 1;

Qy 1 TCAAGAGAAGCGGTACGACCTGGCCCGCTGGGTACAGGTCAACAGAGCTGG 60

Db 26 TCAAGAGAAGCGGTACGACCTGGCCCGCTGGGTACAGGTCAACAGAGCTGG 85

QY 61 GCATCACCAGAGAACCGCGGACACGACGCTGACACGCTGACCGAAGAGGACGTCGTCG 120
Db 86 GCGTCGATGTCGGGAGCCCATCAG---TCGTGACGCTGACCGAAGAGAGCTGTCGG 142
QY 121 CCACCATCGAGTACGTCGTCGTCGTCATCAGGCGGCAAGACGATGACCGTCCCGGTCG 180
Db 143 CCACCATCGAATATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 202
QY 181 GAGTCGAGGTGCGCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 211
Db 203 GCGTCGAGGTGCGCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 233

RESULT 2
PCT-US95-06790-1
; Sequence 1, Application PC/TUS9506790
; GENERAL INFORMATION:
; APPLICANT: Mayo Foundation for Medical Education and Research
; APPLICANT: and Hoffmann-La Roche Inc.
; TITLE OF INVENTION: Detection of a Genetic Locus Encoding
; TITLE OF INVENTION: Resistance to Rifampin
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg & Woessner
; STREET: 3500 IDS Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/06790
; FILING DATE: 26-MAY-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Raasch, Kevin W.
; REGISTRATION NUMBER: 35,651
; REFERENCE/DOCKET NUMBER: 150.105W01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-339-0331
; TELEFAX: 612-339-3061
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 970 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
PCT-US95-06790-1

Query Match 59.8%; Score 126.2; DB 5; Length 970;
Best Local Similarity 78.2%; Pred. No. 9.7e-22;
Matches 165; Conservative 0; Mismatches 43; Indels 3; Gaps 1;
QY 1 TCAAGGAGAGCGCTACGACCTGCGCGGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 60
Db 26 TCAAGGAGAGCGCTACGACCTGCGCGGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 85
QY 61 GCATCACCAGAGAACCGCGGACACGACGCTGACACGCTGACCGAAGAGAGCTGTCGTCG 120
Db 86 GCGTCGATGTCGGGAGCCCATCAG---TCGTGACGCTGACCGAAGAGAGCTGTCGG 142
QY 121 CCACCATCGAGTACCTGTCGTCGTCGTCATCAGGCGGCAAGACGATGACCGTCCCGGTCG 180
Db 143 CCACCATCGAATATCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 202
QY 181 GAGTCGAGGTGCGCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 211
Db 203 GCGTCGAGGTGCGCGTGGAAACCGACGACAT 233

RESULT 3
US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match 59.8%; Score 126.2; DB 3; Length 4403765;
Best Local Similarity 78.2%; Pred. No. 2e-21;
Matches 165; Conservative 0; Mismatches 43; Indels 3; Gaps 1;
QY 1 TCAAGGAGAGCGCTACGACCTGCGCGGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 60
Db 762648 TCAAGGAGAGCGCTACGACCTGCGCGGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 762707
QY 61 GCATCACCAGAGAACCGCGGACACGACGCTGACACGCTGACCGAAGAGAGCTGTCGTCG 120
Db 762708 GCGTCGATGTCGGGAGCCCATCAG---TCGTGACGCTGACCGAAGAGAGCTGTCGG 762764
QY 121 CCACCATCGAGTACCTGTCGTCGTCGTCATCAGGCGGCAAGACGATGACCGTCCCGGTCG 180
Db 762765 CCACCATCGAATATCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 762824
QY 181 GAGTCGAGGTGCGCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 211
Db 762825 CCGTCGAGGTGCGCGTGGAAACCGACGACAT 762855

RESULT 4
US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1
Query Match 59.8%; Score 126.2; DB 3; Length 4411529;

Best Local Similarity 78.2%; Pred. No. 2e-21;
Matches 165; Conservative 0; Mismatches 43; Indels 3; Gaps 1;

QY 1 TCAAGGAGAGCGCTACGACCTGCGCCCGCGTGGTGGTACAGGTCAACAGAGCTGG 60
Db TCAAGGAGAGCGCTACGACCTGCGCCCGCGTGGTGGTGGTACAGGTCAACAGAGCTGG 760747
QY 61 GCATCACCAGAGACCGCGCGGACGACCTCGACCCAGCTGACCCGACAGAGCTGCTGG 120
Db GCGTGCATGTGCGCGAGCCCATCAG---TCGTGCAGCGCTGACCCGAGAGACCTGCTGG 760804
QY 121 CCACCATCGAGTACCTGCTGCGGCTGCATCAGGCGGCAAGAGAGTACCGCTGCCCGGGTG 180
Db CCACCATCGATATCTGCTCGCTTGCACGAGGCTGACACCGAGTACCGCTGCCCGGGTG 760804
QY 181 GAGTCGAGGTGCGCGCTCGAGGTCGACGACAT 211
Db GCGTCGAGGTGCGCGGTGGAACCGACGACAT 760895

RESULT 5

US-08-313-185-57
; Sequence 57, Application US/08313185
; Patent No. 5851763
; GENERAL INFORMATION:
; APPLICANT: Heym, Beate
; APPLICANT: Cole, Stewart
; APPLICANT: Young, Douglas
; APPLICANT: Zhang, Ying
; APPLICANT: Honore, Nadine
; APPLICANT: Telenti, Amalio
; APPLICANT: Bodmer, Thomas
; TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
; TITLE OF INVENTION: in Mycobacterium Tuberculosis
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/313,185
; FILING DATE: 12-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 02356.0068-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3447 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-313-185-57

Query Match 56.8%; Score 119.8; DB 2; Length 3447;
Best Local Similarity 76.3%; Pred. No. 3.6e-20;
Matches 161; Conservative 0; Mismatches 47; Indels 3; Gaps 1;

QY 1 TCAAGGAGAGCGCTACGACCTGCGCCCGCGTGGTGGTACAGGTCAACAGAGCTGG 60

Db 809 TCAAGGAGAGCGCTACGACCTGCGCCCGCGTGGTGGTACAGGTCAACAGAGCTGG 868
QY 61 GCATCACCAGAGACCGCGCGGACGACCTCGACCCAGCTGACCCGACAGAGCTGCTGG 120
Db GGTTCGACG---CCGCTGAGTTGATCAGCTGCTCCAGCTGACCCGAGAGGATGCTCGTG 925
QY 121 CCACCATCGAGTACCTGCTGCGGCTGCATCAGGCGGCAAGAGAGTACCGCTGCCCGGGTG 180
Db CCACCATAGAGTACCTGCTGCTGCTGATGAGGCTGAGTCGACATGACTGTCCCGAGTG 985
QY 181 GAGTCGAGGTGCGCGCTCGAGGTCGACGACAT 211
Db GCGTAGAGTGCACAGTGGRAACTGACGATAT 1016

RESULT 6

US-09-082-614A-57
; Sequence 57, Application US/09082614A
; Patent No. 6124098
; GENERAL INFORMATION:
; APPLICANT: Heym, Beate
; APPLICANT: Cole, Stewart
; APPLICANT: Young, Douglas
; APPLICANT: Zhang, Ying
; APPLICANT: Honore, Nadine
; APPLICANT: Telenti, Amalio
; APPLICANT: Bodmer, Thomas
; TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
; TITLE OF INVENTION: in Mycobacterium Tuberculosis
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/082,614A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/313,185
; FILING DATE: 12-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 02356.0068-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3447 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-082-614A-57

Query Match 56.8%; Score 119.8; DB 3; Length 3447;
Best Local Similarity 76.3%; Pred. No. 3.6e-20;
Matches 161; Conservative 0; Mismatches 47; Indels 3; Gaps 1;

QY 1 TCAAGGAGAGCGCTACGACCTGCGCCCGCGTGGTGGTACAGGTCAACAGAGCTGG 60

Db 809 TCAGGAGAAACGCTACGACCTGGCCAGAGGTGGTGTGTACAGAGGTCAACAAGAGCTCG 868
QY 61 GCATCCAGAGAACCCGCGACACAGACCTCGACCGACGCTGACCGAGAGAGAGCTGCTCG 120
Db 869 GGTTCGACG--CCGGTGAAGTGTATCAGCTGCGTCCACGCTGACCGAAGAGAGTGTGCTCG 925
QY 121 CCACCATCGAGTACCTGCTGGCTGATCAGGCGGCAACAAGACGATGACCGTCCCGGGTGS 180
Db 926 CCACCATAGAGTACCTGCTGGCTGATCAGGCGGCTGATGAGGCTGATGATGCTCCAGGTG 985
QY 181 GATCGAGTGCCTCGCTGAGTGCAGACAT 211
Db 986 GGSTAGAGTGCAGTGGAACTGACGATAT 1016

RESULT 7

US-09-252-991A-16085
; Sequence 16085, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 16085
; LENGTH: 1026
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-16085

Query Match 20.0%; Score 42.2; DB 4; Length 1026;
Best Local Similarity 58.3%; Pred. No. 0.083;
Matches 74; Conservative 0; Mismatches 53; Indels 0; Gaps 0;
QY 80 CGACAGACCTGACACGCTGACCGAGAGAGAGCTGCTGCGCCACCATCGATCGTACCTGGT 139
Db 861 CGGCACACCTGACCGGCTGAATTCGGCGACAACGGCGCTCGCTGCGCTACCTGGT 920
QY 140 GCGGCTGATCAGGCGGCAACAGAGATGACCGTCCCGGGTGGAGTGCAGGTGCCGCTCGA 199
Db 921 GGGCAAGCCGACACCGGCTGGCTGCTATGTTCCAGATGATGAACGAGGCGCGCATCGG 980
QY 200 GGTGAC 206
Db 981 GGTGCGC 987

RESULT 8

US-09-252-991A-15986
; Sequence 15986, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 15986
; LENGTH: 1437
; TYPE: DNA

; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-15986
Query Match 20.0%; Score 42.2; DB 4; Length 1437;
Best Local Similarity 58.3%; Pred. No. 0.085;
Matches 74; Conservative 0; Mismatches 53; Indels 0; Gaps 0;
QY 80 CGACAGACCTGACACGCTGACCGAGAGAGAGCTGCTGCGCCACCATCGATCGTACCTGGT 139
Db 412 CGGCACACCTCCACCGGCTGAATTCGGCGACAACGGCGCTGCTGCGCTACCTGGT 471
QY 140 GCGGCTGATCAGGCGGCAACAAGACGATGACCGTCCCGGGTGGAGTGCAGGTGCCGCTCGA 199
Db 472 GGGCAAGCGCGACCGACCGCTGGCTGCTATGTTCCAGATGATGAACGAGGCGCGCATCGG 531
QY 200 GGTGAC 206
Db 532 GGTGCGC 538

RESULT 9

US-09-199-637A-135/c
; Sequence 135, Application US/09199637A
; Patent No. 6355411
; GENERAL INFORMATION:
; APPLICANT: Ausubel, Frederick
; APPLICANT: Goodman, Howard M.
; APPLICANT: Rahme, Laurence G.
; APPLICANT: Mahajan-Miklos, Shalina
; APPLICANT: Tan, Man-Wah
; APPLICANT: Cao, Hui
; APPLICANT: Drenkard, Eliana
; APPLICANT: Tsongalis, John
; TITLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC ACID
; FILE OF INVENTION: SEQUENCES AND USES THEREOF
; FILE REFERENCE: 00786/361002
; CURRENT APPLICATION NUMBER: US/09/199,637A
; CURRENT FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: 60/066,517
; PRIOR FILING DATE: 1997-11-25
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 135
; LENGTH: 1723
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-199-637A-135

Query Match 19.5%; Score 41.2; DB 4; Length 1723;
Best Local Similarity 50.0%; Pred. No. 0.15;
Matches 103; Conservative 0; Mismatches 103; Indels 0; Gaps 0;
QY 2 CAAGGAGAGCGCTACGACCTGGCCGCGTGGTTCGGTCAAGGTCAACAAGAGCTGGG 61
Db 1222 CATGGGTGGCGCCAGCAGCGGTGAGCGGGGCGCAGTACGAGGATTCGTCGACCTGT 1163
QY 62 CATCACCGAGAACCCGCGCGACACGACTCGACACGCTGACCGAAGAGAGAGCTGCTGTCG 121
Db 1162 CATCCAGGCGATCAAGCGCGCTGGCCCAACGCTGCTGCTCAATTGAGAGACTTCGCCCA 1103
QY 122 CACCATGATGACTGCTGGTGGCTGCTATCATCGGCGCAGACAGATGACCGTCCCGGTGG 181
Db 1102 GACCAATGCCATGCCGCTGCTGAGCGGTCAAGAGGAGAGCTGTGCTGCTTCAACGACGA 1043
QY 182 AGTCAGGTGCCGCTCGAGGTGCAAG 207
Db 1042 CATCAGGCGACCGCGCGGTGGCG 1017

RESULT 10

US-09-252-991A-15231
; Sequence 15231, Application US/09252991A
; Patent No. 6551795

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 17, 2003, 11:54:34 ; Search time 109.82 Seconds
(without alignments)
4726.283 Million cell updates/sec

Title: US-09-697-123B-18

Perfect score: 211
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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1660708 seqs, 1229959015 residues

Total number of hits satisfying chosen parameters: 3321416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_NA.*

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- 3: /cgn2_6/ptodata/1/pubna/US06_PUBCOMB.seq.*
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- 7: /cgn2_6/ptodata/1/pubna/US08_PUBCOMB.seq.*
- 8: /cgn2_6/ptodata/1/pubna/US08_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/1/pubna/US09_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/1/pubna/US09_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/1/pubna/US09_PUBCOMB.seq.*
- 12: /cgn2_6/ptodata/1/pubna/US09_PUBCOMB.seq.*
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- 14: /cgn2_6/ptodata/1/pubna/US10_PUBCOMB.seq.*
- 15: /cgn2_6/ptodata/1/pubna/US10_PUBCOMB.seq.*
- 16: /cgn2_6/ptodata/1/pubna/US10_PUBCOMB.seq.*
- 17: /cgn2_6/ptodata/1/pubna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	83.4	39.5	3495	10	US-09-738-626-547
3	83.4	39.5	5096	10	US-09-984-711-5
4	83.4	39.5	5099	10	US-09-887-052-1
5	83.4	39.5	5099	10	US-09-887-052-3
6	83.4	39.5	5099	10	US-09-887-052-5
7	83.4	39.5	5099	12	US-10-076-406-1
8	83.4	39.5	5099	12	US-10-076-406-3
9	83.4	39.5	5099	12	US-10-076-406-5
10	83.4	39.5	5099	13	US-10-075-460-5
11	83.4	39.5	3309400	10	US-09-738-626-1
12	71	33.6	3543	14	US-10-156-761-4898
13	71	33.6	9025608	14	US-10-156-761-1
14	53.4	25.3	11058	14	US-10-156-761-3629
15	53.4	25.3	9025608	14	US-10-156-761-1
16	43.8	20.8	88421	10	US-09-976-059-1

17	42.6	20.2	3027	14	US-10-156-761-6263
18	42.2	20.0	1242	14	US-10-156-761-365
19	41.8	19.8	1104	14	US-10-156-761-6816
20	41.2	19.5	1035	14	US-10-156-761-5923
21	41.2	19.5	1723	11	US-09-975-719-135
22	40.4	19.1	1728	14	US-10-156-761-3783
23	40.4	19.1	7419	9	US-09-813-242-4009
24	40.2	19.1	2304	14	US-10-156-761-5121
25	40	19.0	267	9	US-09-923-876-1137
26	40	19.0	1254	14	US-10-128-714-2345
27	40	19.0	1254	14	US-10-128-714-2345
28	40	19.0	1416	14	US-10-128-714-1345
29	40	19.0	1416	14	US-10-128-714-6345
30	40	19.0	3415	14	US-10-128-714-345
31	39.8	18.9	3416	14	US-10-128-714-5345
32	39.8	18.9	453	10	US-09-887-576-797
33	39.8	18.9	1392	14	US-10-156-761-2193
34	39.6	18.8	257	9	US-09-923-876-1928
35	39.6	18.8	1548	14	US-10-156-761-3087
36	39.4	18.7	680	9	US-09-841-132-267
37	39.4	18.7	1176	14	US-10-156-761-3069
38	39.4	18.7	2302	14	US-10-037-370-915
39	39.4	18.7	2440	9	US-09-962-436-286
40	39.4	18.7	3756	9	US-09-841-132-425
41	39.2	18.6	529	13	US-10-027-632-287631
42	39.2	18.6	1260	14	US-10-156-761-1993
43	39.2	18.6	12123	11	US-09-764-872-752
44	38.8	18.4	921	14	US-10-156-761-1048
45	38.8	18.4	1083	14	US-10-156-761-4116

ALIGNMENTS

RESULT 1

US-09-712-363-30
Sequence 30, Application US/09712363
Patent No. US20020164588A1
GENERAL INFORMATION:
APPLICANT: Eisenberg, David
APPLICANT: Rotstein, Sergio H.
APPLICANT: Marcotte, Edward M.
TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS
FILE REFERENCE: 07419-032001
CURRENT APPLICATION NUMBER: US/09/712,363
CURRENT FILING DATE: 2000-11-13
PRIOR APPLICATION NUMBER: PCT/US00/02246
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 60/179,531
PRIOR FILING DATE: 2000-02-01
PRIOR APPLICATION NUMBER: 60/117,844
PRIOR FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: 60/118,206,
PRIOR FILING DATE: 1999-02-01
PRIOR APPLICATION NUMBER: 60/126,593
PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: 60/134,093
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 60/134,092
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 60/165,124
PRIOR FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 60/165,086
PRIOR FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 292
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 30
LENGTH: 3519
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
US-09-712-363-30

Sequence 365, App
Sequence 6816, App
Sequence 5923, App
Sequence 135, App
Sequence 3783, App
Sequence 4009, App
Sequence 5121, App
Sequence 1137, App
Sequence 2345, App
Sequence 1345, App
Sequence 6345, App
Sequence 345, App
Sequence 797, App
Sequence 2193, App
Sequence 1928, App
Sequence 3067, App
Sequence 267, App
Sequence 3069, App
Sequence 915, App
Sequence 286, App
Sequence 425, App
Sequence 287631, App
Sequence 1993, App
Sequence 752, App
Sequence 1048, App
Sequence 4116, App

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: GENERAL INFORMATION:
: APPLICANT: MOECKEL, Bettina
: APPLICANT: BATHE, Brigitte
: APPLICANT: HERMANN, Thomas
: APPLICANT: PFEFFERLE, Walter
: APPLICANT: BINDER, Michael
: TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE rpoB GENE
: FILE REFERENCE: 204212USOX
: CURRENT APPLICATION NUMBER: US/09/887,052
: CURRENT FILING DATE: 2001-06-25
: PRIOR APPLICATION NUMBER: DE10107229.5
: PRIOR FILING DATE: 2001-02-16
: NUMBER OF SEQ ID NOS: 8
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 1
: LENGTH: 5099

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; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
US-09-887-052-1

Query Match      39.5%; Score 83.4; DB 10; Length 5099;
Best Local Similarity 67.0%; Pred. No. 2.2e-14;
Matches 136; Conservative 0; Mismatches 61; Indels 6; Gaps 1;

QY 9 AAGCGCTACGACCTGGCCGCGTGGTGGTACAGGTCAACAAGAGCTGGGCATCACC 68
    |||||
Db 1578 AAGCGCTACGACCTGGCTGGTGGTGGTACAGATCAACCGAAGCTGGGCCTTGGT 1637

QY 69 GAGAACCCGGCGACACGCTCGACCGACGAGGACGATGACCGTCCCGGGTGGAGTCGAG 128
    |||||
Db 1638 GCGACCAACGATGGT-----TTGATGACTCTTACTGAAGAGACATCGCAACCACTC 1691

QY 129 GAGTACCTGGTGGCGCTGCATCAGGCGGACAGACGATGACCGTCCCGGGTGGAGTCGAG 188
    |||||
Db 1692 GAGTACCTGGTGGCTGCGACGAGGTGAGCGCGTCATGACTTCTCCAAATGGTGAAGAG 1751

QY 189 GTGCCCGTGGAGTGGACGACAT 211
    |||||
Db 1752 ATCCGAGTCGAGACCGATGACAT 1774

RESULT 5
US-09-887-052-3
; Sequence 3, Application US/09887052
; Patent No. US20020119537A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE TP0B GENE
; FILE REFERENCE: 204212USOX
; CURRENT APPLICATION NUMBER: US/09/887,052
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: DE10107229.5
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 3
; LENGTH: 5099
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
US-09-887-052-5

Query Match      39.5%; Score 83.4; DB 10; Length 5099;
Best Local Similarity 67.0%; Pred. No. 2.2e-14;
Matches 136; Conservative 0; Mismatches 61; Indels 6; Gaps 1;

QY 9 AAGCGCTACGACCTGGCCGCGTGGTGGTACAGGTCAACAAGAGCTGGGCATCACC 68
    |||||
Db 1578 AAGCGCTACGACCTGGCTGGTGGTGGTACAGATCAACCGAAGCTGGGCCTTGGT 1637

QY 69 GAGAACCCGGCGACACGCTCGACCGACGAGGACGATGACCGTCCCGGGTGGAGTCGAG 128
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Db 1638 GCGACCAACGATGGT-----TTGATGACTCTTACTGAAGAGACATCGCAACCACTC 1691

QY 129 GAGTACCTGGTGGCGCTGCATCAGGCGGACAGACGATGACCGTCCCGGGTGGAGTCGAG 188
    |||||
Db 1692 GAGTACCTGGTGGCTGCGACGAGGTGAGCGCGTCATGACTTCTCCAAATGGTGAAGAG 1751

QY 189 GTGCCCGTGGAGTGGACGACAT 211
    |||||
Db 1752 ATCCGAGTCGAGACCGATGACAT 1774

RESULT 6
US-09-887-052-5
; Sequence 5, Application US/09887052
; Patent No. US20020119537A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE TP0B GENE
; FILE REFERENCE: 204212USOX
; CURRENT APPLICATION NUMBER: US/09/887,052
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: DE10107229.5
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 5
; LENGTH: 5099
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
US-09-887-052-5

Query Match      39.5%; Score 83.4; DB 10; Length 5099;
Best Local Similarity 67.0%; Pred. No. 2.2e-14;
Matches 136; Conservative 0; Mismatches 61; Indels 6; Gaps 1;

QY 9 AAGCGCTACGACCTGGCCGCGTGGTGGTACAGGTCAACAAGAGCTGGGCATCACC 68
    |||||
Db 1578 AAGCGCTACGACCTGGCTGGTGGTGGTACAGATCAACCGAAGCTGGGCCTTGGT 1637

QY 69 GAGAACCCGGCGACACGCTCGACCGACGAGGACGATGACCGTCCCGGGTGGAGTCGAG 128
    |||||
Db 1638 GCGACCAACGATGGT-----TTGATGACTCTTACTGAAGAGACATCGCAACCACTC 1691

QY 129 GAGTACCTGGTGGCGCTGCATCAGGCGGACAGACGATGACCGTCCCGGGTGGAGTCGAG 188
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Db 1692 GAGTACCTGGTGGCTGCGACGAGGTGAGCGCGTCATGACTTCTCCAAATGGTGAAGAG 1751

QY 189 GTGCCCGTGGAGTGGACGACAT 211
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Db 1752 ATCCGAGTCGAGACCGATGACAT 1774

RESULT 7
US-10-076-406-1
; Sequence 1, Application US/10076406
; Publication No. US2003016684A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: Nucleotide sequences coding for the tpob gene
; FILE REFERENCE: 219774USOXIP
; CURRENT APPLICATION NUMBER: US/10/076,406
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: DE 10107229.5
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 09/887052
; PRIOR FILING DATE: 2001-06-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1
; LENGTH: 5099
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; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
; OTHER INFORMATION:
US-10-076-406-1

Query Match
  39.5%; Score 83.4; DB 12; Length 5099;
Best Local Similarity 67.0%; Pred. No. 2.2e-14;
Matches 136; Conservative 0; Mismatches 61; Indels 6; Gaps 1;

QY 9 AAGCGCTACGACCTGGCGGCTGCGGTACCAAGGTCAACAAGAGCTGGGATCACC 68
Db 1578 AAGCGCTACGACCTGGCGGCTGCGGTACCAAGGTCAACAAGAGCTGGGATCACC 68
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Db 1578 AAGCGCTACGACCTGGCGGCTGCGGTACCAAGGTCAACAAGAGCTGGGATCACC 68
;
QY 69 GAGAACCCGGCGACACGACCTCGACCGAGAGAGAGAGAGAGAGAGAGAGAGAG 128
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;
QY 129 GAGTACCTGGTGGCGGTGCGGTACCAAGGTCAACAAGAGCTGGGATCACC 188
Db 1692 GAGTACCTGGTGGCGGTGCGGTACCAAGGTCAACAAGAGCTGGGATCACC 188
;
QY 189 GTGCCCGTCGAGTCGACGACAT 211
Db 1752 ATCCAGTCGAGACCGATGACAT 1774
;
RESULT 9
US-10-076-406-5
; Sequence 5, Application US/10076406
; Publication No. US20030166884A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BARHE, Brigitte
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: Nucleotide sequences coding for the rpoB gene
; FILE REFERENCE: 219774US0XCIIP
; CURRENT APPLICATION NUMBER: US/10/076,406
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: DE 10107229-5
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 09/887052
; PRIOR FILING DATE: 2001-06-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 5
; TYPE: DNA
; LENGTH: 5099
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
; OTHER INFORMATION:
; NAME/KEY: mutation
; LOCATION: (2016)..(2016)
; OTHER INFORMATION: Substitution of cytosine by thymine
US-10-076-406-5

Query Match
  39.5%; Score 83.4; DB 12; Length 5099;
Best Local Similarity 67.0%; Pred. No. 2.2e-14;
Matches 136; Conservative 0; Mismatches 61; Indels 6; Gaps 1;

QY 9 AAGCGCTACGACCTGGCGGCTGCGGTACCAAGGTCAACAAGAGCTGGGATCACC 68
Db 1578 AAGCGCTACGACCTGGCGGCTGCGGTACCAAGGTCAACAAGAGCTGGGATCACC 68
;
QY 69 GAGAACCCGGCGACACGACCTCGACCGAGAGAGAGAGAGAGAGAGAGAGAGAG 128
Db 1638 GGCAGACACCATGGT-----TTGATGACTCTTACTGAAGAGGACATCGCAACCATC 1691
;
QY 129 GAGTACCTGGTGGCGGTGCGGTACCAAGGTCAACAAGAGCTGGGATCACC 188
Db 1692 GAGTACCTGGTGGCGGTGCGGTACCAAGGTCAACAAGAGCTGGGATCACC 188
;
QY 189 GTGCCCGTCGAGTCGACGACAT 211
Db 1752 ATCCAGTCGAGACCGATGACAT 1774
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RESULT 10
US-10-075-460-5
; Sequence 5, Application US/10075460
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; Publication No. US2002015557A1
; GENERAL INFORMATION:
; APPLICANT: MCKEL, BETTINA
; APPLICANT: BATHE, BRIGITTE
; APPLICANT: HANS, STEFAN
; APPLICANT: KREUTZER, CAROLINE
; APPLICANT: HERMANN, THOMAS
; APPLICANT: BINDER, MICHAEL
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE IPGL GENE
; FILE REFERENCE: 218472USOX
; CURRENT APPLICATION NUMBER: US/10/075,460
; PRIORITY FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: DE 10107230.9
; PRIORITY FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: DE 10162386.0
; PRIORITY FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 5099
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
; OTHER INFORMATION:

Query Match 39.5%; Score 83.4; DB 13; Length 5099;
Best Local Similarity 67.0%; Pred. No. 2.2e-14;
Matches 136; Conservative 0; Mismatches 61; Indels 6; Gaps 1;

QY 9 AAGCGTAGACACTGGCCGCTGCATCAAGGTTCGAAGAAGCCTGCCCATCACACC 68
Db 1578 AAGCGTTACAGACTGGCTGGTGTTGCGTTACAAGATCAACCGAACGCTGGCCTTGST 1637

QY 69 GAGAAACCCGGCGACACGACCTGCACACACCTGACCGAAGAGAGAGCTGCATCCACCATC 128
Db 1638 GGCGACACAGATTG-----TTGATGACTCTTACTGAAGAGAGATCCGACCATC 1691

QY 129 GAGTAACCTGGTGGCTGCATCAGGGCGACGACGATGACCGTCCCAGGTPGAGTGAG 188
Db 1692 GASTPACTGGTGGCTGCTGCACGAGTGGAGCGGCTGCTCCAAATGTTGAGAG 1751

QY 189 GTGCCGCTGAGTGCAGACAT 211
Db 1752 ATCCAGTCGAGACCGATGACAT 1774

RESULT 11
US-09-738-626-1
Sequence 1, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKIHITO
APPLICANT: IKEDA, MASATO
APPLICANT: OKAZKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
PRIORITY FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07

Prior Application Number: JP 00/280988
Prior Filing Date: 2000-08-03
Number Of Seq Id Nos: 7059
Software: PatentIn ver. 3.0
Seq Id No 1
Length: 3309400
Type: DNA
Organism: Corynebacterium glutamicum
US-09-738-626-1

Query Match 39.5%; Score 83.4; DB 10; Length 3309400;
Best Local Similarity 67.0%; Pred. No. 2.4e-14;
Matches 136; Conservative 0; Mismatches 61; Indels 6; Gaps 1;

QY 9 AAGCGTAGACACTGGCCGCTGGTTCGAAGAAGTCAACAAGAGCTGGGCGATCACACC 68
Db 513789 AAGCGTAGACACTGGCTGGTTCGAAGAATCAACCGCAAGCTCGGCTTGCT 513848

QY 69 GAGAAACCCGGCGACACGACCTGCACACACCTGACCGAAGAGAGAGCTGCATCCACCATC 128
Db 513849 GGCGACACAGATTG-----TTGATGACTCTTACTGAAGAGAGATCCGCAACCATC 513902

QY 129 GASTPACTGGTGGCTGCATCAGGGCGACGACGATGACCGTCCCCGGTGGAGTCGAG 188
Db 513903 GAGTAACCTGGTGGCTGCTGCACGAGTGGAGCGGCTGCTCCAAATGTTGAGAG 513962

QY 189 GTGCCGCTGAGTGCAGACAT 211
Db 513963 ATCCAGTCGAGACCGATGACAT 513985

RESULT 12
US-10-156-761-4898
Sequence 4898, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: ISHKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHITSUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 4898
LENGTH: 3543
TYPE: DNA
ORGANISM: Streptomyces avermitilis
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..
US-10-156-761-4898

Query Match 33.6%; Score 71; DB 14; Length 3543;
Best Local Similarity 62.6%; Pred. No. 6.8e-11;
Matches 132; Conservative 0; Mismatches 70; Indels 9; Gaps 1;

QY 1 TCRAAGGAGAGCGCTACGACCTGGCCGCTGGTGGTTCAGGTCAAGTCAAAGAAGCTGS 60
Db 926 TCACCCGAGAGCGCTACGACTCGGAGAGTGGCCGCTTACAGGTCAAGAAGCTGG 985

QY 61 GCATCACCCGAGAACCGGCGCGACACGACCTCGACACGCTGACCGAGAGAGCTGTG 120
Db 986 CGCGCGAGGGCGCGCTGGAGCGCCGGATC-----CTGACCGTGGAGACATCATCT 1036

```
QY 121 CCACATCGAGTACCTGGTGGCTGCATCAGGCGCAGACGATGATCCGTCGCCGGTG 180
Db 1037 GTCGATCAAGTACCTGGTGAAGCTGCACGCGCGTGAGACCGGCTTGGCAGACG 1096
QY 181 GAGTCGAGGTCGCCGTCGAGGTCGACGACAT 211
Db 1097 GCACCTCGATCGTGGTCGAGACCGACGACAT 1127

RESULT 13
US-10-156-761-1
; Sequence 1, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
; LENGTH: 9025608
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1

Query Match 33.6%; Score 71; DB 14; Length 9025608;
Best Local Similarity 62.8%; Pred. No. 7.5e-11;
Matches 132; Conservative 0; Mismatches 70; Indels 9; Gaps 1;

QY 1 TCAAGGAGAACGCGCTACGACCTGGCGCGCTGGTGCATCAGGTCACCAAGAGCTGG 60
Db 5970494 TCAACCGAAGCGCTAGACCTCGCGAAGGTCGCGCTACAGGTCAACAGAGCTGG 5970553
QY 61 GCATCACCAGAACCGCGCGCGCACACCTCGACACCGTGCAGGACGAGGAGCTGCTCG 120
Db 5970554 GCGGCGAGGCGCGCTGGACGCGCGGATC-----CTGACCGTCGAGGACATCATCT 5970604
QY 121 CCACATCGAGTACCTGGTGGCTGCATCAGGCGCAGACGATGATCCGTCGCCGGTG 180
Db 5970605 GTCGATCAAGTACCTGGTGAAGCTGCACGCGGTGAGACCGGACCGGCTTGGCAGACG 5970664
QY 181 GAGTCGAGGTCGCCGTCGAGGTCGACGACAT 211
Db 5970665 GCACCTCGATCGTGGTCGAGACCGACGACAT 1127

RESULT 14
US-10-156-761-3629
; Sequence 3629, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
```

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; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 3629
; LENGTH: 11058
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(11058)
US-10-156-761-3629

Query Match 25.3%; Score 53.4; DB 14; Length 11058;
Best Local Similarity 55.0%; Pred. No. 6.2e-06;
Matches 105; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

QY 17 GCACCTGGCGCGCTGGTGCATCAGGTCACCAAGAGCTGGGCGATCACCAGACCC 76
Db 2283 GCACCGGTTGGGCTCGACCGGATCGCGCTGTCACATGTACGGGATCACCAGACCC 2342
QY 77 GCGCGACACGACCTCGACCCACCTGACCGAAGAGGAGCTGTCGCCACCATCGAGTACCT 136
Db 2343 GCTCCACACACCTTACCACCGGCTGACCGGAGGAGCTGGACCGCGGGGCGGACACGC 2402
QY 137 GGTGCGGCTGCATCAGGCGCACAGACGATGATCCGCGGTGGAGTCGAGTGCCTCGT 196
Db 2403 GGTGCGGCATCCGCTGCGCGACCTCGCGGTGTACTCTCTGGACCGGACCGACGCTGGT 2462
QY 197 CGAGTGCAGC 207
Db 2463 CCCGTCGCGC 2473

RESULT 15
US-10-156-761-1/c
; Sequence 1, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
; LENGTH: 9025608
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1

Query Match 25.3%; Score 53.4; DB 14; Length 9025608;
Best Local Similarity 55.0%; Pred. No. 6.7e-06;
Matches 105; Conservative 0; Mismatches 86; Indels 0; Gaps 0;
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QY 17 CGACCTGGCCCGCTGGCTCGGTACAGGTCAACAGAGCTGGGCATCACCAGAACCC 76
Db 4508863 CGACCGGTTCCGGGCTCGACCGGATCGCGCTCGTCAACATGTACGGGATCACCAGAGCCAC 4508804
QY 77 GGCGGACAGGACCTCGACACGCTGACCGAGAGGAGCGTCTGCCACCATCGAGTACCT 136
Db 4508803 CGTCCACACCACTTACCACCGGCTGACCGAGCGGGACCTGGACCCCGGGGGCGGCAACGC 4508744
QY 137 GGTGGGCTGTCATCAAGGGGACAAAGACGATGACCGGTCGGGTGGAGTCCGAGGTGCCCGT 196
Db 4508743 GGTGGGCAATCGCTGGCGGACCTCGGGGTGTACCTCTCTGGAGCGGGACCGACAGCTGGT 4508684
QY 197 CGAGGTCGACG 207
Db 4508683 CCGGTCGGCG 4508673
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Search completed: September 17, 2003, 13:08:29
Job time : 135.82 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 17, 2003, 11:54:34 ; Search time 30.1105 Seconds
(without alignments)
3049.028 Million cell updates/sec

Title: US-09-697-123B-19

Perfect score: 208

Sequence: 1 tcaaggagagcgtacgac.....ccggctgaggtgagcagacat 208

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_NA.*

- 1: /cgn2_6/ptodata/1/ina/5A.COMB.seq.*
- 2: /cgn2_6/ptodata/1/ina/5B.COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A.COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B.COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/PCTUS.COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	166.4	80.0	970	1	US-08-250-030-1
2	166.4	80.0	970	5	PCT-US95-06790-1
3	166.4	80.0	4403765	3	US-09-103-840A-2
4	166.4	80.0	4411529	3	US-09-103-840A-1
5	142.4	68.5	3447	2	US-08-313-185-57
6	142.4	68.5	3447	3	US-09-082-614A-57
7	42.8	20.6	1734	6	5352575-8
8	42.2	20.3	1057	4	US-09-452-239-5
9	42.2	20.3	4403765	3	US-09-103-840A-2
10	42.2	20.3	4411529	3	US-09-103-840A-1
11	41.6	20.0	540	4	US-09-252-991A-7249
12	41.6	20.0	1722	4	US-09-252-991A-7450
13	41.2	19.8	1389	4	US-09-252-991A-4243
14	41.2	19.8	2958	4	US-09-252-991A-4323
15	41.2	19.8	2874	4	US-09-252-991A-4533
16	40.8	19.6	795	4	US-09-252-991A-7582
17	40.8	19.6	1755	4	US-09-252-991A-7740
18	39.6	19.0	702	4	US-09-252-991A-3145
19	39.6	19.0	1416	4	US-09-252-991A-3049
20	39.6	19.0	1545	4	US-09-252-991A-2823
21	39.4	18.9	1416	4	US-09-252-991A-2955
22	39.4	18.9	1512	4	US-09-252-991A-2728
23	39.4	18.9	47981	4	US-09-679-279-1
24	38.8	18.7	1450	1	US-07-923-692C-5
25	38.8	18.7	1450	1	US-08-184-237-5
26	38.8	18.7	1450	2	US-08-482-920-5
27	38.8	18.7	1450	3	US-08-484-341-5

28	38.8	18.7	2742	3	US-09-232-458A-1	Sequence 1, Appli
29	38.8	18.7	2742	4	US-09-784-984B-1	Sequence 1, Appli
30	38.8	18.7	4087	6	5196516-7	Patent No. 5196516
31	38.8	18.7	6085	3	US-09-029-603-4	Sequence 4, Appli
32	38.6	18.6	642	4	US-09-252-991A-10515	Sequence 10515, A
33	38.6	18.6	690	4	US-09-252-991A-10422	Sequence 10422, A
34	38.6	18.6	1116	4	US-09-252-991A-7460	Sequence 7460, Ap
c 34	38.6	18.6	1164	1	US-07-640-476-6	Sequence 6, Appli
35	38.6	18.6	1164	4	US-09-252-991A-7184	Sequence 7184, Ap
36	38.6	18.6	1767	4	US-09-252-991A-7241	Sequence 7241, Ap
37	38.6	18.6	1791	4	US-09-252-991A-5303	Sequence 5303, Ap
c 37	38.2	18.4	483	4	US-09-252-991A-5198	Sequence 5198, Ap
39	38.2	18.4	1284	4	US-09-420-211-1	Sequence 1, Appli
40	38	18.3	1131	4	US-09-252-991A-12655	Sequence 12655, A
c 41	38	18.3	1455	4	US-09-252-991A-13312	Sequence 13312, A
42	38	18.3	1488	4	US-09-252-991A-3309	Sequence 3309, Ap
43	37.8	18.2	471	4	US-09-347-801-1	Sequence 1, Appli
44	37.8	18.2	484	3	US-09-252-991A-3366	Sequence 3366, Ap
c 45	37.8	18.2	789	4		

ALIGNMENTS

RESULT 1

US-08-250-030-1
; Sequence 1, Application US/08250030
; Patent No. 5643723

GENERAL INFORMATION:

APPLICANT: Persing, David H.
TITLE OF INVENTION: Detection of a Genetic Locus Encoding
TITLE OF INVENTION: Resistance to Rifampin in Mycobacterial Cultures and in
TITLE OF INVENTION: Clinical Specimens
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman, Lundberg & Woessner
STREET: 3500 IDS Center
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/250,030
FILING DATE: 26-MAY-1994
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Muetling, Ann M. 33,977
REGISTRATION NUMBER: 33,977

REFERENCE/DOCKET NUMBER:

REFERENCE/DOCKET NUMBER: 150.105US1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 612-339-0331

TELEFAX:

TELEFAX: 612-339-3061

INFORMATION FOR SEQ ID NO:

1:

SEQUENCE CHARACTERISTICS:

LENGTH: 970 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

US-08-250-030-1

Query Match 80.0%; Score 166.4; DB 1; Length 970;
Best Local Similarity 87.5%; Pred. No. 7.6e-31;
Matches 182; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 1 TCAAGGAGAGCGGTACGACCTGGCCCGGCTGGCGGCTACAGGTCACACAGAGCTGG 60

DB 26 TCAAGGAGAGCGGTACGACCTGGCCCGGCTGGCGGCTACAGGTCACACAGAGCTGG 85

Best Local Similarity 87.5%; Pred. No. 1.4e-30;
Matches 182; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 1 TCAAGAGAAAGCGCTACGACCTGGCCCGCTGGCCGCTACAGGTCAACAGAGAGCTGG 60
Db 760688 TCAAGAGAAAGCGCTACGACCTGGCCCGCTGGCCGCTACAGGTCAACAGAGAGCTGG 760747
QY 61 GCCTGACGCGCGCGCGCGCGATCAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 120
Db 760748 GCCTGACGCGCGCGCGCGCGATCAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 760807
QY 121 CCATCGATATCTGGTCCGCTGGCAGAGGCGCGACGATGACCGTCCCGCGCGCG 180
Db 760808 CCATCGATATCTGGTCCGCTGGCAGAGGCGCGACGATGACCGTCCCGCGCGCG 760867
QY 181 TCGAGGTCCCGGTGGAGTGGAGCAGCAT 208
Db 760868 TCGAGGTCCCGGTGGAGTGGAGCAGCAT 760895

RESULT 5

US-08-313-185-57
; Sequence 57, Application US/08313185
; Patent No. 5851763

GENERAL INFORMATION:
; APPLICANT: Heym, Beate

; APPLICANT: Cole, Stewart

; APPLICANT: Young, Douglas

; APPLICANT: Zhang, Ying

; APPLICANT: Honore, Nadine

; APPLICANT: Telenti, Amalio

; APPLICANT: Bodmer, Thomas

; TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
; TITLE OF INVENTION: in Mycobacterium Tuberculosis

; NUMBER OF SEQUENCES: 66

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &

; ADDRESSEE: Dunner

; STREET: 1300 I Street, N.W.

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20005-3315

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/313,185

; FILING DATE: 12-OCT-1994

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Meyers, Kenneth J.

; REGISTRATION NUMBER: 25,146

; REFERENCE/DOCKET NUMBER: 02356.0068-00000

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 408-4000

; TELEFAX: (202) 408-4400

; INFORMATION FOR SEQ ID NO: 57:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 3447 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

US-08-313-185-57

Query Match 68.5%; Score 142.4; DB 2; Length 3447;
Best Local Similarity 80.3%; Pred. No. 3.5e-25;
Matches 167; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 1 TCAAGAGAAAGCGCTACGACCTGGCCCGCTGGCCGCTACAGGTCAACAGAGAGCTGG 60

Db 809 TCAAGAGAAAGCGCTACGACCTGGCCCGCTGGCCGCTACAGGTCAACAGAGAGCTGG 868
QY 61 GCCTGACGCGCGCGCGCGATCAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 120
Db 869 GGTTCACGCGCGGTGAGTTGATCAGTGGTCCACGCTGACCGAGAGGATGTCGCTGCCCA 928
QY 121 CCATCGATATCTGGTCCGCTGGCAGAGGCGCGACGATGACCGTCCCGCGCGCG 180
Db 929 CCATGAGTACCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 988
QY 181 TCGAGGTCCCGGTGGAGTGGAGCAGCAT 208
Db 989 TAGAAGTCCCACTGGAACTGACGATAT 1016

RESULT 6

US-09-082-614A-57

; Sequence 57, Application US/09082614A

; Patent No. 6124098

GENERAL INFORMATION:

; APPLICANT: Heym, Beate

; APPLICANT: Cole, Stewart

; APPLICANT: Young, Douglas

; APPLICANT: Zhang, Ying

; APPLICANT: Honore, Nadine

; APPLICANT: Telenti, Amalio

; APPLICANT: Bodmer, Thomas

; TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance

; TITLE OF INVENTION: in Mycobacterium Tuberculosis

; NUMBER OF SEQUENCES: 66

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &

; ADDRESSEE: Dunner

; STREET: 1300 I Street, N.W.

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20005-3315

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/082,614A

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/313,185

; FILING DATE: 12-OCT-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Meyers, Kenneth J.

; REGISTRATION NUMBER: 25,146

; REFERENCE/DOCKET NUMBER: 02356.0068-00000

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 408-4000

; TELEFAX: (202) 408-4400

; INFORMATION FOR SEQ ID NO: 57:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 3447 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

US-09-082-614A-57

Query Match 68.5%; Score 142.4; DB 3; Length 3447;
Best Local Similarity 80.3%; Pred. No. 3.5e-25;
Matches 167; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 1 TCAAGAGAAAGCGCTACGACCTGGCCCGCTGGCCGCTACAGGTCAACAGAGAGCTGG 60

Db	809	TCAGGAGAAACGCTACGACCTCGCCACAGGCTGGTTCAGGTACACAGACGCTCG	868
QY	61	GCCTGAACGCCCGCCAGCCGATCACGTCGCGACTCTGACCGAGGAGAGCTGTCGCCA	120
Db	859	GGTTGCACGCCCGTGGTGTGATCACGTCGCTCCAGCTGACCGAGAGGATGTCGTCGCCA	928
QY	121	CCATCGAGTACTGTGTGCGSCTGTCAGGAGGGCCAGACCGATCACGCTCCCGCGGGCG	180
Db	929	CCATAGAGTACCTGTGTGCTGCTGATGAGGGTCAGTCGACAACTGACTGCCAGGTGGG	988
QY	181	TCGAGGTCCCGGTGAGGTGGACGACAT	208
Db	989	TAGAAGTGCACGTGGAACATCAGCATAT	1016

RESULT 7
5352575-8
Patent No. 5352575
APPLICANT: PETROVSKIS, ERIK A.; POST, LEONARD E.; TIMMINS, JAMES G.
TITLE OF INVENTION: PSEUDORABIES VIRUS PROTEIN
NUMBER OF SEQUENCES: 12
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/513,282
FILING DATE: 20-APR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 100,817
FILING DATE: 29-JUN-1987
APPLICATION NUMBER: 886,260
FILING DATE: 16-JUL-1986
APPLICATION NUMBER: 784,787
FILING DATE: 04-OCT-1985
APPLICATION NUMBER: 801,799
FILING DATE: 26-NOV-1985
APPLICATION NUMBER: 844,113
FILING DATE: 26-MAR-1986
SEQ ID NO: 8
LENGTH: 1734
5352575-8

Query Match	20.6%;	Score 42.8;	DB 6;	Length 1734;
Best Local Similarity	61.8%;	Prod. No. 0.072;		
Matches 68;	Conservative	0;	Mismatches 42;	Indels 0;
Gaps	0;			

QY	99	ACGAGAGAGAGCTGTCGCCACCAATCGAGTACTCTGTGTGCGCTGCACGAGGGCCAGACC	158
Db	1114	ACCGCGCGCGCTACTCAGCGTCACTCAAGAGACTGCAGCGCCCGCGCCCGCGCCCGCGGC	1173
QY	159	ACGATGACCGTCCCGCGGGCGTCGAGGTCCCGCTCGAGGTGGAGCACAT	208
Db	1174	ACCCGCTGGGGCCCCCGCGCGCGCGACGACGGGATCTACGTGGACGGCGT	1223

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RESULT 8
US-09-452-239-5
; Sequence 5, Application US/09452239
; Patent No. 6465229
; GENERAL INFORMATION:
; APPLICANT: Rafalski, Antoni J.
; APPLICANT: Fader, Gary M.
; APPLICANT: Cahoon, Rebecca E.
; TITLE OF INVENTION: Plant Caffeoyl-CoA O-Methyltransferase
; FILE REFERENCE: BEL284 US NA
; CURRENT APPLICATION NUMBER: US/09/452,239
; CURRENT FILING DATE: 1999-12-01
; EARLIER APPLICATION NUMBER: 60/110,594
; EARLIER FILING DATE: 1998-December-02
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 5
; LENGTH: 1057
; TYPE: DNA
; ORGANISM: Zea mays
US-09-452-239-5

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Query Match	20.3%;	Score 42.2;	DB 4;	Length 1057;
Best Local Similarity	51.9%;	Pred. NO. 0.096;		
Matches	95;	Conservative	0;	Mismatches 88; Indels 0; Gaps 0;
QY	21	CTGCCCGCGCTGGCGCGCTACAAAGTCTAACAAAGAGCTGGGCGCTGAACGCGCGGCCACCG	80	
Db	292	CTGATCAAGCTGAGCGCGCGCCGACCCCTGGAGTGGGCGTTCACGGGTACTCG	351	
QY	81	ATCAAGCTGTCGACTGTGACCGGAGGAGAGCTGCTGGCCACCATCGACTACTCTGGTGGCG	140	
Db	352	CTGTGGCGAGCGCTCTGGCGGTGCGCGCGCCGAGGCAAGTCTATCGACTTCGAGCTGAGC	411	
QY	141	CTGCACGAGGGCCAGACCAACGATACCGTCTCCCGGGCGTGGAGGTCCCGGTTCGAGGTG	200	
Db	412	CGGAGTACTACGACATCGCGCGCCCTTCATCGAGCGCGCGGGTGGCGGGCAAGGTG	471	
QY	201	GAC	203	
Db	472	GAC	474	

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RESULT 9
US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

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	Query Match	20.3%	Score 42.2	DB 3	Length 4403765
	Best Local Similarity	52.6%	Prod. No. 0.17		
	Matches 92	Conservative	0	Mismatches 83	Indels 0
	Gaps	0			
QY	32	GGCGCGGTACAAAGTCAACAAGAAGCTGGCGCTCAACGGCGGCACGCGATCAGTCGTC	91		
Db	597306	GGACGCGACCGCGAATCACCCGATGACCTGGACGGCGGCCACAGGATGCTGAT	597247		
QY	92	GACTGTGACGCGAGAAAGCTGCTGCCACCATCGAGTACCTGGTGGCTGCTCAGAGGG	151		
Db	597246	CACCGCTACCCCATAGAACTCGCGGCCACCATGCCCGCGCTCGGCTAAACGGGCGC	597187		
QY	152	CCAGACACGATGACGCTCCCGCGGGCTCGAGGTCCCGTCCAGGTGTGGAGCAC	206		
Db	597186	CTGGGACGCTGCCGAGCTCGGTGCGCGGATATCACGGCAGACATGGTGGCG	597132		

RESULT 10
US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLETSCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.

```
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match      20.3%; Score 42.2; DB 3; Length 4411529;
Best Local Similarity 52.6%; Pred. No. 0.17;
Matches 92; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

QY 32 GGGCGGTACAAAGTCAACAAGAGCTGGGCTGAACGGCGGCCGCGCATCAGTCGTC 91
Db 595945 GGACGGACCGCGAACTACCCAGATGCACTGGACGGCGGCCAGAGGTATGGCTGAT 595886

QY 92 GACTCTGACCGAGGAGAAAGTGTGCTGCCACCATCGAGTACTGGTCGCGCTGCACGAGGG 151
Db 595885 CACCGCTACCCCATAGAACTCGCGGCCACCATCGCCCGCGCTGGGCTTAACCGGCGC 595826

QY 152 CGAGACACAGATGACGTCGCCCGCGCGGTGCGAGGTCCCGGTGAGGTGGACGAC 206
Db 595825 COTGGCACCGTCGCGAGTGTGTCGACGGGATATTCACGGCAGACTGGTCGGC 595771

RESULT 11
US-09-252-991A-7249
; Sequence 7249, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; LENGTH: 540
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7249

Query Match      20.0%; Score 41.6; DB 4; Length 540;
Best Local Similarity 52.3%; Pred. No. 0.13;
Matches 92; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY 21 CTGGCCCGCTGGGCGCTACAAAGTCAACAGAGCTGGGCTGAACCCGCGCCAGCG 80
Db 190 CTGACCCGCTGGGCGCACGATGAGTGTGATCGAGCAGATCACCAGAAACCTCAACAAGCTG 249

QY 81 ATCAGCTGTGACTCTGACCCAGGAGACGTCGTCGCCACCATCGAGTACCTGTGCGC 140
Db 250 ATCGAAGTGTGAAGCTGTGGATCTGTGCGAAAGCCCATATCGAGCGGAGTGATG 309

QY 141 CTGCAGAGGCCACGACGATGACCGTCCCGCGCGCTGCGAGTCCCGTCGA 196
Db 310 CTGGTGAAGGTCAAGGCCAGCGGCCGCCAGCCGCCGAGGTCAAGCGCACCCGA 365

RESULT 12
US-09-252-991A-7450/c
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; Sequence 7450, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 7450
; LENGTH: 1722
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7450

Query Match      20.0%; Score 41.6; DB 4; Length 1722;
Best Local Similarity 52.3%; Pred. No. 0.14;
Matches 92; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY 21 CTGGCCCGCTGGGCGCTACAAAGTCAACAGAGCTGGGCTGAACCGCGCCAGCG 80
Db 1512 CTGACCCGCTGGGCGCACGATGAGTGTGATCGAGCAGATCACAAGACCTCAACAAGCTG 1453

QY 81 ATCAGCTGTGCTGACTCTGACCGAGGAGACGTCGTGCCACCATCGAGTACCTGTGTCGC 140
Db 1452 ATCGAAGTGTGCTGAGCTGGTGTCTCTCGAAAGCCCATATCGAGCGGAGTGATG 1393

QY 141 CTGCACAGAGGCCACGACGATGACCGTCCCGCGCGCTGAGGTCCTCCGGTGA 196
Db 1392 CTGTGTAAGTCAAGGCCACGCGGCCGCCAGCGCGGAGTCAAGCGCACCCGA 1337

RESULT 13
US-09-252-991A-4243/c
; Sequence 4243, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 4243
; LENGTH: 1389
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-4243

Query Match      19.8%; Score 41.2; DB 4; Length 1389;
Best Local Similarity 59.3%; Pred. No. 0.17;
Matches 70; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 5 GGAGAGGCGTACGACCTCGCGCGCGCTGGGCGCTACAAGTCAACAAGAGCTGGGCT 64
Db 691 GCGGAGCGCAGCAAGTGTGTTCGCGGTGATCCGCGGAGTCTCTGTGAAAGAGCTGGCGAT 632

QY 65 GAACCGCGGCCACCGCATCATCGTCGACTCTCACCGAGGAGAGAGCTGTGCGCAC 122
Db 631 CAGCGCCGCGAGGCGGAGAGCGTGTGCGGAGGAGCTGTGCGTAGTGTGCGCGCACCC 574

RESULT 14
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OM nucleic - nucleic search, using sw model

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(without alignments)
4726.283 Million cell updates/sec

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Perfect score: 208
Sequence: 1 tcaagagagagcgctacgac.....ccggtcgagggtgacgacat 208

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1660708 seqs, 1229959015 residues

Total number of hits satisfying chosen parameters: 3321416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

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11: /cgn2.6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2.6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13: /cgn2.6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2.6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2.6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
16: /cgn2.6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
17: /cgn2.6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	166.4	80.0	3519	10	US-09-712-363-30
2	88	42.3	3495	10	US-09-738-626-547
3	88	42.3	5096	10	US-09-884-711-5
4	88	42.3	5099	10	US-09-887-052-1
5	88	42.3	5099	10	US-09-887-052-3
6	88	42.3	5099	10	US-09-887-052-5
7	88	42.3	5099	12	US-10-076-406-1
8	88	42.3	5099	12	US-10-076-406-3
9	88	42.3	5099	12	US-10-076-406-5
10	88	42.3	5099	13	US-10-075-460-5
11	88	42.3	3309400	10	US-09-738-626-1
12	82	39.4	3543	14	US-10-156-761-4898
13	82	39.4	9025608	14	US-10-156-761-1
14	47.4	22.8	11058	14	US-10-156-761-3629
15	47.4	22.8	9025608	14	US-10-156-761-1
16	45.2	21.7	993	14	US-10-156-761-4673

17	44.6	21.4	1395	14	US-10-205-032-21	Sequence 21, Appl
18	44.6	21.4	60196	14	US-10-205-032-1	Sequence 1, Appl
19	43.2	20.8	1800	14	US-10-156-761-5464	Sequence 5464, Ap
20	43	20.7	3828	14	US-10-156-761-2959	Sequence 2959, Ap
21	42.8	20.6	1176	14	US-10-156-761-1625	Sequence 1625, Ap
22	42.4	20.4	1131	14	US-10-156-761-2479	Sequence 2479, Ap
23	42.4	20.4	1320	14	US-10-156-761-6285	Sequence 6285, Ap
24	42.4	20.4	2850	14	US-10-156-761-364	Sequence 364, Appl
25	42.2	20.3	1057	9	US-09-452-339-5	Sequence 5, Appl
26	42.2	20.3	1068	14	US-10-156-761-1261	Sequence 1261, Ap
27	42.2	20.3	86114	15	US-10-080-170-648	Sequence 648, App
28	42	20.2	2693	10	US-09-880-107-3578	Sequence 3578, Ap
29	41.8	20.1	2484	14	US-10-156-761-912	Sequence 912, App
30	41.6	20.0	492	9	US-09-815-242-7946	Sequence 7946, Ap
31	41.6	20.0	792	14	US-10-156-761-6070	Sequence 6070, Ap
32	41.6	20.0	1287	14	US-10-156-761-5314	Sequence 5314, Ap
33	41.6	20.0	5418	14	US-10-156-761-5959	Sequence 5959, Ap
34	41.4	19.9	1149	14	US-10-156-761-6742	Sequence 6742, Ap
35	41.4	19.9	1389	14	US-10-156-761-5431	Sequence 5431, Ap
36	41.2	19.8	948	14	US-10-156-761-3927	Sequence 3927, Ap
37	41	19.7	1215	14	US-10-156-761-2811	Sequence 2811, Ap
38	41	19.7	2565	14	US-10-156-761-7062	Sequence 7062, Ap
39	40.6	19.5	435	14	US-10-156-761-6735	Sequence 6735, Ap
40	40.6	19.5	1003	12	US-10-361-460-33	Sequence 33, Appl
41	40.4	19.4	392	10	US-09-878-574-3598	Sequence 3598, Ap
42	40.4	19.4	1578	14	US-10-156-761-3369	Sequence 3369, Ap
43	40.2	19.3	1164	14	US-10-156-761-7161	Sequence 7161, Ap
44	40	19.2	1344	14	US-10-156-761-4839	Sequence 4839, Ap
45	39.8	19.1	2019	14	US-10-156-761-1314	Sequence 1314, Ap

ALIGNMENTS

RESULT 1
US-09-712-363-30
; Sequence 30, Application US/09712363
; Patent No. US20020164588A1
; GENERAL INFORMATION:
; APPLICANT: Eisenberg, David
; APPLICANT: Rotstein, Sergio H.
; APPLICANT: Marcotte, Edward M.
; TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND
; FILE REFERENCE: 07419-032001
; CURRENT APPLICATION NUMBER: US/09/712,363
; CURRENT FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: PCT/US00/02246
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,531
; PRIOR FILING DATE: 2000-02-01
; PRIOR APPLICATION NUMBER: 60/117,844
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/118,206
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: 60/126,593
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/134,093
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/134,092
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/165,124
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/165,086
; PRIOR FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 292
; SEQ ID NO 30
; SOFTWARE: FastSeq for Windows Version 4.0
; LENGTH: 3519
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-09-712-363-30

Query Match	42.3%;	Score 88;	DB 10;	Length 3495;
Best Local Similarity	68.5%;	Prod. No. 6.5e-16;		
Matches 137;	Conservative	0;	Mismatches 60;	Indels 3; Gaps 1;
QY	9	AAGCGGTACGACTGGCCGCGTGGGCGCGTCAAGGCTCAACAAGAGCTGGCGCTGAAC	68	
Db	877	AAGCGGTACGACTGGCTCGCGTGGTGGTGTACAGATCAACCCACAGCTCGGCGTTGGT	936	
QY	69	GCGGGCCAGCGGATCAGCTCGTGTGATCTCTGACCGAGGAAGACGTGCTGCCACCATCGAG	128	
Db	937	GCGGACACCGAGTGGT---TTGATGACTCTTACTGAAGAGGACATCGCAACCAACCATCGAG	993	
QY	129	TACCTGGTGGCGCTGCAGAGGCGACAGACCGATGACCGTCCCGCGCGCGCTCGAGGTC	188	
Db	994	TACCTGGTGGCTGCAGCGCAGGTGAGCGCGTCAATGACTTCTCCAAATGGTGAAGAGATC	1053	
QY	189	CCGCTCGAGGTTGGACGAAT	208	
Db	1054	CCAGTCGAGACCGATGACAT	1073	

; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
US-09-887-052-1

Query Match 42.3%; Score 88; DB 10; Length 5099;
Best Local Similarity 68.5%; Pred. No. 6.4e-16;
Matches 137; Conservative 0; Mismatches 60; Indels 3; Gaps 1;

QY 9 AAGCGCTACGACCTGGCCGCGCTGACGAGTCAAGGTCAACAGAGCTGGCGCTGAAC 68
DB 1578 AAGCGCTACGACCTGGCTGGCTGCTGTGCTACAGATCAACCGAAGCTGGCTTGGT 1637
QY 69 GCGCGCCAGCGATCAGCTGCTGCTGACCGAGAGAGTGTGTCGCCACCATCGAG 128
DB 1638 GCGGACCAAGATGTTTATGATGACTCTTACTGAAGAGACATCGCAACCAACCATCGAG 1694
QY 129 TACCTGGTGGCGCTGACAGAGGCGCAGACACGATGACCGTCCCGCGGCGTGCAGGTC 188
DB 1695 TACCTGGTGGCTGACAGGCGTGCAGCGGCTCATGACTTCTCCAAATGGTGAAGAGATC 1754
QY 189 CCGGTCGAGGTGGACGACAT 208
DB 1755 CCAGTCGAGACCGATGACAT 1774

RESULT 5
US-09-887-052-3
; Sequence 3, Application US/09887052
; Patent No. US20020119537A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE rpoB GENE
; FILE REFERENCE: 204212USOX
; CURRENT APPLICATION NUMBER: US/09/887,052
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: DE10107229.5
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 5099
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
US-09-887-052-3

Query Match 42.3%; Score 88; DB 10; Length 5099;
Best Local Similarity 68.5%; Pred. No. 6.4e-16;
Matches 137; Conservative 0; Mismatches 60; Indels 3; Gaps 1;

QY 9 AAGCGCTACGACCTGGCCGCGCTGACGAGTCAAGGTCAACAGAGCTGGCGCTGAAC 68
DB 1578 AAGCGCTACGACCTGGCTGGCTGCTGTGCTACAGATCAACCGAAGCTGGCTTGGT 1637
QY 69 GCGCGCCAGCGATCAGCTGCTGCTGACCGAGAGAGCTGCTGCCACCATCGAG 128
DB 1638 GCGGACCAAGATGTTTATGATGACTCTTACTGAAGAGACATCGCAACCAACCATCGAG 1694
QY 129 TACCTGGTGGCGCTGACAGAGGCGCAGACACGATGACCGTCCCGCGGCGTGCAGGTC 188
DB 1695 TACCTGGTGGCTGACAGGCGTGCAGCGGCTCATGACTTCTCCAAATGGTGAAGAGATC 1754
QY 189 CCGGTCGAGGTGGACGACAT 208
DB 1755 CCAGTCGAGACCGATGACAT 1774

DB 1755 CCAGTCGAGACCGATGACAT 1774

RESULT 6
US-09-887-052-5
; Sequence 5, Application US/09887052
; Patent No. US20020119537A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE rpoB GENE
; FILE REFERENCE: 204212USOX
; CURRENT APPLICATION NUMBER: US/09/887,052
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: DE10107229.5
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 5099
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
US-09-887-052-5

Query Match 42.3%; Score 88; DB 10; Length 5099;
Best Local Similarity 68.5%; Pred. No. 6.4e-16;
Matches 137; Conservative 0; Mismatches 60; Indels 3; Gaps 1;

QY 9 AAGCGCTACGACCTGGCCGCGCTGACGAGTCAAGGTCAACAGAGCTGGCGCTGAAC 68
DB 1578 AAGCGCTACGACCTGGCTGGCTGCTGTGCTTACAAGATCAACCGAAGCTGGCTTGGT 1637
QY 69 GCGCGCCAGCGATCAGCTGCTGCTGACCGAGAGAGCTGCTGCCACCATCGAG 128
DB 1638 GCGGACCAAGATGTTTATGATGACTCTTACTGAAGAGACATCGCAACCAACCATCGAG 1694
QY 129 TACCTGGTGGCGCTGACAGAGGCGCAGACACGATGACCGTCCCGCGGCGTGCAGGTC 188
DB 1695 TACCTGGTGGCTGACAGGCGTGCAGCGGCTCATGACTTCTCCAAATGGTGAAGAGATC 1754
QY 189 CCGGTCGAGGTGGACGACAT 208
DB 1755 CCAGTCGAGACCGATGACAT 1774

RESULT 7
US-10-076-406-1
; Sequence 1, Application US/10076406
; Publication No. US20030186884A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: Nucleotide sequences coding for the rpoB gene
; FILE REFERENCE: 219774USOXIP
; CURRENT APPLICATION NUMBER: US/10/076,406
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: DE 10107229.5
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 09/887052
; PRIOR FILING DATE: 2001-06-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 5099

RESULT 10
US-10-075-460-5
; Sequence 5, Application US/10075460

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; Publication No. US20020155557A1
; GENERAL INFORMATION:
; APPLICANT: MCKEL, BETTINA
; APPLICANT: BATHE, BRIGITTE
; APPLICANT: HANS, STEFAN
; APPLICANT: KREUTZER, CAROLINE
; APPLICANT: HERMANN, THOMAS
; APPLICANT: PFEFFERLE, WALTER
; APPLICANT: BINDER, MICHAEL
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE IPSE GENE
; FILE REFERENCE: 218472USX
; CURRENT APPLICATION NUMBER: US/10/075,460
; CURRENT FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: DE 10107230.9
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: DE 10162386.0
; PRIOR FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 5099
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
; OTHER INFORMATION:
US-10-075-460-5

Query Match 42.3%; Score 88; DB 13; Length 5099;
Best Local Similarity 68.5%; Pred. No. 6.4e-16;
Matches 137; Conservative 0; Mismatches 60; Indels 3; Gaps 1;

QY 9 AAGCGCTACGACCTGGCGCGCGCTACAGGTCAACAGAGCTGGCGCTGAAC 68
D 1578 AAGCGCTACGACCTGGCGCGCTGGTGTGTTACAGATCAACCGCAAGCTGGCGCTTGGT 1637
QY 69 GCGCGCCAGCGGATCAGCTGCTGCTGACCGAGGAGAGCTGCTGCCACCATGAG 128
D 1638 GCGGACCCAGATGT---TTGATGACTCTTACTGAGAGGACATCGACCATCGAG 1694
QY 129 TACCTGTGGCGCTGACGAGGCCGCGGACGATGACCGTCCCGCGCGCTGAGGTC 188
D 1695 TACCTGTGGCGCTGACGAGGCCGCGGATGACCGTCCCGCGCGCTGAGGTC 1754
QY 189 CCGGTGAGGTGGGACGAT 208
D 1755 CCAGTCGAGACCGATGACAT 1774

RESULT 11
US-09-738-626-1
; Sequence 1, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENO, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07

; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 1
; LENGTH: 3309400
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-1

Query Match 42.3%; Score 88; DB 10; Length 3309400;
Best Local Similarity 68.5%; Pred. No. 5.2e-16;
Matches 137; Conservative 0; Mismatches 60; Indels 3; Gaps 1;

QY 9 AAGCGCTACGACCTGGCGCGCGCTACAGGTCAACAGAGCTGGCGCTGAAC 68
D 513789 AAGCGCTACGACCTGGCGCGCTGGTGTGTTACAGATCAACCGCAAGCTGGCGCTTGGT 513848
QY 69 GCGCGCCAGCGGATCAGCTGCTGCTGACCGAGGAGAGCTGCTGCCACCATGAG 128
D 513849 GCGGACCCAGATGT---TTGATGACTCTTACTGAGAGGACATCGACCATCGAG 513905
QY 129 TACCTGTGGCGCTGACGAGGCCGCGGACGATGACCGTCCCGCGCGCTGAGGTC 188
D 513906 TACCTGTGGCGCTGACGAGGCCGCGGATGACCGTCCCGCGCGCTGAGGTC 513965
QY 189 CCGGTGAGGTGGGACGAT 208
D 513966 CCAGTCGAGACCGATGACAT 513985

RESULT 12
US-10-156-761-4898
; Sequence 4898, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 4898
; LENGTH: 3543
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3543)
US-10-156-761-4898

Query Match 39.4%; Score 82; DB 14; Length 3543;
Best Local Similarity 65.9%; Pred. No. 3.2e-14;
Matches 137; Conservative 0; Mismatches 65; Indels 6; Gaps 1;

QY 1 TCAAGGAGAGCGCTACGACCTGGCGCGCGCTGAGGTCACAGGTCAACAGAGCTGG 60
D 926 TCAACCCGAGGCGCTACGACCTGGCGCGCTGAGGTCACAGGTCAACAGAGCTGG 985
QY 61 GCCTGAACCGCGCGCGGATCAGCTGCTGACTCTGACCGAGGAGAGCTGCTGCGCA 120
D 986 GCGGCGAGGC-----GCCGCTGAGAGCGCGGATCTCTGACCGGAGGACATCTCTGT 1039
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RESULT 15
US-10-156-761-1/c
; Sequence 1, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
; LENGTH: 9025608
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1

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QY 11 GGGCTAGACCTGGCCCGCGCTGAGCTGACAGAGAGCTGGGCGCTGAACGC 70
 Db 4510921 GCGGGGCGCCCTGACACCGAGGCGCTGACAGGCTGGCACTGCTGGAGCGCA 4510862
 QY 71 CGGGCAGCGGATGACGCTGCTGACGAGGAGAGCTGCGCCACCATCGAGTA 130
 Db 4510861 CGAGATCTTGGGCACCGCTAGCGCTGGACGGCGAGCGCTCCAGATCATCGACGC 4510802
 QY 131 CCTGGTGGCCCTGACAGAGGCGCCAGACCATGATGACCTCCGCGGCGCTCGAGGTCCC 190
 Db 4510801 GCGGGGCGCCCTGACGAGGCTGCGGGGCGCGGAGCGAGCGGTCCGCGCCCT 4510742
 QY 191 GGTGAGGTGGAC 203
 Db 4510741 GGTGAGGCGGAC 4510729

Search completed: September 17, 2003, 13:08:56
 Job time : 135.259 secs

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OM nucleic - nucleic search, using sw model

Run on: September 17, 2003, 11:54:34 ; Search time 30.1105 Seconds
 (without alignments)
 3049.028 Million cell updates/sec

Title: US-09-697-123b-2
 Perfect score: 208
 Sequence: 1 tcaagagagcgctacgac.....cgggtggagaccgacgacat 208

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued Patents, NA: *
 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
 5: /cgn2_6/ptodata/1/ina/PCrus_COMB.seq.*
 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	164.8	79.2	970	1 US-08-250-030-1	Sequence 1, Appli
2	164.8	79.2	970	5 PCT-US95-06790-1	Sequence 1, Appli
3	164.8	79.2	4403765	3 US-09-103-840A-2	Sequence 2, Appli
4	164.8	79.2	4411529	3 US-09-103-840A-1	Sequence 1, Appli
5	144	69.2	3447	2 US-08-313-185-57	Sequence 57, Appli
6	144	69.2	3447	3 US-09-082-614A-57	Sequence 57, Appli
c 7	43	20.7	633	4 US-09-252-991A-8508	Sequence 8508, Ap
8	43	20.7	2712	4 US-09-252-991A-8406	Sequence 8406, Ap
c 9	43	20.7	3528	4 US-09-252-991A-8473	Sequence 8473, Ap
10	41	19.7	480	4 US-09-252-991A-4818	Sequence 4818, Ap
c 11	41	19.7	2865	4 US-09-252-991A-4675	Sequence 4675, Ap
12	41	19.7	4563	4 US-09-252-991A-4765	Sequence 4765, Ap
13	40.6	19.5	6085	3 US-09-029-603-4	Sequence 4, Appli
14	40.2	19.3	603	4 US-09-252-991A-16215	Sequence 16215, A
15	39.4	18.9	642	4 US-09-252-991A-6029	Sequence 6029, Ap
c 16	39.4	18.9	1245	4 US-09-252-991A-4359	Sequence 4359, Ap
17	39.4	18.9	1305	4 US-09-252-991A-4477	Sequence 4477, Ap
18	39.4	18.9	1374	4 US-09-252-991A-4384	Sequence 4384, Ap
19	39	18.8	993	1 US-08-136-993-3	Sequence 3, Appli
20	39	18.8	1218	1 US-08-136-993-8	Sequence 8, Appli
21	39	18.8	1322	1 US-08-136-993-12	Sequence 12, Appli
22	39	18.8	20235	1 US-07-642-734C-3	Sequence 3, Appli
23	39	18.8	20235	3 US-08-439-009A-3	Sequence 3, Appli
c 24	39	18.8	77536	4 US-09-410-551B-1	Sequence 1, Appli
c 25	38.8	18.7	4403765	3 US-09-103-840A-2	Sequence 2, Appli
c 26	38.8	18.7	4411529	3 US-09-103-840A-1	Sequence 1, Appli
c 27	38.4	18.5	276	4 US-09-252-991A-8365	Sequence 8365, Ap

ALIGNMENTS

RESULT 1
 US-08-250-030-1
 : Sequence 1, Application US/08250030
 : Patent No. 5643723
 : GENERAL INFORMATION:
 : APPLICANT: Persing, David H.
 : TITLE OF INVENTION: Detection of a Genetic Locus Encoding
 : TITLE OF INVENTION: Resistance to Rifampin in Mycobacterial Cultures and in
 : TITLE OF INVENTION: Clinical Specimens
 : NUMBER OF SEQUENCES: 15
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Schweigman, Lundberg & Woessner
 : STREET: 3500 IDS Center
 : CITY: Minneapolis
 : STATE: MN
 : COUNTRY: USA
 : ZIP: 55402
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: PatentIn Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA: US/08/250,030
 : APPLICATION NUMBER: US/08/250,030
 : FILING DATE: 26-MAY-1994
 : CLASSIFICATION: 435
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Muetting, Ann M.
 : REGISTRATION NUMBER: 33,977
 : REFERENCE/DOCKET NUMBER: 150.105U51
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 612-339-0331
 : TELEFAX: 612-339-3061
 : INFORMATION FOR SEQ ID NO: 1:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 970 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 : MOLECULE TYPE: DNA
 US-08-250-030-1

Query Match 79.2%; Score 164.8; DB 1; Length 970;
 Best Local Similarity 87.0%; Pred. No. 2.6e-31;
 Matches 181; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

Qy 1 TCAAGGAGAGCGCTACGACCTGGCCCGGTGGCCCGCTACAGGTTCACAGAGAGCTCG 60
 |||||
 Db 26 TCAAGGAGAGCGCTACGACCTGGCCCGGTGGCCCGCTACAGGTTCACAGAGAGCTCG 85
 |||||

QY	61	GTCTCAGCTGCCAAGCCGATCAGCTCGACGCTGACCGAGGAAGACGCTCGTAGCCA	120
Db	86	GGCTCATGTCGCGAGAGCCATCATCGCTCGACCGAAGAAGACGCTCGTGCCA	145
QY	121	CCATCGAGTACCTGCTGCGGCTGCACAGGGGTCAGTCGGCGATGACGTTCCCGGGCGGG	180
Db	146	CCATCGAATATCTGGTTCGCGTTCACAGAGGTCAGACGATGACCTTCGGGGCGGG	205
QY	181	CCGAGGTGCGGTGGAGACCGACGACAT	208
Db	206	TCGAGGTGCGGTGGAAACCGACGACAT	233

RESULT 2

```

PCT-US95-06790-1
: Sequence 1, Application PC/TUS9506790
: GENERAL INFORMATION:
: APPLICANT: Mayo Foundation for Medical Education and Research
: APPLICANT: and Hoffmann-La Roche Inc.
: TITLE OF INVENTION: Detection of a Genetic Locus Encoding
: TITLE OF INVENTION: Resistance to Rifampin
: NUMBER OF SEQUENCES: 15
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Schwegman, Lundberg & Woessner
: STREET: 3500 IDS Center
: CITY: Minneapolis
: STATE: MN
: COUNTRY: USA
: ZIP: 55402
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC Compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US95/06790
: FILING DATE: 26-MAY-1995
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Raasch, Kevin W.
: REGISTRATION NUMBER: 35,651
: REFERENCE/DOCKET NUMBER: 150.105W01
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 612-339-0331
: TELEFAX: 612-339-3061
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 970 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA
: PCT-US95-06790-1

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RESULT 3

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US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

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RESULTS

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US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

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Best Local Similarity 87.0%; Pred. No. 5.6e-31;
Matches 161; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 1 TCAAGAGAACGCTAGACCTGGCCCGGCGGCGGTGACAGGTCACAAAGAGCTCG 60
Db TCAAGAGAACGCTAGACCTGGCCCGGCGGCGGTGACAGGTCACAAAGAGCTCG 760747
QY 61 GTCAGAGCTGCGGCAACCGATCACCAGCTGACGCTGACCGAGGAGAGCTCGTAGCCA 120
Db GGCCTGATGTGCGGAGCCCATCAGCTGCTGACGCTGACCGAGAGAGCTCGTAGCCA 760748
QY 121 CCATGAGTACTGCTGGTGGCTGACGAGGTCAGTGGCGGTGACGCTTCCCGCGCGC 180
Db CCATGATATCTGCTCGCTTGCAGAGGTCAGACCAAGTACCGTTCGCGCGCGC 760807
QY 181 CCGAGTCCGCTGAGAGCAGACAT 208
Db TCGAGTCCGCTGCAACCGAGCAGAT 760895

RESULT 5

US-08-313-185-57
; Sequence 57, Application US/08313185
; Patent No. 5851763
; GENERAL INFORMATION:
; APPLICANT: Heym, Beate
; APPLICANT: Cole, Stewart
; APPLICANT: Young, Douglas
; APPLICANT: Zhang, Ying
; APPLICANT: Honore, Nadine
; APPLICANT: Telenti, Amalio
; APPLICANT: Bodmer, Thomas
; TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
; TITLE OF INVENTION: in Mycobacterium Tuberculosis
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/313,185
; FILING DATE: 12-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 02356.0068-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3447 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-313-185-57

Query Match 69.2%; Score 144; DB 2; Length 3447;
Best Local Similarity 80.8%; Pred. No. 2.8e-26;
Matches 168; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 1 TCAAGAGAACGCTAGACCTGGCCCGGCGGCTGACAGGTCACAAAGAGCTCG 60

Db TCAAGAGAACGCTAGACCTGGCCCGGCGGCTGACAGGTCACAAAGAGCTCG 868
QY 61 GTCAGAGTGGGCAACCGATCACCAGCTGACGCTGACCGAGAGAGCTCGTAGCCA 120
Db GGTTCACGCGGTCAGTTGATCACGCTGCCAGCTGACCGAGAGAGTCTCGTCGCCA 928
QY 121 CCATGAGTACTGCTGGTGGCTGACGAGGTCAGTGGCGGTGACGCTTCCCGCGCGC 180
Db CCATAGAGTACTGCTGGTGGCTGATGAGGTCAGTGGCGGTGACGCTTCCCGAGGTGGG 988
QY 181 CCGAGTCCGCTGAGAGCAGACAT 208
Db TAGAAGTCCAGTGGAACTGACGATAT 1016

RESULT 6

US-09-082-614A-57
; Sequence 57, Application US/09082614A
; Patent No. 6124098
; GENERAL INFORMATION:
; APPLICANT: Heym, Beate
; APPLICANT: Cole, Stewart
; APPLICANT: Young, Douglas
; APPLICANT: Zhang, Ying
; APPLICANT: Honore, Nadine
; APPLICANT: Telenti, Amalio
; APPLICANT: Bodmer, Thomas
; TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
; TITLE OF INVENTION: in Mycobacterium Tuberculosis
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/082,614A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/313,185
; FILING DATE: 12-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 02356.0068-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3447 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-082-614A-57

Query Match 69.2%; Score 144; DB 3; Length 3447;
Best Local Similarity 80.8%; Pred. No. 2.8e-26;
Matches 168; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 1 TCAAGAGAACGCTAGACCTGGCCCGGCGGCTGACAGGTCACAAAGAGCTCG 60

Db 809 TCACGAGAAACCTACGACCTGGCCAGGTTGGCTTACAAAGTCAACAAGAGCTCG 868
Qy 61 GTCTGAAGCTGGCAAGCCGATCACACAGCTCGACGCTGACCGAGGAAGAGCTGTAGCCA 120
Db 869 GGTTCACGCGGTGAGTGTACAGTGTCTCCAGCTGACCGAGAGGATGTCTGCGCA 928
Qy 121 CCATCAGTACCTGGTGGCTGACGAGGCTCAGTGGCGATGAGGTTCCCGCGCGG 180
Db 929 CCATAGATACCTGGTGTCTGTGATGAGGCTCAGTGCACATGATGTCCAGTGGG 988
Qy 181 CGAGGTGCGGTGGAGCCGACGACAT 208
Db 989 TAGAAGTCCAGTGGAACTGACGATAT 1016

RESULT 7
US-09-252-991A-8508/c
; Sequence 8508, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 8508
; LENGTH: 633
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-8508

Query Match 20.7%; Score 43; DB 4; Length 633;
Best Local Similarity 52.5%; Pred. No. 0.041;
Matches 94; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

Qy 22 TGGCCGGTGGCGCTACAAAGTCAACAAGAGCTCGGTGACGTCGCGCAAGCCGA 81
Db 313 TGGCCGGCTTTCGGCAACCGGGCGTATACAACTCCAGTCTCGTGGCGCAGCGCA 254
Qy 82 TCACAGCTCGACGCTGACCGAGGAGAGCTCGTAGCCACATCGAGTACCTGTGGGCG 141
Db 253 CGGGCGGCGCTGCTTGGCGGACCTGCGGGAATCGCGCAACAAGACCTGTGTGTC 194
Qy 142 TCACAGGCTCAGTGGCGATGACGGTTCCCGCGCGCGCGGAGTGGCGTGAGACC 200
Db 193 TCAATGCGCGCGCTGGGGAACAATGCCATCGAGGCTCCGCGGTGATCTCAACACC 135

RESULT 8
US-09-252-991A-8406
; Sequence 8406, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 8406
; LENGTH: 2712
; TYPE: DNA

; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-8406

Query Match 20.7%; Score 43; DB 4; Length 2712;
Best Local Similarity 52.5%; Pred. No. 0.047;
Matches 94; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

Qy 22 TGGCCCGGTGGCGCTACAAAGTCAACAAGAGCTCGGTCTGAACGTCGCGCAAGCCGA 81
Db 317 TGGCCCGCTTTCGGCAACCGAGGCGTATACAACTCCAGTCTCGTGGCGCAGCGCA 376
Qy 82 TCACAGCTCGACGCTGACCGAGGAGAGCTCGTAGCCACATCGAGTACCTGTGGGCG 141
Db 377 CGGGCGGCGCTGCTTGGCGGACCTGCGGGAATCGCGGGAACAAGACCTGTGTGTC 436
Qy 142 TGCACGAGGCTCAGTGGCGATGACGGTTCCCGCGCGCGCGGAGTGGCGTGAGACC 200
Db 437 TCAATGCGCGCGCTGGGGAACAATGCCATCGAGGCTCCGCGGTGATCTCAACACC 495

RESULT 9
US-09-252-991A-8473/c
; Sequence 8473, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 8473
; LENGTH: 3528
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-8473

Query Match 20.7%; Score 43; DB 4; Length 3528;
Best Local Similarity 52.5%; Pred. No. 0.049;
Matches 94; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

Qy 22 TGGCCCGGTGGCGCTACAAAGTCAACAAGAGCTCGGTCTGAACGTCGCGCAAGCCGA 81
Db 2579 TGGCCCGCTTTCGGCAACCGAGGCGTATACAACTCCAGTCTCGTGGCGCAGCGCA 2520
Qy 82 TCACAGCTCGACGCTGACCGAGGAGAGCTCGTAGCCACATCGAGTACCTGTGGGCG 141
Db 2519 CGGGCGGCGCTGCTTGGCGGACCTGCGGGAATCGCGGGAACAAGACCTGTGTGTC 2460
Qy 142 TGCACGAGGCTCAGTGGCGATGACGGTTCCCGCGCGCGCGGAGTGGCGTGAGACC 200
Db 2459 TCAATGCGCGCGCTGGGGAACAATGCCATCGAGGCTCCGCGGTGATCTCAACACC 2401

RESULT 10
US-09-252-991A-4818
; Sequence 4818, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 4818
; LENGTH: 2712
; TYPE: DNA

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; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 4818
; LENGTH: 480
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-4818

Query Match          19.7%; Score 41; DB 4; Length 480;
Best Local Similarity 51.4%; Pred. No. 0.12;
Matches 95; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

QY 21 CTGGCCCGGGTGGCGGCTACAAGGTCACAAAGAGCTCGTCTGAACGTCGCGCAAGCG 80
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 269 CAGGCTGCTGGAGTCCAGGTCACCGACCACTTCGGCGCCCTGGAGATCGCTGGGAC 328
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 81 ATCACCAGCTCGACGCTGACCGAGGAAGACGTCGTAGCCACCAFCGAGTACCTGTGGG 140
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 329 GTACGCTCGGGTTGTTCCCGAGGCGGCAAGCCATGTTCCGACGACTTCGTGCGG 388
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 141 CTCGACGAGGTCAGTCGGCGATGACGGTTCCCGCGCGCGCGGAGTGCGGTGGAGACC 200
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 389 CTCTCCGCGCGCTGGCGCAGAGCCGCGCGCTGGACCGACGCGGATGCCAGGAACCC 448
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 201 GACGA 205
    |||||
Db 449 GTCGA 453
    |||||

RESULT 11
US-09-252-991A-4675/c
; Sequence 4675, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 4675
; LENGTH: 2865
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-4675

Query Match          19.7%; Score 41; DB 4; Length 2865;
Best Local Similarity 51.4%; Pred. No. 0.14;
Matches 95; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

QY 21 CTGGCCCGGGTGGCGGCTACAAGGTCACAAAGAGCTCGTCTGAACGTCGCGCAAGCG 80
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2331 CAGGCTGCTGGAGTCCAGGTCACCGACCACTTCGGCGCCCTGGAGATCGCTGGGAC 2272
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 81 ATCACCAGCTCGACGCTGACCGAGGAAGACGTCGTAGCCACCAFCGAGTACCTGTGGG 140
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2271 GTACGCTCGGGTTGTTCCCGAGGCGGCAAGCCATGTTCCGACGACTTCGTGCGG 2212
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 141 CTCGACGAGGTCAGTCGGCGATGACGGTTCCCGCGCGCGCGGAGTGCGGTGGAGACC 200
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2211 CTGCTCGGCGCTGGCGCAGAGCCCGCGGCTGGACCGAGCGGATGCCAGGAACCC 2152
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 201 GACGA 205
    |||||
Db 2151 GTCGA 2147
    |||||

RESULT 12
US-09-252-991A-4765
; Sequence 4765, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 4765
; LENGTH: 2865
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-4765

Query Match          19.7%; Score 41; DB 4; Length 4563;
Best Local Similarity 51.4%; Pred. No. 0.15;
Matches 95; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

QY 21 CTGGCCCGGGTGGCGGCTACAAGGTCACAAAGAGCTCGTCTGAACGTCGCGCAAGCG 80
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1447 CAGGCTGCTGGAGTCCAGGTCACCGACCACTTCGGCGCCCTGGAGATCGCTGGGAC 1506
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 81 ATCACCAGCTCGACGCTGACCGAGGAAGACGTCGTAGCCACCAFCGAGTACCTGTGGG 140
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1507 GTACGCTCGGGTTGTTCCCGAGGCGGCAAGCCATGTTCCGACGACTTCGTGCGG 1566
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 141 CTCGACGAGGTCAGTCGGCGATGACGGTTCCCGCGCGCGCGGAGTGCGGTGGAGACC 200
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1567 CTGCTCCGCGCGCTGGCGCAGAGCCGCGCGCTGGACCGAGCGGATGCCAGGAACCC 1626
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 201 GACGA 205
    |||||
Db 1627 GTCGA 1631
    |||||

RESULT 13
US-09-029-603-4
; Sequence 4, Application US/09029603
; Patent No. 6210935
; GENERAL INFORMATION:
; APPLICANT: Schupp, Thomas
; APPLICANT: Engel, Natalie
; APPLICANT: Bietenhader, Jurg
; APPLICANT: Toupet, Christine
; APPLICANT: Pospisich, Andreas
; TITLE OF INVENTION: Staurosporin Biosynthesis Gene Clusters
; FILE REFERENCE: 4-20555/A/PCI
; CURRENT APPLICATION NUMBER: US/09/029,603
; CURRENT FILING DATE: 1998-03-20
; EARLIER APPLICATION NUMBER: PCT/EP96/03643
; EARLIER FILING DATE: 1996-08-19
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 6085
; TYPE: DNA
; ORGANISM: Streptomyces longisporoflavus
; FEATURE:
; NAME/KEY: misc_RNA
; LOCATION: (378)..(1665)
; OTHER INFORMATION: ORF
; FEATURE:
; NAME/KEY: misc_RNA
; LOCATION: (1747)..(2553)
; OTHER INFORMATION: ORF
; FEATURE:
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; NAME/KEY: misc_RNA
; LOCATION: (2593)..(4011)
; OTHER INFORMATION: ORF
; FEATURE:
; NAME/KEY: misc_RNA
; LOCATION: (4013)..(4999)
; OTHER INFORMATION: ORF
; FEATURE:
; NAME/KEY: misc_RNA
; LOCATION: (5071)..(6085)
; OTHER INFORMATION: ORF
US-09-029-603-4

Query Match      19.5%; Score 40.6; DB 3; Length 6085;
Best Local Similarity 58.8%; Pred. No. 0.19;
Matches 70; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 18 GACCTGGCCCGGGTGGCCGCTACAAAGGTCAACAGAGTCTGGTGTGAAGCTGGGCAAG 77
   || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1017 GAGGTGGACCGCGCGCGCGGACGACCGGACGATCTGCTCACCCTCTCTCTCGCGGCC 1076

QY 78 CGATACACAGCTCGAGCTGACCGGAGGAGAGCTGCTAGCCACCATCGAGTACTGCT 136
   || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1077 CGGGACACCGGATCACCGCTACCGTGGGACGATCTGCGGACCTGCGTCTCTCTGCT 1135

RESULT 14
US-09-252-991A-16215
; Sequence 16215, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 16215
; LENGTH: 603
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-16215

Query Match      19.3%; Score 40.2; DB 4; Length 603;
Best Local Similarity 50.8%; Pred. No. 0.19;
Matches 96; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

QY 17 CGACCTGGCCCGGGTGGCGGCTACAAAGGTCAACAGAAAGCTGGTCTGAAGCTGGCAA 76
   || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 396 CGTCGTGTGTACTGTGTTCGSCACCAAGCGCTGAGAACTCTGGTTCGAGCTGGGGA 455

QY 77 GCGATACACAGCTCGAGCTGACCGAGGAGAGCTGCTAGCCACCATCGACTCTGCT 136
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 456 AGCATCAAGGCTTCGCGCAAGCGCGTGAACACCGAGGAGAGACGACAAAGAGGACGCC 515

QY 137 GCGGCTGACGACGCTGAGTCGCGGATGACGGTTCGCGGCGCGCGAGGTGCGGTTGA 196
   || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 516 CGCGCGCCAGCGCGCCACCGCTGAACCGCGGACACCATCGACGCCCGGCGGAGAA 575

QY 197 GACCGAGCA 205
   || ||| |||
Db 576 GGTGGAAGA 584

RESULT 15
US-09-252-991A-6029
; Sequence 6029, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 16215
; LENGTH: 603
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-6029

Query Match      18.9%; Score 39.4; DB 4; Length 642;
Best Local Similarity 51.4%; Pred. No. 0.3;
Matches 91; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

QY 21 CTGCCCCGGTGGCGGCTACAGGTCAACAGAGTCTGGTCTGAAGTGGGCAAGCCG 80
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 238 CTGGCGATCGGCGGATTACACCGCGCGGGGATGAGCGCAAGTGGAGACCGCAAGCG 297

QY 81 ATCACACAGCTCGACGCTGACCGAGGAGAGACGTCTGATGCCACCATCGAGTACTCTGTCGG 140
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 298 ATCGGCATCGACAGATGACCTTCGACGAGGTCTGCGCAAGCAGGAGTGGGGCTGACG 357

QY 141 CTGCACAGAGGTCTAGTCGGGATGACGGTTCCTCCGCGCGCGCGAGGTGCCGTTGAG 197
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 358 CTGACGCTACCAATCATCTCTCCAGGAGGAGGCGCGGACGACGAGTGGCGGTGGG 414

Search completed: September 17, 2003, 12:26:03
Job time : 46.1605 secs
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RESULT 3
US-09-984-711-5
; Sequence 5, Application US/09984711
; Patent No. US20020119549A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: STEPHAN, Hans
; APPLICANT: KREUTZER, Caroline
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE rpsL GENE
; FILE REFERENCE: 204209050
; CURRENT APPLICATION NUMBER: US/09/984,711
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: DE10108230.9
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 5096
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
; OTHER INFORMATION:
US-09-984-711-5

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Query Match          42.3%;   Score 88;   DB 10;   Length 3495;
Best Local Similarity 68.5%;   Pred. No. 1.8e-16;
Matches 137;   Conservative 0;   Mismatches 60;   Indels 3;   Gaps 1;

QY      9  AAGGGCTACAGCTGGCGCGCGGCTCAAGAGTCAACAAGAGCTCGGTCTGTAC 68
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      877 AAGGGCTACAGCTGGCTGGCGGTGGCTTACAAGATCAACCGCAGCTGGCGCTGT 936
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      69  GTCCGCAAGCCGATCAACAGCTGACGCTGACCGAGGAAGCTGTCGACCATTCGAG 128
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      937 GCGACCAACGATGGTTGAT--GACCTCTTACTGAGAGGACATCGCAACCATTCGAG 993
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      129 TACCTGTGGCGCTGCACAGAGGTCAGTCGGCGGATGACGGTTTCCCGCGCGCGCGGTG 188
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      994 TACCTGTGTGCTGCACGAGGTGACCGGTCATGACTTCCAAATGTTGAGAGATC 1053
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      189 CCGGTGAGACCGACAGACAT 208
          || || || || || || || || || || || || || || || || || ||
Db      1054 CCAGTCGACACCGATGACAT 1073
          || || || || || || || || || || || || || || || || || ||

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;
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
US-09-887-052-1

Query Match 42.3%; Score 88; DB 10; Length 5099;
Best Local Similarity 68.5%; Pred. No. 1.8e-16;
Matches 137; Conservative 0; Mismatches 60; Indels 3; Gaps 1;

QY 9 AAGCGTACGACCTGGCGCGGCTACAAAGTCAACAAAGAGTGGTCTGAAC 68
|||||
Db 1578 AAGCGTACGACCTGGCGCGGCTGGTGTGTTACAGATCAACGCAAGCTGGCGCTTGGT 1637

QY 69 GTGCGCAAGCGGATACCAAGCTGCGTACCGGAGGAGAGCTGTAGCCACCATCGAG 128
|||||
Db 1638 GCGCACCACAGATGGTTTGTAT--GACTCTTACTGAAGAGGACATCGCAACCATCGAG 1694

QY 129 TACTGTGGCTGCACGAGGTCAGTCGCGGATGACGGTCCCGGGGCGCGAGGTG 188
|||||
Db 1695 TACTGTGGCTGCACGAGGTCAGTCGCGGATGACGGTCCCGGGGCGCGAGGTG 1754

QY 189 CCGGTGGAGACCGAGACAT 208
|||
Db 1755 CCAGTCGAGACCGATGACAT 1774

RESULT 5
US-09-887-052-3
; Sequence 3, Application US/09887052
; Patent No. US20020119537A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE rpoB GENE
; FILE REFERENCE: 204212USOX
; CURRENT APPLICATION NUMBER: US/09/887,052
; PRIOR FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: DE10107229.5
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 5099
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
US-09-887-052-3

Query Match 42.3%; Score 88; DB 10; Length 5099;
Best Local Similarity 68.5%; Pred. No. 1.8e-16;
Matches 137; Conservative 0; Mismatches 60; Indels 3; Gaps 1;

QY 9 AAGCGTACGACCTGGCGCGGCTACAAAGTCAACAAAGAGTGGTCTGAAC 68
|||||
Db 1578 AAGCGTACGACCTGGCGCGGCTGGTGTGTTACAGATCAACGCAAGCTGGCGCTTGGT 1637

QY 69 GTGCGCAAGCGGATACCAAGCTGCGTACCGGAGGAGAGCTGTAGCCACCATCGAG 128
|||||
Db 1638 GCGCACCACAGATGGTTTGTAT--GACTCTTACTGAAGAGGACATCGCAACCATCGAG 1694

QY 129 TACTGTGGCTGCACGAGGTCAGTCGCGGATGACGGTCCCGGGGCGCGAGGTG 188
|||||
Db 1695 TACTGTGGCTGCACGAGGTCAGTCGCGGATGACGGTCCCGGGGCGCGAGGTG 1754

QY 189 CCGGTGGAGACCGAGACAT 208
|||
Db 1755 CCAGTCGAGACCGATGACAT 1774

Db 1755 CCAGTCGAGACCGATGACAT 1774

RESULT 6
US-09-887-052-5
; Sequence 5, Application US/09887052
; Patent No. US20020119537A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE rpoB GENE
; FILE REFERENCE: 204212USOX
; CURRENT APPLICATION NUMBER: US/09/887,052
; PRIOR FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: DE10107229.5
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 5099
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
US-09-887-052-5

Query Match 42.3%; Score 88; DB 10; Length 5099;
Best Local Similarity 68.5%; Pred. No. 1.8e-16;
Matches 137; Conservative 0; Mismatches 60; Indels 3; Gaps 1;

QY 9 AAGCGTACGACCTGGCGCGGCTACAAAGTCAACAAAGAGTGGTCTGAAC 68
|||||
Db 1578 AAGCGTACGACCTGGCGCGGCTGGTGTGTTACAGATCAACGCAAGCTGGCGCTTGGT 1637

QY 69 GTGCGCAAGCGGATACCAAGCTGCGTACCGGAGGAGAGCTGTAGCCACCATCGAG 128
|||||
Db 1638 GCGCACCACAGATGGTTTGTAT--GACTCTTACTGAAGAGGACATCGCAACCATCGAG 1694

QY 129 TACTGTGGCTGCACGAGGTCAGTCGCGGATGACGGTCCCGGGGCGCGAGGTG 188
|||||
Db 1695 TACTGTGGCTGCACGAGGTCAGTCGCGGATGACGGTCCCGGGGCGCGAGGTG 1754

QY 189 CCGGTGGAGACCGAGACAT 208
|||
Db 1755 CCAGTCGAGACCGATGACAT 1774

RESULT 7
US-10-076-406-1
; Sequence 1, Application US/10076406
; Publication No. US2003016684A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: Nucleotide sequences coding for the rpoB gene
; FILE REFERENCE: 219774USOXIP
; CURRENT APPLICATION NUMBER: US/10/076,406
; CURRENT FILING DATE: 2002-02-19
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: DE 10107229.5
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 09/887052
; PRIOR FILING DATE: 2001-06-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 5099

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; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
; OTHER INFORMATION:
US-10-076-406-1

Query Match          42.3%; Score 88; DB 12; Length 5099;
Best Local Similarity 68.5%; Pred. No. 1.8e-16;
Matches 137; Conservative 0; Mismatches 60; Indels 3; Gaps 1;

QY 9 AAGCGCTACGACCTGGCCGGGTGCGCTACCAAGGTCACCAAGAGCTCGTCTGTAAC 68
Db 1578 AAGCGCTACGACCTGGCTCGGTTGCTTACCAAGATCAACCGCAAGCTGGGCTTGGT 1637

QY 69 GTCGGCAAGCCGATCACCAGCTCCAGCTCAGCCCTGACCGAGGAGAGCTGCTAGCACCATCGAG 128
Db 1638 GCGGACCACGATGGTTGAT---GACTCTTACTGAAGAGGACATCGCAACCCATCGAG 1694

QY 129 TACTGTGGTGGCTGCACGAGGTCAGTCGGCGATGACGGTTCCCGGCGCGCGAGGTG 188
Db 1695 TACTGTGGTGGCTGCACGAGGTCAGTCGGCGATGACGGTTCCCAATGGTGAAGAGATC 1754

QY 189 CCGGTGAGACCGACGACAT 208
Db 1755 CCAAGTCGAGACCGATGACAT 1774

RESULT 8
US-10-076-406-3
; Sequence 3, Application US/10076406
; Publication No. US20030166884A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: Nucleotide sequences coding for the rpoB gene
; FILE REFERENCE: 219774USOXIP
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: DE 10107229.5
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 09/887052
; PRIOR FILING DATE: 2001-06-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 3
; LENGTH: 5099
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
; OTHER INFORMATION:
; NAME/KEY: mutation
; LOCATION: (1987)..(1987)
; OTHER INFORMATION: Substitution of adenine by thymine
; NAME/KEY: mutation
; LOCATION: (1288)..(1288)
; OTHER INFORMATION: Substitution of cytosine by thymine
; NAME/KEY: mutation
; LOCATION: (715)..(715)
; OTHER INFORMATION: Substitution of cytosine by thymine
US-10-076-406-3

Query Match          42.3%; Score 88; DB 12; Length 5099;
Best Local Similarity 68.5%; Pred. No. 1.8e-16;
Matches 137; Conservative 0; Mismatches 60; Indels 3; Gaps 1;

QY 9 AAGCGCTACGACCTGGCCGGGTGCGCTACCAAGGTCACCAAGAGCTCGTCTGTAAC 68
```

```
Db 1578 AAGCGCTACGACCTGGCTCGGTTGCTTACCAAGATCAACCGCAAGCTGGGCTTGGT 1637

QY 69 GTCGGCAAGCCGATCACCAGCTCCAGCTCAGCCCTGACCGAGGAGAGCTGCTAGCACCATCGAG 128
Db 1638 GCGGACCACGATGGTTGAT---GACTCTTACTGAAGAGGACATCGCAACCCATCGAG 1694

QY 129 TACTGTGGTGGCTGCACGAGGTCAGTCGGCGATGACGGTTCCCGGCGCGCGAGGTG 188
Db 1695 TACTGTGGTGGCTGCACGAGGTCAGTCGGCGATGACGGTTCCCAATGGTGAAGAGATC 1754

QY 189 CCGGTGAGACCGACGACAT 208
Db 1755 CCAAGTCGAGACCGATGACAT 1774

RESULT 9
US-10-076-406-5
; Sequence 5, Application US/10076406
; Publication No. US20030166884A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: Nucleotide sequences coding for the rpoB gene
; FILE REFERENCE: 219774USOXIP
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: DE 10107229.5
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 09/887052
; PRIOR FILING DATE: 2001-06-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 5
; LENGTH: 5099
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
; OTHER INFORMATION:
; NAME/KEY: mutation
; LOCATION: (2016)..(2016)
; OTHER INFORMATION: Substitution of cytosine by thymine
US-10-076-406-5

Query Match          42.3%; Score 88; DB 12; Length 5099;
Best Local Similarity 68.5%; Pred. No. 1.8e-16;
Matches 137; Conservative 0; Mismatches 60; Indels 3; Gaps 1;

QY 9 AAGCGCTACGACCTGGCCGGGTGCGCTACCAAGGTCACCAAGAGCTCGTCTGTAAC 68
Db 1578 AAGCGCTACGACCTGGCTCGGTTGCTTACCAAGATCAACCGCAAGCTGGGCTTGGT 1637

QY 69 GTCGGCAAGCCGATCACCAGCTCCAGCTGACCGAGGAGAGCTGCTAGCACCATCGAG 128
Db 1638 GCGGACCACGATGGTTGAT---GACTCTTACTGAAGAGGACATCGCAACCCATCGAG 1694

QY 129 TACTGTGGTGGCTGCACGAGGTCAGTCGGCGATGACGGTTCCCGGCGCGCGAGGTG 188
Db 1695 TACTGTGGTGGCTGCACGAGGTCAGTCGGCGATGACGGTTCCCAATGGTGAAGAGATC 1754

QY 189 CCGGTGAGACCGACGACAT 208
Db 1755 CCAAGTCGAGACCGATGACAT 1774

RESULT 10
US-10-075-460-5
; Sequence 5, Application US/10075460
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; Publication No. US2002015557A1
; GENERAL INFORMATION:
; APPLICANT: MCKEL, BETTINA
; APPLICANT: BATHE, BRIGITTE
; APPLICANT: HANS, STEFAN
; APPLICANT: KREUTZER, CAROLINE
; APPLICANT: HERMANN, THOMAS
; APPLICANT: PFEPFERLE, WALTER
; APPLICANT: BINDER, MICHAEL
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE rpsL GENE
; FILE REFERENCE: 218472USOX
; CURRENT APPLICATION NUMBER: US/10/075,460
; CURRENT FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: DE 10107230.9
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: DE 10162386.0
; PRIOR FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 5099
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
; OTHER INFORMATION:
US-10-075-460-5

Query Match 42.3%; Score 88; DB 13; Length 5099;
Best Local Similarity 68.5%; Pred. No. 1.8e-16;
Matches 137; Conservative 0; Mismatches 60; Indels 3; Gaps 1;

QY 9 AAGCGCTACGACCTGGCGCGGCTACAGGTCAACAGAGCTCGGCTGAAC 68
DB 1578 AAGCGCTACGACCTGGCGCGGCTACAGGTCAACAGAGCTCGGCTGAAC 11
QY 69 GTCGGCAAGCGGATCACAGCTCGACGCTGACCGAGGAGAGCTGCTAGCCACCATCGAG 128
DB 1638 GCGGACACAGATGTTTGAT---GACTCTTACTGAAGGACATCCACACCATCGAG 194
QY 129 TACCTGTGGGCTGTCACGAGGTCAGTCGGCGATGACGGTCCCGGGCGCGGAGGTG 188
DB 1695 TACCTGTGGGCTGTCACGAGGTCAGTCGGCGATGACGGTCCCGGGCGCGGAGGTG 11
QY 189 CCGGTGGAGACCGACGACAT 208
DB 1755 CCAGTCGAGACCGATGACAT 1774

RESULT 11
US-09-738-626-1
; Sequence 1, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
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; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 1
; LENGTH: 3309400
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-1

Query Match 42.3%; Score 88; DB 10; Length 3309400;
Best Local Similarity 68.5%; Pred. No. 2.2e-16;
Matches 137; Conservative 0; Mismatches 60; Indels 3; Gaps 1;

QY 9 AAGCGCTACGACCTGGCGCGGCTGACAGGTCAACAGAGCTCGGCTGAAC 68
DB 513789 AAGCGCTACGACCTGGCGCGGCTGACAGGTCAACAGAGCTCGGCTGAAC 11
QY 69 GTCGGCAAGCGGATCACAGCTCGACGCTGACCGAGGAGAGCTGCTAGCCACCATCGAG 128
DB 513849 GCGGACACAGATGTTTGAT---GACTCTTACTGAAGGACATCCACACCATCGAG 513905
QY 129 TACCTGTGGGCTGTCACGAGGTCAGTCGGCGATGACGGTCCCGGGCGCGGAGGTG 188
DB 513906 TACCTGTGGGCTGTCACGAGGTCAGTCGGCGATGACGGTCCCGGGCGCGGAGGTG 11
QY 189 CCGGTGGAGACCGACGACAT 208
DB 513966 CCAGTCGAGACCGATGACAT 513985

RESULT 12
US-10-156-761-4898
; Sequence 4898, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 4898
; LENGTH: 3543
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3543)
US-10-156-761-4898

Query Match 41.0%; Score 85.2; DB 14; Length 3543;
Best Local Similarity 66.8%; Pred. No. 1.2e-15;
Matches 139; Conservative 0; Mismatches 63; Indels 6; Gaps 1;
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QY 1 TCAAGGAGAGCGCTACGACCTGGCGCGGCTGACAGGTCAACAGAGCTCGGCTGAC 60
DB 926 TCAAGGAGAGCGCTACGACCTGGCGCGGCTGACAGGTCAACAGAGCTCGGCTGAC 985
QY 61 GTCTGAAGCTGGCGAAGCGGATCCAGCTCGACGCTGACCGGAGGAGAGCTGCTAGCCA 120
DB 986 G-----CGCGAGGCGCGCTGGAGCGCGGATCTCTGACCGTCGAGGACATCTCTCGT 1039
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QY 121 CCATCGAGTACCTGGTGGCGGTGACGAGGCTCAGTGGCGATGACGGTTCCTCCGGCGCG 180
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1040 CGATCAAGTACCTGGTGAAGTGCACGCCGTGAGACCGGAGACCGCTTGGCGACACGGCA 1099
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 181 CCGAGGTGCGGTGGGAGACCGACGACAT 208
    || || || || || || || || || || || || || || || || || || || || || ||
Db 1100 CCTCGATCGCTGCGAGACCGACGACAT 1127
    || || || || || || || || || || || || || || || || || || || || || ||

RESULT 13
US-10-156-761-1
; Sequence 1, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHITUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
; LENGTH: 9025608
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1

    Query Match 41.0%; Score 85.2; DB 14; Length 9025608;
    Best Local Similarity 66.8%; Pred. No. 1.5e-15;
    Matches 139; Conservative 0; Mismatches 63; Indels 6; Gaps 1;

QY 1 TCAGGAGAGCGCTACGACCTGGCCGGTGGCGCTACAAGTCAACAGAGGTCG 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5970494 TCACCCGAAGCGCTACGACCTGCGAAGTGGCGGTACAAGTCAACAGAGGTCG 5970553
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 61 GTCTGACGTCGCGACGCGATCACCAGCTGACGCTGACCGAGGACGCTGTAGCCA 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5970554 G-----CGCGAGGCGCGCTGGACGCGCGGATCTCTGACCTGAGGACATCTCTCGT 5970607
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 121 CCATCGAGTACCTGGTGGCGGTGACGAGGCTCAGTGGCGATGACGGTTCCTCCGGCGCG 180
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5970608 CGATCAAGTACCTGGTGAAGTGCACGCCGTGAGACCGGACCGCTTGGCGACACGGCA 5970667
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 181 CCGAGGTGCGGTGGGAGACCGACGACAT 208
    || || || || || || || || || || || || || || || || || || || || || ||
Db 5970668 CCTCGATCGCTGCGAGACCGACGACAT 5970695
    || || || || || || || || || || || || || || || || || || || || || ||
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RESULT 14
US-10-199-672-545
; Sequence 545, Application US/10199672
; Publication No. US20030148442A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
```

```
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C1
; CURRENT APPLICATION NUMBER: US/10/199,672
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: US/10/052,586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 545
; LENGTH: 1535
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-199-672-545

    Query Match 21.1%; Score 43.8; DB 12; Length 1535;
    Best Local Similarity 52.5%; Pred. No. 0.0014;
    Matches 96; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

QY 1 TCAGGAGAGCGCTACGACCTGGCCGGTGGCGCTACAAGTCAACAGAGGTCG 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 852 TCCTGGAGACCGCTACCGCGCTGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 911
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 61 GTCTGACGTCGCGACGCGATCACCAGCTGACGCTGACCGAGGACGCTGTAGCCA 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 912 GCATGATGCGAGCCATGAGTACATCAACAGCACTCTGTTTCGGCGATCGGCTCGTCA 971
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 121 CCATCGAGTACCTGGTGGCGGTGACGAGGTCAGTGGCGGATGACGGTTCCTCCGGCGCG 180
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 972 CCATCAGCGACGCTGCGAGATCCACAGCGGGGTGCTGGGGCTACGTGGACCCCGCTGGAAG 1031
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 181 CCG 183
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1032 CCG 1034
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 15
US-10-187-749-545
; Sequence 545, Application US/10187749
; Publication No. US20030153036A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
```

```
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C1
; CURRENT APPLICATION NUMBER: US/10/187,749
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: US/10/052,586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Remaining Prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 545
; LENGTH: 1535
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-187-749-545

Query Match      21.1%; Score 43.8; DB 12; Length 1535;
Best Local Similarity 52.5%; Pred. No. 0.0014;
Matches 96; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

QY      1  TCAAGGAGAGCGCTACGACCTGGCCCGGGTGGCGCTACAGGTCACACAGAGACTCG 60
Db      11  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
852  TCCTGGAGACCCGCTACCGCTGCCGCGGAGAGCGCTGGAGGACGACAGAGGTCATAG 911

QY      61  GTCTGAAGTCGGCAAGCCGATCACAGCTCGACGCTGACCGAGGAGAGAGCTCGTAGCCA 120
Db      11  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
912  GCATGCATGCAGCCATGAAGTATCAACACACTCTGGTTCCGCGCATCGGCTCCGTCA 971

QY      121  CCATCGACTACTGTGGTGGGCTGCACGAGGTCAGTCGGCGATGACGGTTCGCCGCGCG 180
Db      11111 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
972  CCATCAGCGAGCTGCTGGAGATCCACAGCGGGTCTGGGCTAGTGGACCCCGGTGAAG 1031

QY      181  CCG 183
Db      1111
1032 CCG 1034
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Search completed: September 17, 2003, 13:02:39
Job time : 124.259 secs

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OM nucleic - nucleic search, using sw model

Run on: September 17, 2003, 11:54:34 ; Search time 29.6762 Seconds
(without alignments)
3049.028 Million cell updates/sec

Title: US-09-697-123B-20
Perfect score: 205
Sequence: 1 tcaagagacgcgtacgac.....ccggtggacacgacacat 205

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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5: /cgn2_6/ptodata/1/ina/PCFUS.COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	147.2	71.8	970	1 US-08-250-030-1	Sequence 1, Appli
2	147.2	71.8	970	5 PCT-US95-06790-1	Sequence 1, Appli
3	147.2	71.8	4403765	3 US-09-103-840A-2	Sequence 2, Appli
4	147.2	71.8	4411529	3 US-09-103-840A-1	Sequence 1, Appli
5	124.8	60.9	3447	2 US-08-313-185-57	Sequence 57, Appli
6	124.8	60.9	3447	3 US-09-082-614A-57	Sequence 57, Appli
7	42.8	20.9	6085	3 US-09-029-603-4	Sequence 4, Appli
8	42.2	20.6	4403765	3 US-09-103-840A-2	Sequence 2, Appli
9	42.2	20.6	4411529	3 US-09-103-840A-1	Sequence 1, Appli
10	42	20.5	1518	1 US-08-660-765A-1	Sequence 1, Appli
11	41.6	20.3	1008	4 US-09-252-991A-7103	Sequence 7103, Ap
12	41.6	20.3	1263	4 US-09-252-991A-7050	Sequence 7050, Ap
13	41.6	20.3	10083	4 US-09-252-991A-6997	Sequence 6997, Ap
14	41	20.0	672	4 US-09-252-991A-501	Sequence 501, App
15	41	20.0	1434	4 US-09-252-991A-522	Sequence 522, App
16	41	20.0	1458	4 US-09-252-991A-599	Sequence 599, App
17	40.8	19.9	609	4 US-09-252-991A-11904	Sequence 11904, A
18	40.8	19.9	1245	4 US-09-252-991A-12071	Sequence 12071, A
19	40.8	19.9	2313	4 US-09-252-991A-11939	Sequence 11939, A
20	40.6	19.8	1014	4 US-09-252-991A-2663	Sequence 2663, Ap
21	40.6	19.8	1155	4 US-09-252-991A-2762	Sequence 2762, Ap
22	40.6	19.8	1233	4 US-09-252-991A-3203	Sequence 3203, Ap
23	40.4	19.7	4689	3 US-09-105-537-34	Sequence 34, Appli
24	40.4	19.7	36778	3 US-09-105-537-5	Sequence 5, Appli
25	40.4	19.7	38506	3 US-09-320-878-19	Sequence 19, Appli
26	40.4	19.7	38506	4 US-09-141-908-1	Sequence 1, Appli
27	40.4	19.7	38506	4 US-09-657-440-19	Sequence 19, Appli

28	40.2	19.6	471	4 US-09-252-991A-3309	Sequence 3309, Ap
29	40.2	19.6	789	4 US-09-252-991A-3366	Sequence 3366, Ap
30	40.2	19.6	1191	4 US-09-252-991A-3242	Sequence 3242, Ap
31	40.2	19.6	1458	4 US-09-516-914-2	Sequence 2, Appli
32	40.2	19.6	1897	4 US-09-620-312D-94	Sequence 94, Appli
33	40.2	19.6	14272	4 US-09-516-914-23	Sequence 23, Appli
34	39.8	19.4	1450	1 US-07-923-692C-5	Sequence 5, Appli
35	39.8	19.4	1450	1 US-08-184-237-5	Sequence 5, Appli
36	39.8	19.4	1450	2 US-08-482-920-5	Sequence 5, Appli
37	39.8	19.4	1450	3 US-08-484-341-5	Sequence 5, Appli
38	39.8	19.4	1626	4 US-09-252-991A-8639	Sequence 8639, Ap
39	39.4	19.2	927	4 US-09-252-991A-7387	Sequence 7387, Ap
40	39.4	19.2	978	4 US-09-252-991A-7319	Sequence 7319, Ap
41	39.4	19.2	1008	4 US-09-252-991A-7300	Sequence 7300, Ap
42	39.4	19.2	77536	4 US-09-410-551B-1	Sequence 1, Appli
43	39.2	19.1	951	4 US-09-252-991A-16343	Sequence 16343, A
44	39.2	19.1	969	4 US-09-252-991A-15940	Sequence 15940, A
45	39.2	19.1	1119	4 US-09-252-991A-16146	Sequence 16146, A

ALIGNMENTS

RESULT 1
US-08-250-030-1
; Sequence 1, Application US/08250030
; Patent No. 5643723
; GENERAL INFORMATION:
; APPLICANT: Persing, David H.
; TITLE OF INVENTION: Detection of a Genetic Locus Encoding
; TITLE OF INVENTION: Resistance to Rifampin in Mycobacterial Cultures and in
; TITLE OF INVENTION: Clinical Specimens
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg & Woessner
; STREET: 3500 IDS Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/250,030
; FILING DATE: 26-MAY-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Muetting, Ann M.
; REGISTRATION NUMBER: 33,977
; REFERENCE/DOCKET NUMBER: 150.105U51
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-339-0331
; TELEFAX: 612-339-3061
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 970 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-250-030-1

Query Match 71.8%; Score 147.2; DB 1; Length 970;
Best Local Similarity 85.1%; Pred. No. 1.6e-25;
Matches 177; Conservative 0; Mismatches 28; Indels 3; Gaps 1;
Qy 1 TCAAGGAGACGGCTACGACCTGGCGCGTGTGCGCGCTACAGAGTCTACAGAGAGTCTCG 60
Db 26 TCAAGGAGACGGCTACGACCTGGCGCGTGTGCGCGCTACAGAGTCTACAGAGAGTCTCG 85

QY 61 GCGTCGACGCGGCGGAGCGGATCACAGCTCGACGCTGACCGAGAGAGACGCTGTCGCCA 120
 Db 86 GCGTCGATGCGCGGAGCGCCATCAGCTGTCGACGCTGACCGAGAGAGAGCTGTCGCCA 145
 QY 121 CCATCGAGTACCTGCTGCGCTGACGAGGCGCCAGCCACGATGACCGTCC---CGGCA 177
 Db 146 CCATCGAATATCTGCTGCGCTGACGAGGCTGACGAGGCTGACGAGGCTGTCGCCGCGG 205
 QY 178 TCGAGGTGCGGCTGAGAGCCGACGACAT 205
 Db 206 TCGAGGTGCGGCTGAGAGCCGACGACAT 233

RESULT 2

PCT-US95-06790-1
 ; Sequence 1, Application PC/TUS9506790
 ; GENERAL INFORMATION:
 ; APPLICANT: Mayo Foundation for Medical Education and Research
 ; APPLICANT: and Hoffmann-La Roche Inc.
 ; TITLE OF INVENTION: Detection of a Genetic Locus Encoding
 ; TITLE OF INVENTION: Resistance to Rifampin
 ; NUMBER OF SEQUENCES: 15
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Schwegman, Lundberg & Woessner
 ; STREET: 3500 IDS Center
 ; CITY: Minneapolis
 ; STATE: MN
 ; COUNTRY: USA
 ; ZIP: 55402

; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US95/06790
 ; FILING DATE: 26-MAY-1995

CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:
 ; NAME: Raasch, Kevin W.
 ; REGISTRATION NUMBER: 35,651
 ; REFERENCE/DOCKET NUMBER: 150.105W01
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 612-339-0331
 ; TELEFAX: 612-339-3061
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 970 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA
 PCT-US95-06790-1

Query Match 71.8%; Score 147.2; DB 5; Length 970;
 Best Local Similarity 85.1%; Pred. No. 1.6e-25;
 Matches 177; Conservative 0; Mismatches 28; Indels 3; Gaps 1;
 QY 1 TCAAGGAGAACGGCTACGACCTGCGCGCTGCTGCGCGCTACAGGTCAACAAGAGCTCG 60
 Db 26 TCAAGGAGAGAGCGCTACGACCTGCGCGCTGCTGCTGCTATAGGTCAACAGAGAGCTCG 85
 QY 61 GCCTCCACGGGCGGAGCGGATCACAGCTCGACGCTGACCGAGGAGAGAGCTGTCGCCA 120
 Db 86 GCGTCGATCTGCGGAGGCCATCAGCTGCTGCGAGCTGACCGAGAGAGAGCTGTCGCCA 145
 QY 121 CCATCGAGTACCTGCTGCGCTGACGAGGCGCCAGCCACGATGACCGTCC---CGGCA 177
 Db 146 CCATCGAATATCTGCTGCGCTGACGAGGCTGACGAGGCTGACGAGGCTGTCGCCGCGG 205
 QY 178 TCGAGGTGCGGCTGAGAGCCGACGACAT 205
 Db 206 TCGAGGTGCGGCTGAGAGCCGACGACAT 233

RESULT 3

US-09-103-840A-2
 ; Sequence 2, Application US/09103840A
 ; Patent No. 6294328
 ; GENERAL INFORMATION:
 ; APPLICANT: FLEISCHMAN, Robert D.
 ; APPLICANT: WHITE, Owen R.
 ; APPLICANT: FRASER, Claire M.
 ; APPLICANT: VENTER, John C.
 ; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
 ; TITLE OF INVENTION: TUBERCULOSIS
 ; FILE REFERENCE: 24366-20007.00
 ; CURRENT APPLICATION NUMBER: US/09/103,840A
 ; CURRENT FILING DATE: 1998-06-24
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 2
 ; LENGTH: 4403765
 ; TYPE: DNA
 ; ORGANISM: Mycobacterium tuberculosis
 ; FEATURE:
 ; OTHER INFORMATION: CDC 1551
 ; OTHER INFORMATION: "n" bases at various positions throughout the sequence
 ; OTHER INFORMATION: represent a, t, c or g
 US-09-103-840A-2

Query Match 71.8%; Score 147.2; DB 3; Length 4403765;
 Best Local Similarity 85.1%; Pred. No. 2.3e-25;
 Matches 177; Conservative 0; Mismatches 28; Indels 3; Gaps 1;

QY 1 TCAAGGAGAACGGCTACGACCTGCGCGCTGCTGCGCGCTACAGGTCAACAAGAGCTCG 60
 Db 762648 TCAAGGAGAGAGCGCTACGACCTGCGCGCTGCTATAGGTCAACAAGAGCTCG 762707
 QY 61 GCCTGACGCGGCGGAGCGGATCACAGCTCGACGCTGACCGAGGAGAGAGCTGTCGCCA 120
 Db 762708 GCGTCGATGTCGCGGAGGCCATCAGCTGCTGACCGAGGCTGACCGAGAGAGCTGTCGCCA 762767
 QY 121 CCATCGAGTACCTGCTGCGCTGACGAGGCGCCAGCCACGATGACCGTCC---CGGCA 177
 Db 762768 CCATCGAATATCTGCTGCGCTGACGAGGCTGACCGAGGCTGACCGAGAGAGCTGTCGCCA 762827
 QY 178 TCGAGGTGCGGCTGAGAGCCGACGACAT 205
 Db 762828 TCGAGGTGCGGCTGAGAGCCGACGACAT 762855

RESULT 4

US-09-103-840A-1
 ; Sequence 1, Application US/09103840A
 ; Patent No. 6294328
 ; GENERAL INFORMATION:
 ; APPLICANT: FLEISCHMAN, Robert D.
 ; APPLICANT: WHITE, Owen R.
 ; APPLICANT: FRASER, Claire M.
 ; APPLICANT: VENTER, John C.
 ; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
 ; TITLE OF INVENTION: TUBERCULOSIS
 ; FILE REFERENCE: 24366-20007.00
 ; CURRENT APPLICATION NUMBER: US/09/103,840A
 ; CURRENT FILING DATE: 1998-06-24
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 4411529
 ; TYPE: DNA
 ; ORGANISM: Mycobacterium tuberculosis
 ; OTHER INFORMATION: H37Rv
 US-09-103-840A-1

Query Match 71.8%; Score 147.2; DB 3; Length 4411529;

Best Local Similarity 85.1%; Pred. No. 2.3e-25;
Matches 177; Conservative 0; Mismatches 28; Indels 3; Gaps 1;

QY 1 TCAAGAGAAAGCGGTAGACCTGGCGCGCTGTGCGCCGCTACAAAGGTCAACAAAGAGCTCG 60
Db 760688 TCAAGAGAAAGCGGTAGACCTGGCGCGCTGTGCGCCGCTGTGCGCCGCTACAAAGGTCAACAAAGAGCTCG 760747
QY 61 GCCTGCACGGCGGCGGAGCCGATCACCAGCTGCAGCGCTGCAGGAGGAGAGAGCTGCTCGCCA 120
Db 760748 GGCTGCATGTGCGGAGCCCATCAGCTGCTGACGCTGCAGCGGAGGAGGAGAGCTGCTCGCCA 760807
QY 121 CCATCGAGTACTGCTGGTGGCTGCACGAGGCGGAGCCGATCAGATGACCGTCCG---CGGCA 177
Db 760808 CCATCGATATCTGCTGGTCCGCTGCAGGAGGCTCAGACCGATGATGACCGTCCGCGCGCG 760867
QY 178 TCGAGGTCCGCGTGGAGACCGAGCAT 205
Db 760868 TCGAGGTCCGCGTGGAGAACCGAGCAT 760895

RESULT 5

US-08-313-185-57
; Sequence 57, Application US/08313185
; Patent No. 5851763
; GENERAL INFORMATION:
; APPLICANT: Heym, Beate
; APPLICANT: Cole, Stewart
; APPLICANT: Young, Douglas
; APPLICANT: Zhang, Ying
; APPLICANT: Honore, Nadine
; APPLICANT: Telenti, Anallo
; APPLICANT: Bodmer, Thomas
; TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
; TITLE OF INVENTION: in Mycobacterium Tuberculosis
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/313,185
; FILING DATE: 12-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 02356.0068-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3447 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)

US-08-313-185-57

Query Match 60.9%; Score 124.8; DB 2; Length 3447;
Best Local Similarity 78.4%; Pred. No. 2.1e-20;
Matches 163; Conservative 0; Mismatches 42; Indels 3; Gaps 1;

QY 1 TCAAGAGAGACGCTAGACCTGGCGCGTGTGCGCCGCTACAAAGGTCAACAAAGAGCTCG 60

Db 809 TCAGAGAGAAACGCTAGACCTGGCCAGGGTTGGCTTAAAGGTCAACAAAGAGCTCG 868
QY 61 GCCTGCACGGCGGCGGAGCCGATCACCAGCTGCAGCGCTGCAGGAGGAGAGAGCTGCTCGCCA 120
Db 869 GGTTCACGCGGGTGAAGTTGATCAGCTGCTCCACGCTGACCGAGAGGATGTCTGTCGCA 928
QY 121 CCATCGAGTACTGCTGGTGGCTGCAGGAGGCGGAGCCGATGACCGTCCG---CGGCA 177
Db 929 CCATAGATACCTGCTGGTTCCTGCTGATGAGGGTCACTGCACATGACTGTCCAGGTGGG 988
QY 178 TCGAGGTCCGCGTGGAGACCGAGCAT 205
Db 989 TAGAGTCCAGTGGAAACTGACGATAT 1016

RESULT 6

US-09-082-614A-57
; Sequence 57, Application US/09082614A
; Patent No. 6124098
; GENERAL INFORMATION:
; APPLICANT: Heym, Beate
; APPLICANT: Cole, Stewart
; APPLICANT: Young, Douglas
; APPLICANT: Zhang, Ying
; APPLICANT: Honore, Nadine
; APPLICANT: Telenti, Anallo
; APPLICANT: Bodmer, Thomas
; TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
; TITLE OF INVENTION: in Mycobacterium Tuberculosis
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/082,614A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/313,185
; FILING DATE: 12-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 02356.0068-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3447 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)

US-09-082-614A-57

Query Match 60.9%; Score 124.8; DB 3; Length 3447;
Best Local Similarity 78.4%; Pred. No. 2.1e-20;
Matches 163; Conservative 0; Mismatches 42; Indels 3; Gaps 1;

QY 1 TCAAGAGAGACGCTAGACCTGGCGCGTGTGCGCCGCTACAAAGGTCAACAAAGAGCTCG 60
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Db 809 TCAGGAGAAACCTACGACTGCGCCAGGGTTGGTGTACAGGTCAACAAGAAGCTG 868
QY 61 GCCTGCAGCGGCGGAGCGATCACAGCTGCGACGTGACCGAGGAGAGCTGTCGCCA 120
Db 859 GGTTCACGCGCGGTGAGTGTGACGCTGCACGCTGACCGAAGAGATGTCGCCA 928
QY 121 CATCGAGTACCTGCTGCGCTGACGAGGCGCCACGACGATGACCGTCC---CGGCA 177
Db 929 CCATAGATACCTGCTGCTGATGAGGCTCAGTCGACATGACTGCCAGGTGGG 988
QY 178 TCGAGGTGCGGTGAGACCGACGACAT 205
Db 989 TAGAAGTCCAGTGGGAAGTACGATAT 1016

RESULT 7
US-09-029-603-4
; Sequence 4, Application US/09029603
; Patent No. 6210935
; GENERAL INFORMATION:
; APPLICANT: Schupp, Thomas
; APPLICANT: Engel, Natalie
; APPLICANT: Bietenhader, Jurg
; APPLICANT: Toupet, Christine
; APPLICANT: Pospiech, Andreas
; TITLE OF INVENTION: Staurosporin Biosynthesis Gene Clusters
; FILE REFERENCE: 4-20555/A/PCT
; CURRENT APPLICATION NUMBER: US/09/029,603
; CURRENT FILING DATE: 1998-03-20
; EARLIER APPLICATION NUMBER: PCT/EP96/03643
; EARLIER FILING DATE: 1996-08-19
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 6085
; TYPE: DNA
; ORGANISM: Streptomyces longisporoflavus
; FEATURE:
; NAME/KEY: misc_RNA
; LOCATION: (378)..(1665)
; OTHER INFORMATION: ORF
; FEATURE:
; NAME/KEY: misc_RNA
; LOCATION: (1747)..(2553)
; OTHER INFORMATION: ORF
; FEATURE:
; NAME/KEY: misc_RNA
; LOCATION: (2593)..(4011)
; OTHER INFORMATION: ORF
; FEATURE:
; NAME/KEY: misc_RNA
; LOCATION: (4013)..(4999)
; OTHER INFORMATION: ORF
; FEATURE:
; NAME/KEY: misc_RNA
; LOCATION: (5071)..(5085)
; OTHER INFORMATION: ORF
US-09-029-603-4

Query Match 20.9%; Score 42.8; DB 3; Length 6085;
Best Local Similarity 54.4%; Pred. No. 0.11; Mismatches 0; Gaps 0;
Matches 86; Conservative 0; Indels 72; Indels 0; Gaps 0;

QY 18 GACCTGGCGCTGTCGCGCTTACAGGTCAACAAGAAGCTGCGCTGCACGCGGGGAG 77
Db 1017 GAGGTGGACCGCGCGCGGCGGACGCGGACGATGCTGTCAACCTCCTGTCGCGGCC 1076

QY 78 CGGATCACAGCTCGACGCTGACGAGAGAGTGTGTCGCCACCATGACTGCTGGT 137
Db 1077 CGGGACACCGGATCACCGCTGACGCTGACGCGATCGTCGGACATGCTGCTCCTC 1136

QY 138 CGCTGCACGAGGGCGAGCCGACGATGACGCTCCCGG 175

Db 1137 ACCGCGGCGCAGAGACCAACCACTGCTGCGCAG 1174

RESULT 8
US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match 20.6%; Score 42.2; DB 3; Length 4403765;
Best Local Similarity 53.3%; Pred. No. 0.2; Mismatches 0; Gaps 0;
Matches 89; Conservative 0; Indels 78; Indels 0; Gaps 0;

QY 26 GCGTGTGCGCGCTCAAGGTCAACAAGAGCTGCGCTGCACGCGGCGGAGCGATCAC 85
Db 1629474 GCAACTGGGCAACCTCATCGTGTCTACGACCGCACAGATCTCGATCGAGGACGAC 1629415

QY 86 CAGCTCGACCTGACCGAGGAGACGTCGTCGCGCCACATCGATCGATGCTGGTGGCCTGCA 145
Db 1629414 CAACATCGCGCTGTGTGAGGACACCGCGGCGCGCTACCGCGGTGCGGCTGCA 1629355

QY 146 CGAGGCGCCACCATGATGACGTCGCCCGCATCGAGTGCCTGG 192
Db 1629354 AGAGTTGAGGCGGTGAGACGCTGTCGGCATCGAGGAGGCCATCG 1629308

RESULT 9
US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match 20.6%; Score 42.2; DB 3; Length 4411529;
Best Local Similarity 53.3%; Pred. No. 0.2; Mismatches 0; Gaps 0;
Matches 89; Conservative 0; Indels 78; Indels 0; Gaps 0;

Db 1629493 AGAGGTTGAGGGCGGTGAGAACGTCTCGGCATCGAGGAGGCCATCG 1629447

50 240 GTCAGCCGATCGTGTATCCAGCCGAGGTCGACATCCTCGGCTTC

Db 246 GTCCAGCCGATCGTGAACCAAGCCGAGGTGGGCATCCTCGGCTTCCTGGTGAAGGAG 303

 $\bar{Q}y$

QY 128 GTACCTGGTGGCCTGCACGAGGCCAGCCACGATGACCGTCCCCGGCATC

TGCC 187

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OM nucleic - nucleic search, using sw model

Run on: September 17, 2003, 11:54:34 ; Search time 106.698 Seconds
(without alignments)
4726.283 Million cell updates/sec

Title: US-09-697-123B-20

Perfect score: 205

Sequence: 1 tcaagagaacgcgtacgac.....ccggtgagacgacgacat 205

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1660708 seqs, 122959015 residues

Total number of hits satisfying chosen parameters: 3321416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:*

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10:	/cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
11:	/cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12:	/cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13:	/cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
14:	/cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
15:	/cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
16:	/cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
17:	/cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	147.2	71.8	3519	10	US-09-712-363-30
2	70.8	34.5	3543	14	US-10-156-761-4898
3	70.8	34.5	9025608	14	US-10-156-761-1
4	69.2	33.8	3495	10	US-09-738-626-547
5	69.2	33.8	5096	10	US-09-984-711-5
6	69.2	33.8	5099	10	US-09-887-052-1
7	69.2	33.8	5099	10	US-09-887-052-3
8	69.2	33.8	5099	10	US-09-887-052-5
9	69.2	33.8	5099	12	US-10-076-406-1
10	69.2	33.8	5099	12	US-10-076-406-3
11	69.2	33.8	5099	12	US-10-076-406-5
12	69.2	33.8	5099	13	US-10-075-460-5
13	69.2	33.8	3309400	10	US-09-738-626-1
14	44	21.5	1542	14	US-10-156-761-5967
15	44	21.5	9025608	14	US-10-156-761-1
16	43.4	21.2	1215	14	US-10-156-761-2811

17	43.4	21.2	2334	14	US-10-156-761-5079
18	43.2	21.1	16692	14	US-10-156-761-414
19	43.2	21.1	100000	14	US-10-156-761-15103
20	42.6	20.8	2484	14	US-10-156-761-912
21	41.6	20.3	603	14	US-10-156-761-1568
22	41.6	20.3	1287	14	US-10-156-761-5314
23	41.6	20.3	13029	9	US-09-815-242-4052
24	41.4	20.2	6798	11	US-09-918-740-57
25	41.4	20.2	6798	12	US-10-204-434A-13
26	41.4	20.2	8077	11	US-09-918-740-63
27	41	20.0	906	14	US-10-156-761-3122
28	41	20.0	993	14	US-10-156-761-4673
29	41	20.0	1353	9	US-09-815-242-4159
30	40.8	19.9	2277	14	US-10-156-761-3085
31	40.8	19.9	63158	12	US-10-292-198-1
32	40.6	19.8	984	14	US-10-156-761-1305
33	40.6	19.8	1806	12	US-10-259-165-239
34	40.4	19.7	1065	14	US-10-156-761-2215
35	40.4	19.7	1200	14	US-10-156-761-5930
36	40.4	19.7	4689	10	US-09-861-289-34
37	40.4	19.7	4689	10	US-09-860-846-34
38	40.4	19.7	4689	11	US-09-988-384B-34
39	40.4	19.7	4689	11	US-09-836-821-34
40	40.4	19.7	36778	10	US-09-861-289-5
41	40.4	19.7	36778	10	US-09-860-846-5
42	40.4	19.7	36778	11	US-09-836-821-5
43	40.4	19.7	37948	11	US-09-988-384B-5
44	40.4	19.7	38506	11	US-09-793-708-19
45	40.4	19.7	38506	12	US-10-201-365-1

ALIGNMENTS

RESULT 1

US-09-712-363-30
; Sequence 30, Application US/09712363
; Patent No. US20020164588A1
; GENERAL INFORMATION:
; APPLICANT: Eisenberg, David
; APPLICANT: Rotstein, Sergio H.
; APPLICANT: Marcotte, Edward M.
; TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND
; FILE REFERENCE: 07419-032001
; CURRENT APPLICATION NUMBER: US/09/712,363
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: PCT/US00/02246
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,531
; PRIOR FILING DATE: 2000-02-01
; PRIOR APPLICATION NUMBER: 60/117,844
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/118,206,
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: 60/126,593
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/134,093
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/134,092
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/165,124
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/165,086
; PRIOR FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 3519
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-09-712-363-30

Sequence 5079, Ap
Sequence 414, App
Sequence 15103, A
Sequence 912, App
Sequence 1568, Ap
Sequence 5314, Ap
Sequence 4052, Ap
Sequence 57, Appl
Sequence 13, Appl
Sequence 63, Appl
Sequence 3122, Ap
Sequence 4673, Ap
Sequence 4159, Ap
Sequence 3085, Ap
Sequence 1, Appl
Sequence 1305, Ap
Sequence 239, App
Sequence 2215, Ap
Sequence 5930, Ap
Sequence 34, Appl
Sequence 34, Appl
Sequence 34, Appl
Sequence 5, Appl
Sequence 5, Appl
Sequence 5, Appl
Sequence 19, Appl
Sequence 1, Appl

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Query Match 71.8%; Score 147.2; DB 10; Length 3519;
Best Local Similarity 85.1%; Pred. No. 1.6e-30;
Matches 177; Conservative 0; Mismatches 28; Indels 3; Gaps 1;

QY 1 TCAGGAGACGGCTACGACCTGCGCGGTGTCGGCGCTACAGGTCAACAGAGCTCG 60
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Db 884 TCAGGAGACGGCTACGACCTGCGCGGTGTCGGCGCTACAGGTCAACAGAGCTCG 943
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 GCTTCGACGGCGGCGGACCGGTACACAGCTGACGCTGACCGAGGAGAGCTGTCGCCA 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 944 GCTTCGATGTCGGCGAGCGCCATCACGCTGCTGCGAGCTGACCGAGAGAGCTGTCGCCA 1003
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 121 CCATCGAGTACCTGGTGGCCCTGCACGAGGCGCCAGCCACGATGACCGTCC---CGGCA 177
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1004 CCATCGAATATCTGGTCCGCTTGCACGAGGCTCAGACCCAGATGACCGTTCGGGGCGGG 1063
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 178 TCGAGGTGCGGTGGAGACCGAGCAT 205
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1064 TCGAGGTGCGGTGGAAACCGAGCAT 1091
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 2
US-10-156-761-4898
; Sequence 4898, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 4898
; LENGTH: 3543
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3543)
US-10-156-761-4898

Query Match 34.5%; Score 70.8; DB 14; Length 3543;
Best Local Similarity 65.9%; Pred. No. 3.8e-10;
Matches 137; Conservative 0; Mismatches 62; Indels 9; Gaps 2;

QY 1 TCAGGAGACGGCTACGACCTGTCGGCGCTACAGGTCAACAGAGCTCG 60
    |||| |||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 926 TCACCCGGAAGCGCTACGACCTTCGGAAAGTTCGGCGCTACAGGTCAACAGAGCTCG 985
    |||| |||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 GCTTCGACGGCGGCGGACCGATCACGCTGACGCTGACCGGAGGAGACGCTCGGCCA 120
    |||| |||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 986 GCGGCGAGGC-----GCGGCTGGACCGCGGATCTGACCGTCGAGGACATCATCTCGT 1039
    |||| |||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 121 CCATCGAGTACCTGGTGGCCCTGCACGAGGCGCCAGCC---ACGATGACCGTCCCGGCA 177
    |||| |||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1040 CGATCAAGTACCTGGTGAAGCTGACGCGGTGAGACCGGAGACCGCTTGGCCACAACGGCA 1099
    |||| |||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 178 TCGAGGTGCGGTGGAGACCGAGCAT 205
    |||| |||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1100 CCTCGATCGTCTGGAGACCGAGCAT 1127
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RESULT 3
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US-10-156-761-1
; Sequence 1, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
; LENGTH: 9025608
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1

Query Match 34.5%; Score 70.8; DB 14; Length 9025608;
Best Local Similarity 65.9%; Pred. No. 1.8e-10;
Matches 137; Conservative 0; Mismatches 62; Indels 9; Gaps 2;

QY 1 TCAGGAGACGGCTACGACCTGTCGGCGCTACAGGTCAACAGAGCTCG 60
    |||| |||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 5970494 TCACCCGGAAGCGCTACGACCTTCGGAAAGTTCGGCGCTACAGGTCAACAGAGCTCG 5970553
    |||| |||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 GCTTCGACGGCGGCGGACCGATCACGCTGACGCTGACCGGAGGAGACGCTCGGCCA 120
    |||| |||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 5970554 GCGGCGAGGC-----GCGGCTGGACCGCGGATCTCGCCGTCGAGGACATCATCTCGT 5970607
    |||| |||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 121 CCATCGAGTACCTGGTGGCCCTGCACGAGGCGCCAGCC---ACGATGACCGTCCCGGCA 177
    |||| |||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 5970608 CGATCAAGTACCTGGTGAAGCTGTCACGCGGTGAGACCGGAGACCGCTTGGCCACAACGGCA 5970667
    |||| |||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 178 TCGAGGTGCGGTGGAGACCGAGCAT 205
    |||| |||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 5970668 CCTCGATCGTCTGGAGACCGAGCAT 5970695
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RESULT 4
US-09-738-626-547
; Sequence 547, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US/09/738,626
; PRIOR FILING DATE: 2000-12-16
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
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; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 5099
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
US-09-887-052-3

Query Match      33.8%; Score 69.2; DB 10; Length 5099;
Best Local Similarity 67.0%; Pred. No. 9.9e-10;
Matches 130; Conservative 0; Mismatches 58; Indels 6; Gaps 2;

QY 15 TAGCACTGGCGCGTGTGGCGGCTACAGGTCACAGAGAGCTCGGCGCTGCACGGGGC 74
Db 1584 TAGCACTGGCTGCGGTGGTTCACAGATCAACCGCAAGCTCGGCCCTT---GGTGGC 1640

QY 75 GAGCCGATCAACAGCTGACGCTGACGAGGAGAGCTGCGCCACCATCGAGTACCTG 134
Db 1641 GACCAAGATGTTGATGACTCTTACTGAGAGGACATCGCAACCATCGAGTACCTG 1700

QY 135 GTGCGCTGCAGAGGGCCACCCAGATGACGGTCCC---CGCATCGAGGTGCGGGT 191
Db 1701 GTGCGCTGCAGAGGTGAGCGCGTATGACTTCTCCAAATGGTGAAGATCCCACTC 1760

QY 192 GAGACCGAGCAT 205
Db 1761 GAGACCGATGACAT 1774

RESULT 8
US-09-887-052-5
; Sequence 5, Application US/09887052
; Patent No. US20020119537A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE rpoB GENE
; FILE REFERENCE: 204212USOX
; CURRENT APPLICATION NUMBER: US/09/887,052
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: DE10107229.5
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 5099
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
US-09-887-052-5

Query Match      33.8%; Score 69.2; DB 10; Length 5099;
Best Local Similarity 67.0%; Pred. No. 9.9e-10;
Matches 130; Conservative 0; Mismatches 58; Indels 6; Gaps 2;

QY 15 TAGCACTGGCGGTGTGGCGGCTACAGGTCACAGAGCTCGGCCCTGCACGGGGC 74
Db 1584 TAGCACTGGCTGCGGTGGTTCACAGATCAACCGCAAGCTCGGCCCTT---GGTGGC 1640

QY 75 GAGCCGATCAACAGCTGACGCTGACGAGGAGAGCTGCGCCACCATCGAGTACCTG 134
Db 1641 GACCAAGATGTTGATGACTCTTACTGAGAGGACATCGCAACCATCGAGTACCTG 1700

QY 135 GTGCGCTGCAGAGGGCCACCCAGATGACGGTCCC---CGCATCGAGGTGCGGGT 191
Db 1701 GTGCGCTGCAGAGGTGAGCGCGTATGACTTCTCCAAATGGTGAAGATCCCACTC 1760

QY 192 GAGACCGAGCAT 205
Db 1761 GAGACCGATGACAT 1774

RESULT 9
US-10-076-406-1
; Sequence 1, Application US/10076406
; Publication No. US20030166884A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: Nucleotide sequences coding for the rpoB gene
; FILE REFERENCE: 219774USOXCP
; CURRENT APPLICATION NUMBER: US/10/076,406
; PRIOR FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: DE 10107229.5
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 09/887052
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 5099
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
; OTHER INFORMATION:
US-10-076-406-1

Query Match      33.8%; Score 69.2; DB 12; Length 5099;
Best Local Similarity 67.0%; Pred. No. 9.9e-10;
Matches 130; Conservative 0; Mismatches 58; Indels 6; Gaps 2;

QY 15 TAGCACTGGCGGTGTGGCGGCTACAGGTCACAGAGAGCTCGGCCCTGCACGGGGC 74
Db 1584 TAGCACTGGCTGCGGTGGTTCACAGATCAACCGCAAGCTCGGCCCTT---GGTGGC 1640

QY 75 GAGCCGATCAACAGCTGACGCTGACGAGGAGAGCTGCGCCACCATCGAGTACCTG 134
Db 1641 GACCAAGATGTTGATGACTCTTACTGAGAGGACATCGCAACCATCGAGTACCTG 1700

QY 135 GTGCGCTGCAGAGGGCCACCCAGATGACGGTCCC---CGCATCGAGGTGCGGGT 191
Db 1701 GTGCGCTGCAGCGAGGTGAGCGCGTATGACTTCTCCAAATGGTGAAGATCCCACTC 1760

QY 192 GAGACCGAGCAT 205
Db 1761 GAGACCGATGACAT 1774

RESULT 10
US-10-076-406-3
; Sequence 3, Application US/10076406
; Publication No. US20030166884A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: Nucleotide sequences coding for the rpoB gene
; FILE REFERENCE: 219774USOXCP
; CURRENT APPLICATION NUMBER: US/10/076,406
; PRIOR FILING DATE: 2002-02-19

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; PRIOR APPLICATION NUMBER: DE 10107229.5
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 09/887052
; PRIOR FILING DATE: 2001-06-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 5099
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
; OTHER INFORMATION:
; NAME/KEY: mutation
; LOCATION: (1987)..(1987)
; OTHER INFORMATION: Substitution of adenine by thymine
; NAME/KEY: mutation
; LOCATION: (1288)..(1288)
; OTHER INFORMATION: Substitution of cytosine by thymine
; NAME/KEY: mutation
; LOCATION: (715)..(715)
; OTHER INFORMATION: Substitution of cytosine by thymine
US-10-076-406-3

Query Match          33.8%; Score 69.2; DB 12; Length 5099;
Best Local Similarity 67.0%; Pred. No. 9.9e-10;
Matches 130; Conservative 0; Mismatches 58; Indels 6; Gaps 2;

QY 15 TAGGACCTGGCGGCTGTGCGCGCTACAAAGGTCAACAAGAGCTCGGCGCTGCACGCGGGC 74
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1584 TAGGACCTGGCGGCTGTGCGGTGCTTACAAAGATCAACGCAAGCTCGGCCCTT---GGTGGC 1640

QY 75 GAGCGATCACAGCTCGAGCTGACCGGTCACGAGGAAGACGTCTGCCACCATCGAGTACCTG 134
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1641 GACCACGATGGTTTGATGACTCTTACTGAAGAGGACATCGCAACCAACCATCGAGTACCTG 1700

QY 135 GTGGCGCTGCACGAGGGCCAGCCACGATGACCGTCCC---CGGCATCGAGGTGCGGGTG 191
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1701 GTGGCTGTCACGAGGTGAGCGGTGATGACTTCTCCAAATGTTGAAGAGATCCCGATC 1760

QY 192 GAGACCGACGACAT 205
    ||||| ||||| |||||
Db 1761 GAGACCGATGACAT 1774

RESULT 11
US-10-076-406-5
; Sequence 5, Application US/10076406
; Publication No. US20030166884A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: Nucleotide sequences coding for the rpoB gene
; FILE REFERENCE: 219774USXCIP
; CURRENT APPLICATION NUMBER: US/10/076,406
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: DE 10107229.5
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 09/887052
; PRIOR FILING DATE: 2001-06-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 5099
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
; OTHER INFORMATION:

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; OTHER INFORMATION:
; NAME/KEY: mutation
; LOCATION: (2016)..(2016)
; OTHER INFORMATION: Substitution of cytosine by thymine
US-10-076-406-5

Query Match          33.8%; Score 69.2; DB 12; Length 5099;
Best Local Similarity 67.0%; Pred. No. 9.9e-10;
Matches 130; Conservative 0; Mismatches 58; Indels 6; Gaps 2;

QY 15 TAGGACCTGGCGGCTGTGCGCGCTACAAAGGTCAACAAGAGCTCGGCGCTGCACGCGGGC 74
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1584 TAGGACCTGGCGGCTGTGCGGTGCTTACAAAGATCAACGCAAGCTCGGCCCTT---GGTGGC 1640

QY 75 GAGCGATCACAGCTCGAGCTGACCGGTCACGAGGAAGACGTCTGCCACCATCGAGTACCTG 134
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1641 GACCACGATGGTTTGATGACTCTTACTGAAGAGGACATCGCAACCAACCATCGAGTACCTG 1700

QY 135 GTGGCGCTGCACGAGGGCCAGCCACGATGACCGTCCC---CGGCATCGAGGTGCGGGTG 191
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1701 GTGGCTGTCACGAGGTGAGCGGTGATGACTTCTCCAAATGTTGAAGAGATCCCGATC 1760

QY 192 GAGACCGACGACAT 205
    ||||| ||||| |||||
Db 1761 GAGACCGATGACAT 1774

RESULT 12
US-10-075-460-5
; Sequence 5, Application US/10075460
; Publication No. US20020155557A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: HANS, STEFAN
; APPLICANT: KREUTZER, CAROLINE
; APPLICANT: HERMANN, THOMAS
; APPLICANT: PFEFFERLE, WALTER
; APPLICANT: BINDER, MICHAEL
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE rpsL GENE
; FILE REFERENCE: 218472USUX
; CURRENT APPLICATION NUMBER: US/10/075,460
; CURRENT FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: DE 10107230.9
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: DE 10162386.0
; PRIOR FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 5099
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
; OTHER INFORMATION:
US-10-075-460-5

Query Match          33.8%; Score 69.2; DB 13; Length 5099;
Best Local Similarity 67.0%; Pred. No. 9.9e-10;
Matches 130; Conservative 0; Mismatches 58; Indels 6; Gaps 2;

QY 15 TAGGACCTGGCGGCTGTGCGCGCTACAAAGGTCAACAAGAGCTCGGCGCTGCACGCGGGC 74
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1584 TAGGACCTGGCGGCTGTGCGGTGCTTACAAAGATCAACGCAAGCTCGGCCCTT---GGTGGC 1640

QY 75 GAGCGATCACAGCTCGAGCTGACCGGTCACGAGGAAGACGTCTGCCACCATCGAGTACCTG 134
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1641 GACCACGATGGTTTGATGACTCTTACTGAAGAGGACATCGCAACCAACCATCGAGTACCTG 1700

QY 135 GTGGCGCTGCACGAGGGCCAGCCACGATGACCGTCCC---CGGCATCGAGGTGCGGGTG 191
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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Db      1701 GTGCTGTGACGAGGTGAGCGGTGATGACTTCTCCAAATGGTGAAGAGATCCCGATC 1760
QY      192 GAGACCGAGACAT 205
Db      1761 GAGACCGATGACAT 1774

RESULT 13
US-09-738-626-1
; Sequence 1, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAORO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 1
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-1

Query Match      33.8%; Score 69.2; DB 10; Length 3309400;
Best Local Similarity 67.0%; Pred. No. 5.4e-10;
Matches 130; Conservative 0; Mismatches 58; Indels 6; Gaps 2;

QY      15 TAGACCTGCGCGGTGTCGGCGCTACAAGGTCAACAGAGCTCGGCTGCACGGCGGC 74
Db      513795 TAGACCTGCGTGGGTGTCGTTACAAGATCAACCGCAAGCTCGGCCTT---GGTGGC 513851

QY      75 GAGCGGATCACCAGCTCGACGCTGACCGAGAGAGCTGTCGGCCACCATCGAGTACCTG 134
Db      513852 GACCACGATGGTTGATGACTTCTTACTGAAGAGGACATCGCAACCATCGAGTACCTG 513911

QY      135 GTGGGCTGCAGAGGGCCAGCCACCATGACCGTCCC---CGGCATCGAGTCCGGTG 191
Db      513912 GTGGCTGCAGCGAGGTGAGCGGCTGATGACTTCTCCAAATGGTGAAGAGATCCCGATC 513971

QY      192 GAGACCGAGACAT 205
Db      513972 GAGACCGATGACAT 513985

RESULT 14
US-10-156-761-5967
; Sequence 5967, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
; LENGTH: 9025608
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1

Query Match      21.5%; Score 44; DB 14; Length 9025608;
Best Local Similarity 51.0%; Pred. No. 0.0026;
Matches 104; Conservative 0; Mismatches 100; Indels 0; Gaps 0;
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; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 5967
; LENGTH: 1542
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1542)
US-10-156-761-5967

Query Match      21.5%; Score 44; DB 14; Length 1542;
Best Local Similarity 51.0%; Pred. No. 0.0059;
Matches 104; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

QY      1 TCAGGAGAACGCTGACGACCTGCGCGCTGTCGGCGCTACAGGTCAACAGAGCTCG 60
Db      683 TCCAGGCGAAGGCCCGGGCCCGGCGTGGCTCGACCGGCACGTTCCAGAGTTCCTGGG 742

QY      61 GCCTGCACGCGGGCGAGCGGATCACAGCTCGACGCTGACGAGGAGAGAGCTGTCGCCA 120
Db      743 GTGTGAACGCCCAACAAAGATTCAACACCGACACGCTGATGTCGGCGCCGGTGTCAACA 802

QY      121 CCATCGAGTACCTGTCGCGCTGTCGACGAGGGCCAGCCACGATGACCGTCCCGGGCATCG 180
Db      803 ACGGCGCGCACCCACCTGCAAGACTACGTGCGGCAACCAACGAGTCGAACGACGCTTCGCCAACA 862

QY      181 AGTGCGCGGTGGAGACCGACGACA 204
Db      863 ACGACACGTTTCGCGCGGCCCGACA 886

RESULT 15
US-10-156-761-1/c
; Sequence 1, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
; LENGTH: 9025608
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1

Query Match      21.5%; Score 44; DB 14; Length 9025608;
Best Local Similarity 51.0%; Pred. No. 0.0026;
Matches 104; Conservative 0; Mismatches 100; Indels 0; Gaps 0;
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QY 1 TCAGGAGACGCTACGACCTGGCGGTGTGCGCGCTACAAAGCTCAACAAGAGCTCG 60
Db 7217845 TCCAGGCGAAGGCCCGCGGCCAGGGCGGTGGCTCGACCGGCACGTTACAGAGTTCCCTGCCG 7217786
QY 61 GCCTGCACGCGCGCGAGCCGATCACACGCTCGACGCTGACCGAGGAGACGCTCGTCGCCA 120
Db 7217785 GTGTGACGCCACACAGAGATTCAACACCGACACGCTGATCGTGGCGCGCGGTGTCACCA 7217726
QY 121 CCATCGAGTACCTGTGGCTGCGACGAGGGCCAGCCACGATGACCGTCCCGCGGATCG 180
Db 7217725 ACGGCGCGCACCACTGCTGACGCTGCGCAACCGACGTCGAACGACGCTTCGCCAACA 7217666
QY 181 AGGTGCGCGTGGAGACCGACGACA 204
Db 7217665 ACGACACGTTCCGCGCGGCCGAGA 7217642
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Search completed: September 17, 2003, 13:09:22
Job time : 132.698 secs

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OM nucleic - nucleic search, using sw model

Run on: September 17, 2003, 12:31:22 ; Search time 38.6597 Seconds
(without alignments)
2443.269 Million cell updates/sec

Title: US-09-697-123B-21

Perfect score: 214
Sequence: 1 tcaggagagcgctacgat.....ccggtggtgacgacat 214

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2.6/ptodata/1/ina/5A_COMB.seq.*
- 2: /cgn2.6/ptodata/1/ina/5B_COMB.seq.*
- 3: /cgn2.6/ptodata/1/ina/6A_COMB.seq.*
- 4: /cgn2.6/ptodata/1/ina/6B_COMB.seq.*
- 5: /cgn2.6/ptodata/1/ina/PCTUS_COMB.seq.*
- 6: /cgn2.6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	129.6	60.6	970	1	US-08-250-030-1
2	129.6	60.6	970	5	PCT-US95-06790-1
3	129.6	60.6	4403765	3	US-09-103-840A-2
4	129.6	60.6	4411529	3	US-09-103-840A-1
5	108.8	50.8	3447	2	US-08-313-185-57
6	108.8	50.8	3447	3	US-09-082-614A-57
7	42.8	20.0	77536	4	US-09-410-551B-1
8	42.2	19.7	1734	6	5352575-8
9	40.6	19.0	1158	4	US-09-252-991A-1555
10	40.6	19.0	1314	4	US-09-252-991A-1611
11	39	18.2	777	4	US-09-252-991A-12568
12	39	18.2	786	4	US-09-252-991A-13239
13	39	18.2	2325	4	US-09-252-991A-12916
14	38.4	17.9	68750	3	US-09-335-403-1
15	38.4	17.9	68750	4	US-09-568-102-1
16	38.4	17.9	68750	4	US-09-567-969-1
17	38.4	17.9	68750	4	US-09-568-480-1
18	38.4	17.9	68750	4	US-09-568-486-1
19	38.4	17.9	68750	4	US-09-568-472-1
20	38.4	17.9	68750	4	US-09-567-899-1
21	38.2	17.9	1110	4	US-09-252-991A-16244
22	38.2	17.9	2034	4	US-09-252-991A-16353
23	38.2	17.9	2355	4	US-09-252-991A-16238
24	38	17.8	1665	3	US-08-881-784-8
25	38	17.8	1665	3	US-09-292-768-3
26	38	17.8	1665	3	US-09-292-768-67
27	38	17.8	1665	3	US-09-292-768-69

28	37.8	17.7	378	4	US-09-252-991A-7345	Sequence 7345, Ap
c 29	37.8	17.7	1134	4	US-09-252-991A-7137	Sequence 7137, Ap
30	37.8	17.7	1248	4	US-09-252-991A-7361	Sequence 7361, Ap
c 31	37.8	17.7	2541	4	US-09-252-991A-7209	Sequence 7209, Ap
32	37.8	17.7	3099	4	US-09-252-991A-7487	Sequence 7487, Ap
33	37.6	17.6	888	4	US-09-252-991A-6566	Sequence 6566, Ap
c 34	37.6	17.6	1074	4	US-09-252-991A-6658	Sequence 6658, Ap
35	37.6	17.6	11958	3	US-09-134-246-8	Sequence 8, Appl
c 36	37.4	17.5	2681	3	US-08-928-213B-7	Sequence 7, Appl
37	37.4	17.5	47981	4	US-09-679-279-1	Sequence 1, Appl
38	37.2	17.4	702	4	US-09-252-991A-3145	Sequence 3145, Ap
39	37.2	17.4	1416	4	US-09-252-991A-3049	Sequence 3049, Ap
40	37.2	17.4	1533	4	US-09-252-991A-2957	Sequence 2957, Ap
c 41	37.2	17.4	1545	4	US-09-252-991A-2823	Sequence 2823, Ap
42	37	17.3	879	3	US-09-105-537-11	Sequence 11, Appl
43	37	17.3	3292	3	US-09-320-878-22	Sequence 22, Appl
44	37	17.3	3292	4	US-09-141-908-15	Sequence 15, Appl
45	37	17.3	3292	4	US-09-657-440-22	Sequence 22, Appl

ALIGNMENTS

RESULT 1

US-08-250-030-1
; Sequence 1, Application US/08250030
; Patent No. 5643723
; GENERAL INFORMATION:
; APPLICANT: Persing, David H.
; TITLE OF INVENTION: Detection of a Genetic Locus Encoding
; TITLE OF INVENTION: Resistance to Rifampin in Mycobacterial Cultures and in
; TITLE OF INVENTION: Clinical Specimens
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg & Woessner
; STREET: 3500 IDS Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/250,030
; APPLICATION NUMBER: US/08/250,030
; FILING DATE: 26-MAY-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Muetting, Ann M.
; REGISTRATION NUMBER: 33,977
; REFERENCE/DOCKET NUMBER: 150.105US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-339-0331
; TELEFAX: 612-339-3061
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 970 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-250-030-1

Query Match 60.6%; Score 129.6; DB 1; Length 970;
Best Local Similarity 79.0%; Pred. No. 9.6e-22;
Matches 169; Conservative 0; Mismatches 39; Indels 6; Gaps 1;

QY 1 TCAGGAGAGCGCTACGATCTGCGCGCTGCGTACAGGTGACACAGAGCTGG 60

DB 26 TCAGGAGAGCGCTACGATCTGCGCGCTGCGTACAGGTGACACAGAGCTGG 85

Best Local Similarity 79.0%; Pred. No. 2e-21;
Matches 169; Conservative 0; Mismatches 39; Indels 6; Gaps 1;

QY 1 TCAAGGAGAAGCGTACGATCTGGCCCGGCTGGGTGCGGTACAGGTGACACAGAGAGCTGG 60
Db 760688 TCAAGGAGAAGCGTACGATCTGGCCCGGCTGGGTGCGGTATAGGTCAACAAGAGCTGG 760747

QY 61 GCGTGGGGGGACCAATCCGGCTCAGGTGACACACACACCCCTCACCGAGGAGAGCTGG 120
Db 760748 GCGTGGGTGGGGAGCC-----CATCAGCTGTCGACGCTGACCGAGAGAGCTGG 760801

QY 121 TCGCCACCATCAGTACCTGGTCCGCTGCAGAGGGCCAGACACCAAGATGACCGCCCGG 180
Db 760802 TCGCCACCATCAGTATCTGCTCCGCTTGCAGAGGCTCAGACACAGATGACCGTCCGG 760861

QY 181 GCGGCGTGCAGGTCCGGTGGGTGGAGGACAT 214
Db 760862 GCGGCGTGCAGGTCCGGTGGGAAACCGAGACAT 760895

RESULT 5
US-08-313-185-57
; Sequence 57, Application US/08313185
; Patent No. 5851763
; GENERAL INFORMATION:
; APPLICANT: Heym, Beate
; APPLICANT: Cole, Stewart
; APPLICANT: Young, Douglas
; APPLICANT: Zhang, Ying
; APPLICANT: Honore, Nadine
; APPLICANT: Telenti, Amalio
; APPLICANT: Bodmer, Thomas
; TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
; TITLE OF INVENTION: in Mycobacterium Tuberculosis
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/313,185
; FILING DATE: 12-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 02356.0068-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3447 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-313-185-57

Query Match 50.8%; Score 108.8; DB 2; Length 3447;
Best Local Similarity 72.9%; Pred. No. 6.7e-17;
Matches 156; Conservative 0; Mismatches 52; Indels 6; Gaps 1;

QY 1 TCAAGGAGAAGCGTACGATCTGGCCCGGCTGGGTGCGGTACAGGTGACACAGAGCTGG 60

Db 809 TCAAGGAGAAGCGTACGATCTGGCCCGGCTGGGTGCGGTACAGGTGACACAGAGCTGG 868

QY 61 GCGTGGGGGGACCAATCCGGCTCAGGTGACACACACACCCCTCACCGAGGAGAGCTGG 120
Db 869 GGTGTGACGCGGCTGAGTTGA-----TCAAGTCTGCTCCAGCTGACCGAAGAGGATGCG 922

QY 121 TCGCCACCATCAGTACCTGGTCCGCTGCAGAGGGCCAGACACCAAGATGACCGCCCGG 180
Db 923 TCGCCACCATCAGTACCTGGTCCGCTGCATGAGGCTCAGTCCGACAATGACTGTCCGAG 982

QY 181 GCGGCGTGCAGGTCCGGTGGGTGGAGGACAT 214
Db 983 GTGGGGTAGAGTCCCACTGGAACCTGACGATAT 1016

RESULT 6
US-09-082-614A-57
; Sequence 57, Application US/09082614A
; Patent No. 6124098
; GENERAL INFORMATION:
; APPLICANT: Heym, Beate
; APPLICANT: Cole, Stewart
; APPLICANT: Young, Douglas
; APPLICANT: Zhang, Ying
; APPLICANT: Honore, Nadine
; APPLICANT: Telenti, Amalio
; APPLICANT: Bodmer, Thomas
; TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
; TITLE OF INVENTION: in Mycobacterium Tuberculosis
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/082,614A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/313,185
; FILING DATE: 12-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 02356.0068-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3447 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-082-614A-57

Query Match 50.8%; Score 108.8; DB 3; Length 3447;
Best Local Similarity 72.9%; Pred. No. 6.7e-17;
Matches 156; Conservative 0; Mismatches 52; Indels 6; Gaps 1;

QY 1 TCAAGGAGAAGCGTACGATCTGGCCCGGCTGGGTGCGGTACAGGTGACACAGAGCTGG 60

Db 809 TCAAGGAAACCTACGACCTGCCAGGCTTGCTTACAGGTCAACAGAGCTCG 868
QY 61 GCCTGGGCGCACCAATCGGCTCAGGTGACCCACCACTCACCAGGAGAACGTCG 120
Db 869 GGTTCACGCGGTGAGTTGA-----TCAGTCTCCACGCTGACCGAAGAGATCG 922
QY 121 TCGCCACCATGATGACCTGCTGCGCTGCACGAGGCGCCAGACCATGATGACCGCCCG 180
Db 923 TCGCCACCATGATGACCTGCTGCTGCTGATGAGGCTCAGTCGACATGACTGTCCAG 982
QY 181 GCGGCTGAGGTGCGCGTGGATGGAGACAT 214
Db 983 GTGGGTAGAGTGCAGTGGAACTGACGATAT 1016

RESULT 7

US-09-410-551B-1/c
; Sequence 1, Application US/09410551B
; Patent No. 6503737
; GENERAL INFORMATION:
; APPLICANT: KOSAN BIOSCIENCES, Inc.
; APPLICANT: REEVES, CHRISTOPHER
; APPLICANT: CHU, DANIEL
; APPLICANT: KHOSLA, CHAITAN
; APPLICANT: SANTI, DANIEL
; APPLICANT: WU, KAI
; TITLE OF INVENTION: POLYKETIDE SYNTHASE ENZYMES AND RECOMBINANT DNA
; TITLE OF INVENTION: CONSTRUCTS THEREFOR
; FILE REFERENCE: 30062-20026.00
; CURRENT APPLICATION NUMBER: US/09/410,551B
; CURRENT FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: US 60/139,650
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: US 60/123,810
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 60/102,748
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 77536
; TYPE: DNA
; ORGANISM: Streptomyces hygroscopicus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (52275)...(71465)
US-09-410-551B-1

Query Match 20.0%; Score 42.8; DB 4; Length 77536;
Best Local Similarity 61.8%; Pred. No. 0.15;
Matches 68; Conservative 0; Mismatches 42; Indels 0; Gaps 0;
QY 69 GGCACCATCGGCTCAGGTGACCCACCACTCACCAGGAGAACGTCGTGCCACC 128
Db 2439 GCCGCCACCGGCGCCAGACACCATCAGCTGACCTGGAACCCGTGCGCGGCC 2380
QY 129 ATCGAGTACCTGTGCGCTGCACGAGGCGCCAGACCATGATGACCGCCCG 178
Db 2379 ACCGACTACGCGCTCCACCGCGAGCTGCCAGATCACCACGCTCCGCCAC 2330

RESULT 8

5352575-8
; Patent No. 5352575
; APPLICANT: PETROVSKIS, ERIK A.; POST, LEONARD E.; TIMMINS, JAMES G.
; TITLE OF INVENTION: PSEUDORABIES VIRUS PROTEIN
; NUMBER OF SEQUENCES: 12
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/513,282
; FILING DATE: 20-APR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 100,817
; FILING DATE: 29-JUN-1987

; APPLICATION NUMBER: 886,260
; FILING DATE: 16-JUL-1986
; APPLICATION NUMBER: 784,787
; FILING DATE: 04-OCT-1985
; APPLICATION NUMBER: 801,799
; FILING DATE: 26-NOV-1985
; APPLICATION NUMBER: 844,113
; FILING DATE: 26-MAR-1986
; SEQ ID NO: 8
; LENGTH: 1734
5352575-8
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Best Local Similarity 54.1%; Pred. No. 0.15;
Matches 86; Conservative 0; Mismatches 73; Indels 0; Gaps 0;
QY 56 GCTGGGCTGGGCGGACCAATCGGCTCAGGTGACCAACCACTCACCAGGAGAGA 115
Db 1065 GATGACCCACACGCGCCACGTCGCCACCTGGGACTACAGCTCTCGCCACCGCGCGCA 1124
QY 116 CGTGTGCGCCACCATCGAGTACCTGCTGCGCTGCACGAGGCGCCAGACCATGACCGC 175
Db 1125 GTAGTCACTCGTCACTCAAGGACTGACGGCCCGCGGCCCGCGGCACCCCGTGGGG 1184
QY 176 CCCGCGCGGCTCGAGGTGCGGTCGGTGGATGGAGACAT 214
Db 1185 CCCGCGCGGCGGACGACGCGATCTACGTGGACGGCGT 1223

RESULT 9

US-09-252-991A-1555
; Sequence 1555, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONA:
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 1555
; LENGTH: 1158
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1555

Query Match 19.0%; Score 40.6; DB 4; Length 1158;
Best Local Similarity 60.4%; Pred. No. 0.33;
Matches 67; Conservative 0; Mismatches 44; Indels 0; Gaps 0;
QY 57 CTGGGCTGGGCGGACCAATCGGCTCAGGTGACCAACCACTCACCAGGAGAGAC 116
Db 181 CTGGGCTGGGCGGCGAGCCTCGCCAGCGCCACCACTCAGCTCAGGTATACGCG 240
QY 117 GTGCTGCCACCATCGAGTACCTGCTGCGCTGCACGAGGCGCCAGACCAAG 167
Db 241 GCCGCGACGAGGAGAGACCTGTGACCTGTTCGCCAGCACTCAAG 291

RESULT 10

US-09-252-991A-1611/c
; Sequence 1611, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONA:
; FILE REFERENCE: 107196.136

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 17, 2003, 13:09:27 : Search time 132.69 Seconds
(without alignments)
3967.311 Million cell updates/sec

Title: US-09-697-123B-21
Perfect score: 214
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1660708 seqs, 1229959015 residues

Total number of hits satisfying chosen parameters: 3321415

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_NA:*

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13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
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15: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	129.6	60.6	3519	US-09-712-363-30
2	80.4	37.6	3495	Sequence 30, Appl
3	80.4	37.6	5096	Sequence 547, Appl
4	80.4	37.6	5099	Sequence 5, Appl
5	80.4	37.6	5099	US-09-984-711-5
6	80.4	37.6	5099	US-09-887-052-1
7	80.4	37.6	5099	US-09-887-052-3
8	80.4	37.6	5099	US-09-887-052-5
9	80.4	37.6	5099	US-10-076-406-1
10	80.4	37.6	5099	US-10-076-406-3
11	80.4	37.6	5099	US-10-076-406-5
12	80.4	37.6	3309400	US-10-075-460-5
13	66.4	31.0	3543	US-09-738-626-1
14	46.6	21.8	984	US-10-156-761-1
15	46.6	21.8	9025608	US-10-156-761-1305
16	43.6	20.4	963	US-10-156-761-1
				Sequence 5097, Appl

17	43.2	20.2	1860	14	US-10-156-761-6889
18	42	19.6	294	14	US-10-156-761-711
19	41.2	19.3	1074	14	US-10-156-761-5848
20	41	19.2	392	10	US-09-878-574-3598
21	41	19.2	1584	14	US-10-156-761-5604
22	40.8	19.1	1041	14	US-10-156-761-594
23	40.6	19.0	2304	14	US-10-156-761-5121
24	40.2	18.8	1629	14	US-10-156-761-3590
25	39.8	18.6	1905	14	US-10-156-761-3164
26	39.8	18.6	2475	14	US-10-156-761-6867
27	39.8	18.6	2715	14	US-10-156-761-2245
28	39.6	18.5	1107	14	US-10-156-761-3873
29	39.4	18.4	645	14	US-10-156-761-1690
30	39.2	18.3	1887	14	US-10-156-761-99
31	39	18.2	1176	14	US-10-156-761-1256
32	39	18.2	1254	14	US-10-128-714-2345
33	39	18.2	1254	14	US-10-128-714-7345
34	39	18.2	1285	12	US-10-183-708-1
35	39	18.2	1416	14	US-10-128-714-1345
36	39	18.2	1416	14	US-10-128-714-6345
37	39	18.2	1707	14	US-10-156-761-4723
38	39	18.2	3415	14	US-10-128-714-345
39	39	18.2	3416	14	US-10-128-714-5345
40	38.8	18.1	1134	12	US-10-259-165-740
41	38.6	18.0	399	9	US-09-861-893-29
42	38.6	18.0	431	10	US-09-954-456-1034
43	38.6	18.0	933	14	US-10-156-761-4618
44	38.6	18.0	1503	14	US-10-156-761-2732
45	38.4	17.9	68750	13	US-10-014-717-1

ALIGNMENTS

RESULT 1

US-09-712-363-30
Sequence 30, Application US/09712363
Patent No. US20020164588A1
GENERAL INFORMATION:
APPLICANT: Eisenberg, David
APPLICANT: Rotstein, Sergio H.
APPLICANT: Marcotte, Edward M.
TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND
FILE REFERENCE: 07419-032001
CURRENT APPLICATION NUMBER: US/09/712,363
CURRENT FILING DATE: 2000-11-13
PRIOR APPLICATION NUMBER: PCT/US00/02246
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 60/179,531
PRIOR FILING DATE: 2000-02-01
PRIOR APPLICATION NUMBER: 60/117,844
PRIOR FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: 60/118,206,
PRIOR FILING DATE: 1999-02-01
PRIOR APPLICATION NUMBER: 60/126,593
PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: 60/134,093
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 60/134,092
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 60/165,124
PRIOR FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 60/165,086
PRIOR FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 292
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 30
LENGTH: 3519
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis

US-09-712-363-30


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QY 121 TCGCCACCATCGAGTACCTGGTGGCGCTGCACAGGCGCCAGACACGATGACCGCCCGG 180
    || | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1034 TCTGCTGATCAAGTACCTGGTGAAGCTGCACGCGCGGTGAGCCGAGACCGTTGGCGACA 1093
    || | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 181 GCGGGGTGCGAGGTGCGCGGTGGATGTGGACGACAT 214
    ||| | || | || | || | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1094 ACGGCACCTCGATCGTGGTGGACGACGACAT 1127
    ||| | || | || | || | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 13
US-10-156-761-1
; Sequence 1, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
; LENGTH: 9025608
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1

Query Match 31.0%; Score 66.4; DB 14; Length 9025608;
Best Local Similarity 61.2%; Pred. No. 2.8e-09;
Matches 131; Conservative 0; Mismatches 71; Indels 12; Gaps 1;

QY 1 TCAAGGAGAAGCGGTACGATCTGGCCCGCGTGGCTGCTACAGGTGACACAGAGCTGG 60
    ||| | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5970494 TCAACCGGAAGCGGTACGATCTGGCCCGCGTGGCTGCTACAGGTGACACAGAGCTGG 5970553
    ||| | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 61 GCGTGGGCGGACCATCCGCTCAGGTGACACACACCCCTCACCAGGAGGACGCTCG 120
    || | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5970554 GCGGCGA-----GGCGCGCTGGACCGCGGGATCCTGACCGCTCGAGGACATCA 5970601
    || | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 121 TCGCCACCATCGAGTACCTGGTGGCGCTGCACAGGCGCCAGACACGATGACCGCCCGG 180
    || | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5970602 TCTGCTGATCAAGTACCTGGTGGCTGCACGCGCGGTGAGACCGGACCGTTGGCGACA 5970661
    ||| | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 181 GCGGCGTGCAGGTGCCGGTGGATGTGGACGACAT 214
    ||| | || | || | || | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5970662 ACGGCACCTCGATCGTGGTGGACGACGACAT 5970695
    ||| | || | || | || | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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RESULT 14
US-10-156-761-1305
; Sequence 1305, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRO
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; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1305
; LENGTH: 984
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(984)
US-10-156-761-1305

Query Match 21.8%; Score 46.6; DB 14; Length 984;
Best Local Similarity 51.2%; Pred. No. 0.00098;
Matches 109; Conservative 0; Mismatches 104; Indels 0; Gaps 0;

QY 1 TCAAGGAGAAGCGGTACGATCTGGCCCGCGTGGCTGCTACAGGTGACACAGAGCTGG 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 56 TCGAGGGGATCCACTACGGGTCCGCTGGTGTCTCGGCGCGGACGGAACGTGGACCTGC 115
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 61 GCGTGGGCGGACCAATCCGGGTTCAGGTGACACACACCCCTCACCAGGAGGACGCTCG 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 116 AGATCGGCGACATCGAGGGCGGCTTCTATCCACCTCGGCGCTCAAGCCCGGTACAGGCG 175
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 121 TCGCCACCATCGAGTACCTGGTGGCGCTGCACAGGCGCCAGACACGATGACCGCCCGG 180
    || | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 176 TGGCGATGCTGGGCGCGGCTCGCCCTCGACGGGGAAGTCTCTCTGCTGGCGCGCGCA 235
    || | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 181 GCGGCGTGCAGGTCCGCGTGGATGTGGACGACA 213
    || | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 236 GCCACTCGGCGAGGAGCGGCACTCTGGCGCGCA 268
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RESULT 15
US-10-156-761-1/c
; Sequence 1, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
; LENGTH: 9025608
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1

Query Match 21.8%; Score 46.6; DB 14; Length 9025608;
Best Local Similarity 51.2%; Pred. No. 0.0007;
Matches 109; Conservative 0; Mismatches 104; Indels 0; Gaps 0;
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Db      1628326  TCGAGGCGATCCACTACGGGTCCGTCGTGGTCTCGGCGCCGACGGGACGTGGACCTGC 1628267
QY      61  GCCTGGGGGGACCAATCCGGCTCAGGTGACCAACCAACCCCTCACCGAGGAAGACGTGG 120
Db      1628266  AGATCGGCGACATCGAGGCGGCCCTTCTATCCACGCTCGGCCCTCAAGCCCGTACAGGCCG 1628207
QY     121  TCGCCACCATCGAGTACCTGCTGGCTTCACAGAGGGCCAGACACGATGACCGCCCGG 180
Db     1628206  TGGCGATGCTCGGCGCGGGCTGCCCTCGACGGGGAATGCTCTGCTGGCGCGGCA 1628147
QY     181  GCGGCGTCGAGGTGCCGTGGATGTGGACGACA 213
Db     1628146  GCCACTCCGGCGAGGAGCGGCATCTGGCCGGCA 1628114
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Job time : 162.69 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 17, 2003, 12:31:22 : Search time 37.5758 Seconds
(without alignments)
2443.269 Million cell updates/sec

Title: US-09-697-123B-22

Perfect score: 208

Sequence: 1 tcaaggagaagcgtacgac.....ccggtggaacgagacat 208

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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5: /cgn2.6/ptodata/1/ina/PTUS_COMB.seq.*
6: /cgn2.6/ptodata/1/ina/backfiles1.seq.*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	206.4	99.2	4403765	3	US-09-103-840A-2
4	206.4	99.2	4411529	3	US-09-103-840A-1
5	147.2	70.8	3447	2	US-08-313-185-57
6	147.2	70.8	3447	3	US-09-082-614A-57
7	40.2	19.3	924	4	US-09-252-991A-969
8	40.2	19.3	939	4	US-09-252-991A-925
c	39.8	19.1	768	4	US-09-252-991A-1114
9	38.8	18.7	1412	1	US-08-097-831-1
c	37.2	17.9	1452	4	US-09-252-991A-13650
11	37.2	17.9	1980	4	US-09-252-991A-13782
12	37.2	17.9	6085	3	US-09-029-603-4
13	37	17.8	1748	4	US-09-252-991A-13457
c	36.4	17.5	258	4	US-09-252-991A-13899
15	36.4	17.5	615	4	US-09-252-991A-13899
16	36.4	17.5	1695	4	US-09-252-991A-13695
17	36	17.3	1894	3	US-09-329-350-32
c	35.4	17.0	894	4	US-09-252-991A-10907
18	35.4	17.0	1848	4	US-09-252-991A-10829
19	35.2	16.9	1326	4	US-09-252-991A-10931
20	35.2	16.9	2211	4	US-09-252-991A-11256
c	35.2	16.9	2289	4	US-09-252-991A-10995
22	35.2	16.9	1621	1	US-08-722-001-13
23	34.6	16.6	1621	1	US-08-722-001-13
24	34.6	16.6	1776	1	US-08-722-001-29
25	34.6	16.6	2002	4	US-09-016-434-1172
26	34.6	16.6	2140	1	US-08-334-698-1
27	34.6	16.6	2140	1	US-08-228-932-1

28	34.6	16.6	2140	1	US-08-468-939-1	Sequence 1, Appli
29	34.6	16.6	2140	2	US-08-406-855A-1	Sequence 1, Appli
30	34.6	16.6	2140	2	US-08-722-190-1	Sequence 1, Appli
31	34.6	16.6	2140	3	US-08-244-354-1	Sequence 1, Appli
32	34.6	16.6	2140	3	US-09-206-899-1	Sequence 1, Appli
33	34.6	16.6	2140	4	US-09-444-783-1	Sequence 1, Appli
34	34.6	16.6	2140	4	US-09-688-415-1	Sequence 1, Appli
35	34.6	16.6	2140	5	PCT-US95-04203-1	Sequence 1, Appli
36	34.6	16.5	870	4	US-09-252-991A-7157	Sequence 7157, Ap
C 37	34.4	16.5	2415	4	US-09-252-991A-7480	Sequence 7480, Ap
38	34.4	16.5	2667	4	US-09-252-991A-7216	Sequence 7216, Ap
C 39	34.2	16.4	22306	4	US-09-453-702B-251	Sequence 251, App
40	34	16.3	680	4	US-09-556-877-267	Sequence 267, App
41	34	16.3	680	4	US-09-620-412C-267	Sequence 267, App
42	34	16.3	680	4	US-09-598-419-267	Sequence 267, App
C 43	33.2	16.0	1089	4	US-09-252-991A-14778	Sequence 14778, A
C 44	33.2	16.0	1347	4	US-09-252-991A-14972	Sequence 14972, A
45	33.2	16.0	1482	4	US-09-252-991A-14656	Sequence 14656, A

ALIGNMENTS

RESULT 1
US-08-250-030-1
; Sequence 1, Application US/08250030
; Patent No. 5643723
; GENERAL INFORMATION:
; APPLICANT: Persing, David H.
; TITLE OF INVENTION: Detection of a Genetic Locus Encoding
; TITLE OF INVENTION: Resistance to Rifampin in Mycobacterial Cultures and in
; TITLE OF INVENTION: Clinical Specimens
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg & Woessner
; STREET: 3500 IDS Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/250,030
; FILING DATE: 26-MAY-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Muetting, Ann M.
; REGISTRATION NUMBER: 33,977
; REFERENCE/DOCKET NUMBER: 150.105US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-339-0331
; TELEFAX: 612-339-3061
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 970 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-250-030-1

Query Match 99.2%; Score 206.4; DB 1; Length 970;
Best Local Similarity 99.5%; Pred. No. 6.2e-48;
Matches 207; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCAAGGAGAGCGCTACGACCTGCCCGCGTGGTGTATAGGTCAACAAGAGCTCG 60

Db 26 TCAAGGAGAGCGCTACGACCTGCCCGCGTGGTGTATAGGTCAACAAGAGCTCG 85

QY 61 GGCTGCATATCGCGAGCCCAATCAGTGTGTCAGCGTGTGACCGAAGAAGACGCTGTGGCCA 120
Db 86 GGCTGCATATCGCGAGCCCAATCAGTGTGTCAGCGTGTGACCGAAGAAGACGCTGTGGCCA 145
QY 121 CCATCGAATATCTGCTGCGCTTGCACGAGGTCAGACGATGATGCTTCGGGGGGCG 180
Db 146 CCATCGAATATCTGCTGCGCTTGCACGAGGTCAGACGATGATGCTTCGGGGGGCG 205
QY 181 TCGAGGTGCGCGTGGAAACCGACGACAT 208
Db 206 TCGAGGTGCGCGTGGAAACCGACGACAT 233

RESULT 2

PCT-US95-06790-1
; Sequence 1, Application PC/TUS9506790
; GENERAL INFORMATION:
; APPLICANT: Mayo Foundation for Medical Education and Research
; APPLICANT: and Hoffmann-La Roche Inc.
; TITLE OF INVENTION: Detection of a Genetic Locus Encoding
; TITLE OF INVENTION: Resistance to Rifampin
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg & Woessner
; STREET: 3500 IDS Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/06790
; FILING DATE: 26-MAY-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Raasch, Kevin W.
; REGISTRATION NUMBER: 35,651
; REFERENCE/DOCKET NUMBER: 150.105W01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-339-0331
; TELEFAX: 612-339-3061
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 970 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
PCT-US95-06790-1

Query Match 99.2%; Score 206.4; DB 5; Length 970;
Best Local Similarity 99.5%; Pred. No. 6.2e-48;
Matches 207; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TCAAGGAGAGCGCTACGACCTGGCCCGCTGCTGCTATAGGTCAACAGAGCTCG 60
Db 26 TCAAGGAGAGCGCTACGACCTGGCCCGCTGCTGCTATAGGTCAACAGAGCTCG 85
QY 61 GGCTGCATATCTGCTGCGCTTGCACGAGGTCAGACGATGATGCTTCGGGGGGCG 120
Db 86 GGCTGCATATCTGCTGCGCTTGCACGAGGTCAGACGATGATGCTTCGGGGGGCG 145
QY 121 CCATCGAATATCTGCTGCGCTTGCACGAGGTCAGACGATGATGCTTCGGGGGGCG 180
Db 146 CCATCGAATATCTGCTGCGCTTGCACGAGGTCAGACGATGATGCTTCGGGGGGCG 205
QY 181 TCGAGGTGCGCGTGGAAACCGACGACAT 208
Db 206 TCGAGGTGCGCGTGGAAACCGACGACAT 233

RESULT 3

US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match 99.2%; Score 206.4; DB 3; Length 4403765;
Best Local Similarity 99.5%; Pred. No. 2.6e-47;
Matches 207; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TCAAGGAGAGCGCTACGACCTGGCCCGCTGCTGCTATAGGTCAACAGAGCTCG 60
Db 762648 TCAAGGAGAGCGCTACGACCTGGCCCGCTGCTGCTATAGGTCAACAGAGCTCG 762707
QY 61 GGCTGCATATCTGCTGCGCTTGCACGAGGTCAGACGATGATGCTTCGGGGGGCG 120
Db 762708 GGCTGCATATCTGCTGCGCTTGCACGAGGTCAGACGATGATGCTTCGGGGGGCG 180
QY 121 CCATCGAATATCTGCTGCGCTTGCACGAGGTCAGACGATGATGCTTCGGGGGGCG 180
Db 762768 CCATCGAATATCTGCTGCGCTTGCACGAGGTCAGACGATGATGCTTCGGGGGGCG 762827
QY 181 TCGAGGTGCGCGTGGAAACCGACGACAT 208
Db 762828 TCGAGGTGCGCGTGGAAACCGACGACAT 762855

RESULT 4

US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match 99.2%; Score 206.4; DB 3; Length 4411529;

Best Local Similarity 99.5%; Pred. No. 2.6e-47;
Matches 207; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCAAGAGAGAGCGGTACGACCTGGCCCGCGTGTGCTATAGGTCAACAAGAGCTCG 60
DB 760688 TCAAGAGAGAGCGGTACGACCTGGCCCGCGTGTGCTATAGGTCAACAAGAGCTCG 760747
QY 61 GCGTCANGTGGGAGCCCATCAGCTGTGCGACGCTGACCGAGAGAGCTGTCGGCCA 120
DB 760748 GCGTCANGTGGGAGCCCATCAGCTGTGCGACGCTGACCGAGAGAGCTGTCGGCCA 760807
QY 121 CCATCGAATATCTGCTCCGCTTGCAGAGGCTCAGACCATGATGCTTCCGGGCGCG 180
DB 760808 CCATCGAATATCTGCTCCGCTTGCAGAGGCTCAGACCATGATGCTTCCGGGCGCG 760867
QY 181 TCGAGGTCCGCGTGAACCGAGACAT 208
DB 760868 TCGAGGTCCGCGTGAACCGAGACAT 760895

RESULT 5

US-08-313-185-57
; Sequence 57, Application US/08313185
; Patent No. 5851763

GENERAL INFORMATION:

APPLICANT: Heym, Beate
APPLICANT: Cole, Stewart
APPLICANT: Young, Douglas
APPLICANT: Zhang, Ying
APPLICANT: Honore, Nadine
APPLICANT: Telenti, Amalio
APPLICANT: Bodmer, Thomas
TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
TITLE OF INVENTION: in Mycobacterium Tuberculosis
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 12-OCT-1994
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 02356.0068-00600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400

INFORMATION FOR SEQ ID NO: 57:

SEQUENCE CHARACTERISTICS:
LENGTH: 3447 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-313-185-57

Query Match 70.8%; Score 147.2; DB 2; Length 3447;
Best Local Similarity 81.7%; Pred. No. 1.3e-31;
Matches 170; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 1 TCAAGAGAGAGCGGTACGACCTGGCCCGCGTGTGCTATAGGTCAACAAGAGCTCG 60

DB 809 TCAGAGAGAGCGGTACGACCTGGCCCGCGTGTGCTATAGGTCAACAAGAGCTCG 868
QY 61 GCGTCANGTGGGAGCCCATCAGCTGTGCGACGCTGACCGAGAGAGCTGTCGGCCA 120
DB 869 GGTTCGACCGCGGTGAGTTGATCACTGCTCCACGCTGACCGAGAGAGATGTCGTGCGCA 928
QY 121 CCATCGAATATCTGCTCCGCTTGCAGAGGCTCAGACCATGATGCTTCCGGGCGCG 180
DB 929 CCATAGAGTACTGCTGCTCGTCTGATGAGGCTCAGTCAATGACTGTCCAGAGTGGGG 988
QY 181 TCGAGGTCCGCGTGAACCGAGACAT 208
DB 989 TAGAGTCCGAGTGAACCTGACGATAT 1016

RESULT 6

US-09-082-614A-57
; Sequence 57, Application US/09082614A
; Patent No. 6124098

GENERAL INFORMATION:

APPLICANT: Heym, Beate
APPLICANT: Cole, Stewart
APPLICANT: Young, Douglas
APPLICANT: Zhang, Ying
APPLICANT: Honore, Nadine
APPLICANT: Telenti, Amalio
APPLICANT: Bodmer, Thomas
TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
TITLE OF INVENTION: in Mycobacterium Tuberculosis
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 12-OCT-1994
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 02356.0068-00600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400

INFORMATION FOR SEQ ID NO: 57:

SEQUENCE CHARACTERISTICS:
LENGTH: 3447 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-082-614A-57

Query Match 70.8%; Score 147.2; DB 3; Length 3447;
Best Local Similarity 81.7%; Pred. No. 1.3e-31;
Matches 170; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 1 TCAAGAGAGAGCGGTACGACCTGGCCCGCGTGTGCTATAGGTCAACAAGAGCTCG 60

Db 809 TCAGGAGAAAGCTACGACCTGCCAGGCTGGTTCGTTACAAAGTCAACAAGAAAGCTCG 868
QY 61 GGCTGATGTCGCGAGCCCATACGTCGTCGAGCTGACCGAAGAGAGCTGTCGGCCA 120
Db 869 GTTTCACGCCGGTGAGTTGATACGTCGTCACGTCGACGTCACGAGAGAGAGTGTGTCGCCA 928
QY 121 CCAATGAAATATGTCGCTTCGACGAGGTCAGACCATGATGCTTCCGGGGCGCG 180
Db 929 CCATAGAGTACCTGGTTCGTCGATGAGGTCAGTCGACATGACTGCCAGGTTGGG 988
QY 181 TCGAGTGGCGGTGAACCCAGCACAT 208
Db 989 TAGAAGTGCAGTGGAACTGACGATAT 1016

RESULT 7
US-09-252-991A-969
; Sequence 969, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 969
; LENGTH: 924
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-969

Query Match 19.3%; Score 40.2; DB 4; Length 924;
Best Local Similarity 52.0%; Pred. No. 0.021;
Matches 90; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

QY 17 CGACTGGCCGCGTCTGCTATAGGTCACAAAGAGCTCGGGCTGCTGTCGCGCA 76
Db 597 CGACCGCTCGCGTCTGCTCGCGACCCCGCGAGCGGTCGCGCGCGACCTGTGAG 656
QY 77 GCCCATCACGTCTGCTGACGCTGACCGAAGAGAGCTGTCGCGCAATATCTGTT 136
Db 657 CACCGAGTGTGGCTCTGATGGCGCAGGAGAGCGCGCGCGCATCGCCCTGTT 716
QY 137 CCGTTTCACAGAGGTCAGACCATGATGCTTCCGGGGCGCGTCGAGGTTC 189
Db 717 CCGTCCCTACAGGTGAACGCGCGCTTCTCGATGGGGCGCGCGACGATGTAC 769

RESULT 8
US-09-252-991A-925
; Sequence 925, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 925
; LENGTH: 939
; TYPE: DNA

; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-925

Query Match 19.3%; Score 40.2; DB 4; Length 939;
Best Local Similarity 52.0%; Pred. No. 0.021;
Matches 90; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

QY 17 CGACTGGCCGCGTCTGCTATAGGTCACAAAGAGCTCGGGCTGCTGTCGCGCA 76
Db 604 CGACCGCTCGCGTCTGCTCGCGACCCCGCGAGGCGGTGGCGCGCACCTGTGTAG 663
QY 77 GCCCATCACGTCTGCTGACGCTGACCGAAGAGAGCTGTCGCGCACCATCTGATCTGTT 136
Db 664 CACCGAGTGTGGCTCTGATGGCGCGAGGAGAGAGCGCGCGCATCGCCCTGTT 723
QY 137 CCGTTTCACAGAGGTCAGACCATGATGCTTCCGGGGCGCGTCGAGGTTC 189
Db 724 CCGTCCCTACAGGTGAACGCGCGCTTCTCGATGGGGCGCGCGACGATGTAC 776

RESULT 9
US-09-252-991A-1114/C
; Sequence 1114, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 1114
; LENGTH: 768
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1114

Query Match 19.1%; Score 39.8; DB 4; Length 768;
Best Local Similarity 52.0%; Pred. No. 0.026;
Matches 89; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

QY 17 CGACTGGCCGCGTCTGCTATAGGTCACAAAGAGCTCGGGCTGCTGTCGCGCA 76
Db 172 CGACCGCTCGCGTCTGCTCGCGACCCCGCGAGGCGGTGGCGCGCACCTGTGTAG 113
QY 77 GCCCATCACGTCTGCTGACGCTGACCGAAGAGAGCTGTCGCGCACCATCTGATCTGTT 136
Db 112 CACCGAGTGTGGCTCTGATGGGGCGCGAGGAGAGAGCGCGCGCATCGCCCTGTT 53
QY 137 CCGTTTCACAGAGGTCAGACCATGATGCTTCCGGGGCGCGTCGAGGTTC 187
Db 52 CCGTCCCTACAGGTGAACGCGCGCTTCTCGATGGGGCGCGCGACGATGT 2

RESULT 10
US-08-097-831-1
; Sequence 1, Application US/08097831
; Patent No. 5510473
; GENERAL INFORMATION:
; APPLICANT: Camerini-Otero, Rafael D.
; APPLICANT: Anzov, Evangelina
; TITLE OF INVENTION: Cloning and Expression of Taq reca
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KNOBBE, MARTENS, OLSON AND BEAR
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA

COUNTRY: USA
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/097,831
FILING DATE: 19930726
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E.
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: NIH066.001A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
TELEFAX: 714-760-9502
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1412 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: taq reca
FEATURE:
NAME/KEY: CDS
LOCATION: 62..1082
US-08-097-831-1

Query Match 18.7%; Score 38.8; DB 1; Length 1412;
Best Local Similarity 54.1%; Pred. No. 0.054;
Matches 79; Conservative 0; Mismatches 67; Indels 0; Gaps 0;
QY 50 CAAGAAGTCGGGTGCTGCGGCGAGCCCATCAGCTGCGACGCTGACCGAGAGA 109
DB 370 CAAGAAGTCGGGTGCGAGCTGCGAGGCTTCTGCTCCAGCCGAGACCGGGGACA 429
QY 110 CGTCGTGCCACCATCGAATATCTGGTCGCTTGACAGAGGTCAGACCATGATCGT 169
DB 430 GCCTTTGAGATCGTGGAGCTTCTGCGCGCTCGGGGGCGGTGACGTGTCGTGGA 489
QY 170 TCGGGCGCGTCTGAGTGCCGGTGG 195
DB 490 TTCGGTGGCCGCTTTGCTGCCAAG 515

RESULT 11
US-09-252-991A-13650/C
; Sequence 13650, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 13650
; LENGTH: 1452
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13650

Query Match 17.9%; Score 37.2; DB 4; Length 1452;
Best Local Similarity 51.2%; Pred. No. 0.15; Indels 0; Gaps 0;
Matches 87; Conservative 0; Mismatches 83; Indels 0; Gaps 0;
QY 13 GCTACGACTGGCCCGGCTGCTGCTATAGGTCAACAAGAGCTGGGCTGCAATGCG 72
DB 806 GCGCTACTGTGTTGGAAGGCTTCGAGAAGATGCCCAATACTGCCCCATGAGG 747
QY 73 GCGAGCCCATCAGCTGCTGAGCGCTGACCGAAGAGAGCTGGGCCACCATGCAATTC 132
DB 746 ACAGCAGCCGCGAGGCGCTGCGGCCCAATGTCAGCTGGCGCGCTGGAAAAGC 687
QY 133 TGGTCGGTTGACAGAGGTCAGACCATGATGCTTCGCGGGCGGCTC 182
DB 686 AGAAGATCGCGGCGGATCCGTACCGACTTCATCTCTCGCGGAAATC 637

RESULT 12
US-09-252-991A-13782
; Sequence 13782, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 13782
; LENGTH: 1980
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13782

Query Match 17.9%; Score 37.2; DB 4; Length 1980;
Best Local Similarity 51.2%; Pred. No. 0.16;
Matches 87; Conservative 0; Mismatches 83; Indels 0; Gaps 0;
QY 13 GCTACGACTGGCCCGGCTGCTGCTATAGGTCAACAAGAGCTGGGCTGCAATGCG 72
DB 1340 GCGCTACTGTGTTGGAAGGCTTCGAGAAGATGCCCAATACTGCCCCATGAGG 1399
QY 73 GCGAGCCCATCAGCTGCTGAGCGCTGACCGAAGAGAGCTGGGCCACCATGCAATTC 132
DB 1400 ACAGCAGCCGCGAGGCGCTGCGGCCCAATGTCAGCTGGCGCGCTGGAAAAGC 1459
QY 133 TGGTCGGTTGACAGAGGTCAGACCATGATGCTTCGCGGGCGGCTC 182
DB 1460 AGAAGATCGCGGCGGATCCGTACCGACTTCATCTCTCGCGGAAATC 1509

RESULT 13
US-09-029-603-4
; Sequence 4, Application US/09029603
; Patent No. 6210935
; GENERAL INFORMATION:
; APPLICANT: Schupp, Thomas
; APPLICANT: Engel, Natalie
; APPLICANT: Bietenhadex, Jurg
; APPLICANT: Toupet, Christine
; APPLICANT: Pospiech, Andreas
; TITLE OF INVENTION: Staurosporin Biosynthesis Gene Clusters
; FILE REFERENCE: 4-20535/A/PCT
; CURRENT APPLICATION NUMBER: US/09/029,603
; PRIOR FILING DATE: 1998-03-20
; EARLIER APPLICATION NUMBER: PCT/EP96/03643
; EARLIER FILING DATE: 1996-08-19
; NUMBER OF SEQ ID NOS: 11

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OM nucleic - nucleic search, using sw model

Run on: September 17, 2003, 13:09:27 ; Search time 128.97 Seconds
(without alignments)
3967.311 Million cell updates/sec

Title: US-09-697-123B-22
Perfect score: 208
Sequence: 1 tcaagggaagcgtacgac.....ccggtgaaacgacgacat 208

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1660708 seqs, 1229959015 residues

Total number of hits satisfying chosen parameters: 3321416

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA.*

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12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
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14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
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16: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
17: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	206.4	99.2	3519	10 US-09-712-363-30	Sequence 30, Appl
2	88	42.3	3495	10 US-09-738-626-547	Sequence 547, App
3	88	42.3	5096	10 US-09-984-711-5	Sequence 5, Appli
4	88	42.3	5099	10 US-09-887-052-1	Sequence 1, Appli
5	88	42.3	5099	10 US-09-887-052-3	Sequence 3, Appli
6	88	42.3	5099	10 US-09-887-052-5	Sequence 5, Appli
7	88	42.3	5099	12 US-10-076-406-1	Sequence 1, Appli
8	88	42.3	5099	12 US-10-076-406-3	Sequence 3, Appli
9	88	42.3	5099	12 US-10-076-406-5	Sequence 5, Appli
10	88	42.3	5099	13 US-10-073-460-5	Sequence 5, Appli
11	88	42.3	3309400	10 US-09-738-626-1	Sequence 1, Appli
12	69.2	33.3	3543	14 US-10-156-761-4898	Sequence 4898, Ap
13	69.2	33.3	9025608	14 US-10-156-761-1	Sequence 1, Appli
14	40.4	19.4	1215	14 US-10-156-761-2811	Sequence 2811, Ap
15	40.2	19.3	1131	14 US-10-156-761-2479	Sequence 2479, Ap
16	40.2	19.3	9025608	14 US-10-156-761-1	Sequence 1, Appli

c

17	36.6	17.6	1395	14	US-10-205-032-21	Sequence 21, Appl	
18	36.6	17.6	60196	14	US-10-205-032-1	Sequence 1, Appli	
19	36.2	17.4	1458	14	US-10-156-761-4634	Sequence 4634, Ap	
20	36	17.3	1894	8	US-08-841-636A-32	Sequence 32, Appl	
21	35.8	17.2	1509	12	US-09-967-464-64	Sequence 64, Appl	
22	35.8	17.2	1509	12	US-09-967-464-68	Sequence 68, Appl	
23	35.6	17.1	3756	9	US-09-841-132-425	Sequence 425, Appl	
24	35.4	17.0	1029	14	US-10-156-761-5440	Sequence 5440, Ap	
25	35.4	17.0	1284	14	US-10-156-761-5434	Sequence 5434, Ap	
26	35.4	17.0	1461	14	US-10-156-761-2120	Sequence 2120, Ap	
27	35	16.8	3774	14	US-10-156-761-2845	Sequence 2845, Ap	
c	27	35	16.8	14	US-10-156-761-5853	Sequence 5853, Ap	
28	34.8	16.7	588	14	US-10-225-567A-33	Sequence 33, Appl	
29	34.6	16.6	2130	14	US-10-185-991-1	Sequence 1, Appli	
30	34.6	16.6	2140	14	US-10-238-129-1	Sequence 1, Appli	
31	34.6	16.6	2140	14	US-10-238-667-1	Sequence 1, Appli	
32	34.6	16.6	2140	14	US-10-156-761-553	Sequence 553, App	
33	34.4	16.5	615	14	US-10-156-761-1671	Sequence 1671, App	
34	34.2	16.4	1191	14	US-10-156-761-1671	Sequence 1671, App	
35	34.2	16.4	1398	14	US-10-156-761-2212	Sequence 2212, Ap	
36	34.2	16.4	2334	14	US-10-156-761-5079	Sequence 5079, Ap	
c	37	34.2	16.4	22306	14	US-10-114-170-251	Sequence 251, App
38	34	16.3	252	10	US-09-878-574-8901	Sequence 8901, App	
39	34	16.3	680	9	US-09-841-132-267	Sequence 267, App	
40	34	16.3	993	14	US-10-156-761-4673	Sequence 4673, Ap	
c	41	34	16.3	1509	14	US-10-156-761-1592	Sequence 1592, Ap
c	42	34	16.3	5203	12	US-10-238-075-1038	Sequence 1038, Ap
c	43	34	16.3	14066	12	US-10-085-959-90	Sequence 90, Appl
c	44	33.6	16.2	1059	14	US-10-166-087-11	Sequence 11, Appl
c	45	33.6	16.2	32539	14	US-10-166-087-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-712-363-30
; Sequence 30, Application US/09712363
; Patent No. US20020164588A1
; GENERAL INFORMATION:
; APPLICANT: Eisenberg, David
; APPLICANT: Rotstein, Sergio H.
; APPLICANT: Marcotte, Edward M.
; TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND
; FILE REFERENCE: 07419-032001
; CURRENT APPLICATION NUMBER: US/09/712,363
; CURRENT FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: PCT/US00/02246
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,531
; PRIOR FILING DATE: 2000-02-01
; PRIOR APPLICATION NUMBER: 60/117,844
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/118,206,
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: 60/126,593
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/134,093
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/134,092
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/165,124
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/165,086
; PRIOR FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 3519
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-09-712-363-30

Query Match 99.2%; Score 206.4; DB 10; Length 3519;
Best Local Similarity 99.5%; Pred. No. 7.6e-58;
Matches 207; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCAGGAGAGCGCTACGACCTGGCCCGCTGCTATATAGGTCAACAGAGCTCG 60
DB 884 TCAAGGAGAGCGCTACGACCTGGCCCGCTGCTATATAGGTCAACAGAGCTCG 943
QY 61 GCGTGCATGTGGCGAGCCCATCAGCTGCTGACGCTGACCGAAGAGAGCTCGTGCCCA 120
DB 944 GCGTGCATGTGGCGAGCCCATCAGCTGCTGACGCTGACCGAAGAGAGCTCGTGCCCA 1003
QY 121 CCATCGAATATCGTTCGCTGCTGACGAGGCTCAGACCATGATGCTCGGCGCGCG 180
DB 1004 CCATCGAATATCGTTCGCTGCTGACGAGGCTCAGACCATGATGCTCGGCGCGCG 1063
QY 181 TCGAGGTGCGGTGGAAACCGAGGACAT 208
DB 1064 TCGAGGTGCGGTGGAAACCGAGGACAT 1091

RESULT 2

US-09-738-626-547

; Sequence 547, Application US/09738626

; Publication No. US20020197605A1

; GENERAL INFORMATION:

; APPLICANT: NAKAGAWA, SATOSHI

; APPLICANT: MIZOGUCHI, HIROSHI

; APPLICANT: ANDO, SEIKO

; APPLICANT: HAYASHI, MIKIO

; APPLICANT: OCHIAI, KEIKO

; APPLICANT: YOKOI, HARUHIKO

; APPLICANT: TATEISHI, NAOKO

; APPLICANT: SENO, AKIHIRO

; APPLICANT: IKEDA, MASATO

; APPLICANT: OZAKI, AKIO

; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES

; FILE REFERENCE: 249-125

; CURRENT APPLICATION NUMBER: US/09/738,626

; CURRENT FILING DATE: 2000-12-18

; PRIOR APPLICATION NUMBER: JP 99/377484

; PRIOR FILING DATE: 1999-12-16

; PRIOR APPLICATION NUMBER: JP 00/159162

; PRIOR FILING DATE: 2000-04-07

; PRIOR APPLICATION NUMBER: JP 00/280988

; PRIOR FILING DATE: 2000-08-03

; NUMBER OF SEQ ID NOS: 7059

; SOFTWARE: PatentIn ver. 3.0

; SEQ ID NO 547

; LENGTH: 3495

; TYPE: DNA

; ORGANISM: Corynebacterium glutamicum

US-09-738-626-547

Query Match 42.3%; Score 88; DB 10; Length 3495;
Best Local Similarity 68.5%; Pred. No. 4.3e-19;
Matches 137; Conservative 0; Mismatches 60; Indels 3; Gaps 1;

QY 9 AAGCGCTACGACCTGGCCCGCTGCTATATAGGTCAACAGAGCTCGGCTGCAT 68
DB 877 AAGCGCTACGACCTGGCTCGCTGCTTACAGATCAACCGAAGCTCGGCT--T 933
QY 69 GTCGGCGAGCCCATCAGCTGCTGACGCTGACCGAAGAGAGCTCGTCCGACCATCGAA 128
DB 934 GGTGGCGACCATGATGTTGATGACTCTTACTGAAGAGGACATCGAACCATCGAG 993
QY 129 TATCTGTCCTGCTGACGAGGCTCAGACCATGATGCTTCCGGCGGCGCTCGAGTG 188
DB 994 TACCTGGTGGCTGCTGACGAGGCTGAGCGGCTCATGACTTCTCCAAATGGTGAAGAGATC 1053
QY 189 CCGGTGGAACCGAGGACAT 208
DB 1054 CCAGTCGAGACCGATGACAT 1073

RESULT 3

US-09-984-711-5

; Sequence 5, Application US/09984711

; Patent No. US20020119549A1

; GENERAL INFORMATION:

; APPLICANT: MOECKEL, Bettina

; APPLICANT: BATHE, Brigitte

; APPLICANT: STEPHAN, Hans

; APPLICANT: KREUTZER, Caroline

; APPLICANT: HERMANN, Thomas

; APPLICANT: PFEFFERLE, Walter

; APPLICANT: BINDER, Michael

; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE ipsl GENE

; FILE REFERENCE: 204209US0

; CURRENT APPLICATION NUMBER: US/09/984,711

; CURRENT FILING DATE: 2001-10-31

; PRIOR APPLICATION NUMBER: DE10108230.9

; PRIOR FILING DATE: 2001-02-16

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 5

; LENGTH: 5096

; TYPE: DNA

; ORGANISM: Corynebacterium glutamicum

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (702)..(4196)

; OTHER INFORMATION:

US-09-984-711-5

Query Match 42.3%; Score 88; DB 10; Length 5096;
Best Local Similarity 68.5%; Pred. No. 4.5e-19;
Matches 137; Conservative 0; Mismatches 60; Indels 3; Gaps 1;

QY 9 AAGCGCTACGACCTGGCCCGCTGCTATATAGGTCAACAGAGCTCGGCTGCAT 68
DB 1578 AAGCGCTACGACCTGGCTCGCTTGTGCTTACAGATCAACCGAAGCTCGGCT--T 1634
QY 69 GTCGGCGAGCCCATCAGCTGCTGACGCTGACCGAAGAGAGCTCGTCCGACCATCGAA 128
DB 1635 GGTGGCGACCATGATGTTGATGACTCTTACTGAAGAGGACATCGAACCATCGAG 1694
QY 129 TATCTGTCCTGCTGACGAGGCTCAGACCATGATGCTTCCGGCGGCGCTCGAGTG 188
DB 1695 TACCTGGTGGCTGCTGACGAGGCTGAGCGGCTCATGACTTCTCCAAATGGTGAAGAGATC 1754
QY 189 CCGGTGGAACCGAGGACAT 208
DB 1755 CCAGTCGAGACCGATGACAT 1774

RESULT 4

US-09-887-052-1

; Sequence 1, Application US/09887052

; Patent No. US20020119537A1

; GENERAL INFORMATION:

; APPLICANT: MOECKEL, Bettina

; APPLICANT: BATHE, Brigitte

; APPLICANT: HERMANN, Thomas

; APPLICANT: PFEFFERLE, Walter

; APPLICANT: BINDER, Michael

; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE ipob GENE

; FILE REFERENCE: 204212US0X

; CURRENT APPLICATION NUMBER: US/09/887,052

; CURRENT FILING DATE: 2001-06-25

; PRIOR APPLICATION NUMBER: DE10107229.5

; PRIOR FILING DATE: 2001-02-16

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 1

; LENGTH: 5099

QY 9 AAGCGTACGACCTGGCCCGGTCGGTCGCTAAGGTCACAGAAGCTCGGCGCTGCAT 68

US-10-075-460-5
; Sequence 5, Application US/10075460

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; Publication No. US2002015557A1
; GENERAL INFORMATION:
; APPLICANT: MOCKEL, BETTINA
; APPLICANT: BATHE, BRIGITTE
; APPLICANT: HANS, STEFAN
; APPLICANT: KREUTZER, CAROLINE
; APPLICANT: HERMANN, THOMAS
; APPLICANT: PFEFFERLE, WALTER
; APPLICANT: BINDER, MICHAEL
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE IPdL GENE
; FILE REFERENCE: 218472US0X
; CURRENT APPLICATION NUMBER: US/10/075,460
; CURRENT FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: DE 10107230.9
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: DE 10162386.0
; PRIOR FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent version 3.1
; SEQ ID NO 5
; LENGTH: 5099
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
; OTHER INFORMATION:
US-10-075-460-5

Query Match      42.3%; Score 88; DB 13; Length 5099;
Best Local Similarity 68.5%; Pred. No. 4.5e-19;
Matches 137; Conservative 0; Mismatches 60; Indels 3; Gaps 1;

QY      9 AACGCTAGACCTGGCCGCGTCGCTGCTATAGGTCACAAAGAGCTCGGCTGCAT 68
Db      1578 AACGCTAGACCTGGCTGGCTGCTTACAGATCAACCCGAGCTCGGCCCT---T 1634
QY      69 GTGCGGAGCCCATCAGCTGCTGACGCTGACGAGAGAGAGCTGCGGCCACCATCGAA 128
Db      1635 GTGCGGAGCCAGATGTTGATGACTCTTACTGAGAGAGACATCGCAACCATCGAG 1694
QY      129 TATCTGTCGCTGACGAGGTCAGACACAGATGATCGTTCCGGCGGCGCTCGAGGTG 188
Db      1695 TACTTGGTGGCTGTCGACGAGGTGAGCGCTCATCTTCCAAATGTTGAAGAGATC 1754
QY      189 CCGTGGAAACCGACGACAT 208
Db      1755 CCACTCGAGACCGATGACAT 1774

RESULT 11
US-09-738-626-1
; Sequence 1, Application US/09738626
; Publication No. US20020197603A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIALI, KEIKO
; APPLICANT: YOKOL, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
```

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; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: Patent ver. 3.0
; SEQ ID NO 1
; LENGTH: 3309400
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-1

Query Match      42.3%; Score 88; DB 10; Length 3309400;
Best Local Similarity 68.5%; Pred. No. 1e-18;
Matches 137; Conservative 0; Mismatches 60; Indels 3; Gaps 1;

QY      9 AACGCTAGACCTGGCCGCGTCGCTGCTATAGGTCACAAAGAGCTCGGCTGCAT 68
Db      513789 AACGCTAGACCTGGCTGGCTGCTTACAAAGATCAACCCGAGCTCGGCCCT---T 513845
QY      69 GTGCGGAGCCCATCAGCTGCTGACGCTGACGAGAGAGAGCTGCGGCCACCATCGAA 128
Db      513846 GTGCGGAGCCAGATGTTGATGACTCTTACTGAGAGAGACATCGCAACCATCGAG 513905
QY      129 TATCTGTCGCTGACGAGGTCAGACACAGATGATCGTTCCGGCGGCGCTCGAGGTG 188
Db      513906 TACTTGGTGGCTGTCGACGAGGTGAGCGCTCATCTTCCAAATGTTGAAGAGATC 513965
QY      189 CCGTGGAAACCGACGACAT 208
Db      513966 CCACTCGAGACCGATGACAT 513985

RESULT 12
US-10-156-761-4898
; Sequence 4898, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 4898
; LENGTH: 3543
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3543)
US-10-156-761-4898

Query Match      33.3%; Score 69.2; DB 14; Length 3543;
Best Local Similarity 62.0%; Pred. No. 6.1e-13;
Matches 129; Conservative 0; Mismatches 73; Indels 6; Gaps 1;
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QY      1 TCAAGAGAGAGCGCTAGCACTGGCCGCGCTCGTTCGCTATAGGTCACAAAGAGCTCG 60
Db      926 TCAACCCGAGAGCGCTAGCACTGGCCGCGCTAGCAAGGTCAACAGGTCAACAAAGAGCTGG 985
QY      61 GGCTGCATGTCGGCGAGGCCCATCAGCTCGTCCGACCTGACCGGAGAGAGAGAGCTCGTGGCCA 120
Db      986 GC-----GGCGAGGCGCGCTGAGCGCGGGATCCTGCGTCGAGGACATCATCTCCT 1039
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QY 121 CCATCGAATATCTGGTCGGCTGCAGAGGTCAGACACGATGATCGTTCGGGCGCG 180
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1040 CGATCACTACTGGTGAAGCTGCAGCGGTCAGACCGGTGGCCGACACGGCA 1099
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 181 TCGAGTCCCGGTGGAACCGACGACAT 208
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1100 CCTGATCGTCTGCAGACCGACGACAT 1127
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 13
US-10-156-761-1
; Sequence 1, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
; LENGTH: 9025608
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1

Query Match 33.3%; Score 69.2; DB 14; Length 9025608;
Best Local Similarity 62.0%; Pred. No. 1.7e-12;
Matches 129; Conservative 0; Mismatches 73; Indels 6; Gaps 1;

QY 1 TCAAGGAGACCGCTACGACCTGGCCGCGTGGCTGCGTATAGGTCAACAAGAGCTCG 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5970494 TCAACCCGAGCGCTAGACCTCGCGAAGTGGCGGCTACAAGGTCAACAAGAGCTGG 5970553
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 61 GGCTGCATGTCGGGAGCCCATCAGCTGTCGACGCTGACGAGAGAGCTGCTGGCCA 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5970554 GC-----GGCGAGCGCGCTGGAGCGGATCTCTGACCGTCGAGGACATCTCTGT 5970607
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 121 CCATCGAATATCTGGTCGGCTGCACGAGGTCAGACACGATGATCGTTCGGGCGCG 180
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5970608 CGATCAAGTACTGGTGAAGCTCCAGCGGTCGAGACCGGTCGCGGACACGGCA 1099
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 181 TCGAGTCCCGGTGGAACCGACGACAT 208
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5970668 CCTGATGCTGTCGAGACCGAGACAT 5970695
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 14
US-10-156-761-2811
; Sequence 2811, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
```

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; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 2811
; LENGTH: 1215
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1215)
US-10-156-761-2811

Query Match 19.4%; Score 40.4; DB 14; Length 1215;
Best Local Similarity 58.2%; Pred. No. 0.0014;
Matches 71; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 55 AGCTCGGCTGCTATGTCGGGAGGAGCCCATCATCAGCTGTCGACGCTGACCGAAGAGCTCG 114
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 275 ACCGGTGGTGCACGGCGCGAGGTCTCTTCCAGGAGCGGACCGCTCATCGACGACGCTCC 334
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 115 TGGCCACCATCGAATATCTGGTCCGCTTGACGAGGTCAGACCGAGATGATCGTTCGG 174
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 335 TCGCGAGATCGAGCGGCTGATCCCGGCGGCTGTCACACCGCGGACCTCACCG 394
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 175 GC 176
    ||
Db 395 GC 396
    ||

RESULT 15
US-10-156-761-2479
; Sequence 2479, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 2479
; LENGTH: 1131
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1131)
US-10-156-761-2479

Query Match 19.3%; Score 40.2; DB 14; Length 1131;
Best Local Similarity 55.3%; Pred. No. 0.0016;
Matches 78; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 51 AAGAAGCTCGGCTGCATGTCGGGAGGAGCCCATCAGCTGTCGACGCTGACCGAAGAGAC 110
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 313 AAGAAGCTCGGCTGCATGTCGACATCGACACCTGATCTCTGTCGCGCGGACGACGCTGAGCAG 372
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

```
QY 111 GTCGTGGCCACCACATCGAATATCTGTGTCCTGCTCCAGAGGCTCAGACCAAGATGATCGTT 170
Db 373 GCTCTGGAGATCGTGGACATCTGCTCCGCTCCGGGGGCTCGACCTGATCGTCATCGAC 432
QY 171 CCGGGCGCGCTCGAGGTGCCG 191
Db 433 TCGGTGGCGGCGCTGCTGCCG 453
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Search completed: September 17, 2003, 23:29:53
Job time : 148.97 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 17, 2003, 12:31:22 ; Search time 37.5758 Seconds
(without alignments)
2443.269 Million cell updates/sec

Title: US-09-697-123B-23

Perfect score: 208

Sequence: 1 tcagggagagcctacgac.....ccagtgatactgacgacat 208

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents NA:*
- 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
 - 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
 - 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
 - 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
 - 5: /cgn2_6/ptodata/1/ina/PTUS_COMB.seq:*
 - 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	176	84.6	3447	2	US-08-313-185-57
2	176	84.6	3447	3	US-09-082-614A-57
3	166.4	80.0	970	1	US-08-250-030-1
4	166.4	80.0	970	5	PCT-US95-06790-1
5	166.4	80.0	4403765	3	US-09-103-840A-2
6	166.4	80.0	4411529	3	US-09-103-840A-1
7	35.2	16.9	1480	4	US-09-252-991A-8286
8	35.2	16.9	1419	4	US-09-252-991A-8286
9	35.2	16.9	1506	4	US-09-252-991A-8077
10	35.2	16.9	1506	4	US-09-252-991A-8236
11	35.2	16.9	6085	3	US-09-029-603-4
12	35.2	16.9	53500	4	US-09-256-965-76
13	34.8	16.7	771	4	US-08-252-991A-13613
14	34.8	16.7	1389	4	US-09-252-991A-4243
15	34.8	16.7	1641	4	US-09-252-991A-13507
16	34.8	16.7	2598	4	US-09-252-991A-4323
17	34.8	16.7	2874	4	US-09-252-991A-4533
18	34	16.3	1626	4	US-09-252-991A-8639
19	33.8	16.2	4403765	3	US-09-103-840A-2
20	33.8	16.2	4411529	3	US-09-103-840A-1
21	33	15.9	819	4	US-09-199-637A-284
22	33	15.9	819	4	US-09-252-991A-4858
23	33	15.9	897	4	US-09-252-991A-4831
24	33	15.9	903	4	US-09-252-991A-9467
25	33	15.9	996	4	US-09-252-991A-9363
26	33	15.9	1677	4	US-09-199-637A-276
27	33	15.9	1686	4	US-09-252-991A-9439

28	33	15.9	2580	4	US-09-199-637A-280	Sequence 280, Appl
29	33	15.9	2580	4	US-09-252-991A-4842	Sequence 4842, Ap
30	33	15.9	2970	4	US-09-199-637A-272	Sequence 272, Appl
31	33	15.9	2970	4	US-09-252-991A-4897	Sequence 4897, Ap
32	33	15.9	42235	4	US-09-199-637A-1	Sequence 1, Appli
33	32.8	15.8	1077	4	US-09-252-991A-3406	Sequence 3406, Ap
34	32.8	15.8	1104	4	US-09-252-991A-3275	Sequence 3275, Ap
35	32.6	15.7	1347	4	US-09-252-991A-4472	Sequence 4472, Ap
36	32.6	15.7	1449	4	US-09-252-991A-4361	Sequence 4361, Ap
37	32.6	15.7	1776	4	US-09-252-991A-4380	Sequence 4380, Ap
38	32.6	15.7	77536	4	US-09-410-551B-1	Sequence 1, Appli
39	32.4	15.6	621	4	US-09-252-991A-12526	Sequence 12526, A
40	32.4	15.6	1026	4	US-09-252-991A-13274	Sequence 13274, A
41	32.4	15.6	1412	1	US-08-097-831-1	Sequence 1, Appli
42	32.4	15.6	1476	4	US-09-107-532A-2726	Sequence 2726, Ap
43	32.4	15.6	3257	5	PCT-US91-09784-1	Sequence 1, Appli
44	32.2	15.5	450	4	US-09-252-991A-8210	Sequence 8210, Ap
45	32.2	15.5	762	4	US-09-252-991A-7992	Sequence 7992, Ap

ALIGNMENTS

RESULT 1
US-08-313-185-57
; Sequence 57, Application US/08313185
; Patent No. 5851763
; GENERAL INFORMATION:
; APPLICANT: Heym, Beate
; APPLICANT: Cole, Stewart
; APPLICANT: Young, Douglas
; APPLICANT: Zhang, Ying
; APPLICANT: Honore, Nadine
; APPLICANT: Telenti, Ramello
; APPLICANT: Bodmer, Thomas
; TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
; TITLE OF INVENTION: in Mycobacterium Tuberculosis
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/313,185
; FILING DATE: 12-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 02356.0068-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3447 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-313-185-57
Query Match 84.6%; Score 176; DB 2; Length 3447;
Best Local Similarity 90.4%; Pred. No. 6.5e-39;

Matches 188; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

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QY 1 TCAAGGAGAGCGCTACGACCTGGCCCGGGTTGGTTCACAGGTCACACAGAGCTCG 60
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Db 809 TCAAGGAGAGCGCTACGACCTGGCCCGGGTTGGTTCACAGGTCACACAGAGCTCG 868
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 GGTTCACGCGCGGTGAGCCGATCAGAGCTCGACGCTGACCGAAGAGGAGCTCGTCCGCA 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 869 GGTTCACGCGCGGTGAGTTGATCAGCTGCTCCAGCTGACCGAAGAGGATGCTCGTCCCA 928
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 121 CCATCGAGTACCTGGTCCGGCTGCATGAGGTCAGTCGACGATGACCCGTCAGGTGGCG 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 929 CCATGAGTACCTGGTTCGCTGTCATGAGGTCAGTCGACGATGACCAATGACTGCCAGGTGGG 988
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 181 TCGAGGTGCCAGTGGATACGACGACAT 208
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 989 TAGAGTGCCAGTGGAACTGACGATAT 1016
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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RESULT 2

US-09-082-614A-57
; Sequence 57, Application US/09082614A
; Patent No. 6124098

GENERAL INFORMATION:

APPLICANT: Heym, Beate
APPLICANT: Cole, Stewart
APPLICANT: Young, Douglas
APPLICANT: Zhang, Ying
APPLICANT: Honore, Nadine
APPLICANT: Telenti, Amalio
APPLICANT: Bodmer, Thomas
TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
TITLE OF INVENTION: in Mycobacterium Tuberculosis
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/082.614A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/313,185
FILING DATE: 12-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 02356.0068-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400

INFORMATION FOR SEQ ID NO:

SEQUENCE CHARACTERISTICS:
LENGTH: 3447 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-082-614A-57

Query Match 84.6%; Score 176; DB 3; Length 3447;
Best Local Similarity 90.4%; Pred. No. 6.5e-39;
Matches 188; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

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QY 1 TCAAGGAGAGCGCTACGACCTGGCCCGGGTTGGTTCACAGGTCACACAGAGCTCG 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 809 TCAAGGAGAGCGCTACGACCTGGCCCGGGTTGGTTCACAGGTCACACAGAGCTCG 868
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 GGTTCACGCGCGGTGAGCCGATCAGAGCTCGACGCTGACCGAAGAGGAGCTCGTCCGCA 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 869 GGTTCACGCGCGGTGAGTTGATCAGCTGCTCCAGCTGACCGAAGAGGATGCTCGTCCCA 928
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 121 CCATCGAGTACCTGGTCCGGCTGCATGAGGTCAGTCGACGATGACCCGTCAGGTGGCG 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 929 CCATGAGTACCTGGTTCGCTGTCATGAGGTCAGTCGACGATGACCAATGACTGCCAGGTGGG 988
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 181 TCGAGGTGCCAGTGGATACGACGACAT 208
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 989 TAGAGTGCCAGTGGAACTGACGATAT 1016
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

RESULT 3

US-08-250-030-1
; Sequence 1, Application US/08250030
; Patent No. 5643723

GENERAL INFORMATION:

APPLICANT: Persing, David H.
TITLE OF INVENTION: Detection of a Genetic Locus Encoding
TITLE OF INVENTION: Resistance to Rifampin in Mycobacterial Cultures and in
TITLE OF INVENTION: Clinical Specimens
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman, Lundberg & Woessner
STREET: 3500 IDS Center
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/250.030
FILING DATE: 26-MAY-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mueting, Ann M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 150.105051
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-0331
TELEFAX: 612-339-3061

INFORMATION FOR SEQ ID NO:

SEQUENCE CHARACTERISTICS:
LENGTH: 970 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-250-030-1

Query Match 80.0%; Score 166.4; DB 1; Length 970;
Best Local Similarity 87.5%; Pred. No. 2.1e-36;
Matches 182; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

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QY 1 TCAAGGAGAGCGCTACGACCTGGCCCGGGTTGGTTCACAGGTCACACAGAGCTCG 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 26 TCAAGGAGAGCGCTACGACCTGGCCCGGGTTGGTTCACAGGTCACACAGAGCTCG 85
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 GGTTCACGCGCGGTGAGCCGATCAGAGCTCGACGCTGACCGAAGAGGAGCTCGTCCGCA 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 86 GGTTCGATGTCGGCGAGGCCATCAGCTGCTGCGAGGTCAGCCGGAAGAGAGCTCGTCCCA 145
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 121 CCATCGAGTACCTGGTTCGCGCTGTCATGAGGTCAGTCGACGATGACCCGTCAGGTGGCG 180
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```

```

; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match      80.0%; Score 166.4; DB 3; Length 4403765;
Best Local Similarity 87.5%; Pred. No. 9.1e-36;
Matches 182; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 1 TCAAGAGAGCGCTACGACCTGCGCGGGTGGTTCGTTACAGGTCAACAAGAAGCTCG 60
Db 762648 TCAAGAGAGCGCTACGACCTGCGCGGGTGGTTCGTTACAGGTCAACAAGAAGCTCG 762707
QY 61 GGTTCACGCGGTGAGCGGATCACGAGCTCGACGCTGACGAGAGAGAGAGAGAGAGAGAG 120
Db 762708 GGCTGCTGTGGGAGCGCCATCAGCTGCTGCGAGCTGACCGAGAGAGAGAGAGAGAGAG 120
QY 121 CCATCAGTACCTGCTCGCGGTGCATGAGGTGAGTTCGAGTACGACGATCACCGTTCCAGGTGGCG 180
Db 762768 CCATCGAATATCTGCTGCGGTTCGACGAGGTTCAGACACGATGACCGTTCGCGGGCGG 762827
QY 181 TCGAGTGCCAGTGGATGACGACAT 208
Db 762828 TCGAGTGCCGCTGGTGAACCGACGACAT 762855

RESULT 6
US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37RV
US-09-103-840A-1

Query Match      80.0%; Score 166.4; DB 3; Length 4411529;
Best Local Similarity 87.5%; Pred. No. 9.1e-36;
Matches 182; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 1 TCAAGAGAGCGCTACGACCTGCGCGGGTGGTTCGTTACAGGTCAACAAGAAGCTCG 60
; Sequence 2, Application US/09103840A

; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37RV
US-09-103-840A-1

Query Match      80.0%; Score 166.4; DB 3; Length 4411529;
Best Local Similarity 87.5%; Pred. No. 9.1e-36;
Matches 182; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 1 TCAAGAGAGCGCTACGACCTGCGCGGGTGGTTCGTTACAGGTCAACAAGAAGCTCG 60
; Sequence 2, Application US/09103840A

; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37RV
US-09-103-840A-1

Query Match      80.0%; Score 166.4; DB 5; Length 970;
Best Local Similarity 87.5%; Pred. No. 2.1e-36;
Matches 182; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 1 TCAAGAGAGCGCTACGACCTGCGCGGGTGGTTCGTTACAGGTCAACAAGAAGCTCG 60
Db 26 TCAAGAGAGCGCTACGACCTGCGCGGGTGGTTCGTTACAGGTCAACAAGAAGCTCG 85
QY 61 GGTTCACGCGGTGAGCGGATCACGAGCTCGACGCTGACGAGAGAGAGAGAGAGAGAGAG 120
Db 86 GGCTGCTGTGGGAGCGCCATCAGCTGCTGCGAGCTGACCGAGAGAGAGAGAGAGAGAGAG 145
QY 121 CCATCAGTACCTGCTCGCGGTGCATGAGGTGAGTTCGAGTACGACGATCACCGTTCCAGGTGGCG 180
Db 146 CCATCGAATATCTGCTGCGGTTCGACGAGGTTCAGACACGATGACCGTTCGCGGGCGG 205
QY 181 TCGAGTGCCAGTGGATGACGACAT 208
Db 206 TCGAGTGCCGCTGGTGAACCGACGACAT 233

RESULT 5
US-09-103-840A-2
; Sequence 2, Application US/09103840A
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; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match      80.0%; Score 166.4; DB 3; Length 4403765;
Best Local Similarity 87.5%; Pred. No. 9.1e-36;
Matches 182; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 1 TCAAGAGAGCGCTACGACCTGCGCGGGTGGTTCGTTACAGGTCAACAAGAAGCTCG 60
Db 762648 TCAAGAGAGCGCTACGACCTGCGCGGGTGGTTCGTTACAGGTCAACAAGAAGCTCG 762707
QY 61 GGTTCACGCGGTGAGCGGATCACGAGCTCGACGCTGACGAGAGAGAGAGAGAGAGAGAG 120
Db 762708 GGCTGCTGTGGGAGCGCCATCAGCTGCTGCGAGCTGACCGAGAGAGAGAGAGAGAGAG 120
QY 121 CCATCAGTACCTGCTCGCGGTGCATGAGGTGAGTTCGAGTACGACGATCACCGTTCCAGGTGGCG 180
Db 762768 CCATCGAATATCTGCTGCGGTTCGACGAGGTTCAGACACGATGACCGTTCGCGGGCGG 762827
QY 181 TCGAGTGCCAGTGGATGACGACAT 208
Db 762828 TCGAGTGCCGCTGGTGAACCGACGACAT 762855

RESULT 6
US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37RV
US-09-103-840A-1

Query Match      80.0%; Score 166.4; DB 3; Length 4411529;
Best Local Similarity 87.5%; Pred. No. 9.1e-36;
Matches 182; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 1 TCAAGAGAGCGCTACGACCTGCGCGGGTGGTTCGTTACAGGTCAACAAGAAGCTCG 60
; Sequence 2, Application US/09103840A

; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37RV
US-09-103-840A-1

Query Match      80.0%; Score 166.4; DB 3; Length 4411529;
Best Local Similarity 87.5%; Pred. No. 9.1e-36;
Matches 182; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 1 TCAAGAGAGCGCTACGACCTGCGCGGGTGGTTCGTTACAGGTCAACAAGAAGCTCG 60
; Sequence 2, Application US/09103840A

; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37RV
US-09-103-840A-1

Query Match      80.0%; Score 166.4; DB 5; Length 970;
Best Local Similarity 87.5%; Pred. No. 2.1e-36;
Matches 182; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 1 TCAAGAGAGCGCTACGACCTGCGCGGGTGGTTCGTTACAGGTCAACAAGAAGCTCG 60
Db 26 TCAAGAGAGCGCTACGACCTGCGCGGGTGGTTCGTTACAGGTCAACAAGAAGCTCG 85
QY 61 GGTTCACGCGGTGAGCGGATCACGAGCTCGACGCTGACGAGAGAGAGAGAGAGAGAGAG 120
Db 86 GGCTGCTGTGGGAGCGCCATCAGCTGCTGCGAGCTGACCGAGAGAGAGAGAGAGAGAGAG 145
QY 121 CCATCAGTACCTGCTCGCGGTGCATGAGGTGAGTTCGAGTACGACGATCACCGTTCCAGGTGGCG 180
Db 146 CCATCGAATATCTGCTGCGGTTCGACGAGGTTCAGACACGATGACCGTTCGCGGGCGG 205
QY 181 TCGAGTGCCAGTGGATGACGACAT 208
Db 206 TCGAGTGCCGCTGGTGAACCGACGACAT 233

RESULT 5
US-09-103-840A-2
; Sequence 2, Application US/09103840A
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Db 760688 TCAAGGAGAGCGCTACGACCTGGCCCGCTCGCTGCTATAGGTCAACAGAGCTCG 760747
QY 61 GGTTCGACCGCGGTGAGCGATACGAGCTCGACGCTGACCGAGGAGGACGCTCGTCGCCA 120
Db 760748 GGCTGATGTCGCGAGCCATCAGCTGCTGACGCTGACCGAAGAGACGCTCGTCGCCA 760807
QY 121 CCATCGAGTACCTGCTCGCGCTGCATGAGGCTCAGTCGACGATGACCGCTCCAGGTGGCG 180
Db 760808 CCATCGAATATCTGGTCCGCTTGCACGAGGCTCAGACGATGACCGCTCCGCGGGCGG 760867
QY 181 TCGAGGTCGCGAGTGGATGACGACAT 208
Db 760868 TCGAGGTGCGGCTGGAAACCGACGACAT 760895

RESULT 7
US-09-252-991A-8286/c
; Sequence 8286, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 8286
; LENGTH: 480
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-8286

Query Match 16.9%; Score 35.2; DB 4; Length 480;
Best Local Similarity 52.0%; Pred. No. 0.54;
Matches 79; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

QY 13 GCTACGACCTGGCCCGGTTGCTGTACAGGTCAACAGAGCTCGGTTGACCGCG 72
Db 304 GCAACCTGCGCGACCTGCGACACATACCACCATGATCGAATGTTGCGCGCGATGGGCG 245
QY 73 GTGAGCGGATCAGCAGCTCGAGCTGACCGAGAGGAGGAGCTGCTGCGCCACATCGAGTACC 132
Db 244 TGCAGCGGATCAGCAGGAGAGCTCAACGTCGAGTGCATGCCAGCAGCATCAGACCC 185
QY 133 TGGTCCGGCTGCATGAGGTGCTGACGAGTGC 164
Db 184 TGGTCCGGCGGTATGAAGTGGTGAAGACCATG 153

RESULT 8
US-09-266-965-61
; Sequence 61, Application US/09266965
; Patent No. 6495348
; GENERAL INFORMATION:
; APPLICANT: Sherman, D
; APPLICANT: Mao, Y
; APPLICANT: Varoglu, M
; APPLICANT: He, M
; APPLICANT: Sheldon, P
; TITLE OF INVENTION: Mitomycin biosynthetic gene cluster
; FILE REFERENCE: 600.456US1
; CURRENT FILING DATE: 1999-03-12
; EARLIER APPLICATION NUMBER: US 08/624,447
; EARLIER FILING DATE: 1996-08-19
; EARLIER APPLICATION NUMBER: PCT/US94/11279
; EARLIER FILING DATE: 1994-10-06
; EARLIER APPLICATION NUMBER: US 08/133,963

; EARLIER FILING DATE: 1993-10-07
; NUMBER OF SEQ ID NOS: 145
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 61
; LENGTH: 1419
; TYPE: DNA
; ORGANISM: Streptomyces lavendulae
US-09-266-965-61

Query Match 16.9%; Score 35.2; DB 4; Length 1419;
Best Local Similarity 49.5%; Pred. No. 0.66; 93; Indels 0; Gaps 0;
Matches 91; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

QY 23 GGCCCGGCTGGTCTGTACAGGTCAACAGAGCTCGGTTGACCGCGGTGAGCGGAT 82
Db 354 GCGCGGCTGCTGGGAGCAGGTGATCCAGAGGCGGCGGCGGCTTGTGACCGCT 413
QY 83 CACGAGCTCGACCTGACCGAAGAGAGGAGTGTGCGCACCAATCGAGTACCTGGTCCGGCT 142
Db 414 GAGCGGCTCGGCGCGCTTGTGCGCGCGGTCTCTACTCTCTCGCGCGGCGCTCGGGCT 473
QY 143 GCATGAGGTCAGTCCGACGATGACCGTTCCAGGTGGGCTCGAGTCCCGAGTCCGATCTGA 202
Db 474 TCTGTCGGGAAGTACGGGTTGCGCGGCGACCATGTGCTGCTCGACCTGGTGACGGC 533
QY 203 CGAC 206
Db 534 CGAC 537

RESULT 9
US-09-252-991A-8077
; Sequence 8077, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONA
; FILE REFERENCE: 107196.136
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 8077
; LENGTH: 1506
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-8077

Query Match 16.9%; Score 35.2; DB 4; Length 1506;
Best Local Similarity 52.0%; Pred. No. 0.67; 73; Indels 0; Gaps 0;
Matches 79; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

QY 13 GCTACGACCTGGCCCGGTTGCTGTACAGGTCAACAGAGTCAACAGAGCTCGGTTGACCGCG 72
Db 365 GCAACCTGCGCGACCTGCGACACATACCACCATGATCGAATGTTGCGCGCGATGGGCG 424
QY 73 GTGAGCGGATCAGCAGCTGCGAGCTGACCGAAGAGGAGGAGCTGCTGCGCCACATCGAGTACC 132
Db 425 TGCAGCGGATCATCGACGAGAGAGCTCAACGTCGAGTGCATGCCAGCAGCATCAAGACCC 484
QY 133 TGGTCCGGCTGCATGAGGTGCTGACGAGTGC 164
Db 485 TGGTCCGGCGGTATGAAGTGGTGAAGACCATG 516

RESULT 10
US-09-252-991A-8236/c
; Sequence 8236, Application US/09252991A
; Patent No. 6551795


```
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 8236
; LENGTH: 1506
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-8236

Query Match      16.9%; Score 35.2; DB 4; Length 1506;
Best Local Similarity 52.0%; Pred. No. 0.67;
Matches 79; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

QY 13 GTACGACCTGCCCGGTTGGTGTACAGGTCAACAGAGAGCTCGGGTTGCACGCG 72
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1268 GCAACCTGCCGACCTGCACGACATACACCATGATCGAACTGTTCGGCGCATGGCG 1209

QY 73 GTGACCGGATCAGAGCTCGACGCTGACCGAGAGAGAGCTGTCGCCACCATCGATACC 132
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1208 TGCAGCGGATCATCGAGAGAGCTCAACGTCAAGTGTGATGCCAGCAGATCAAGACC 1149

QY 133 TGTGTCGGTGTGATGAGGTCAGTCGACGATG 164
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1148 TGTGTCGGCGTGTGATGAGTGTGAGACCATG 1117

RESULT 11
US-09-029-603-4
; Sequence 4, Application US/09029603
; Patent No. 6210935
; GENERAL INFORMATION:
; APPLICANT: Schupp, Thomas
; APPLICANT: Engel, Natalie
; APPLICANT: Bietenhader, Jurg
; APPLICANT: Toupet, Christine
; APPLICANT: Pospiech, Andreas
; TITLE OF INVENTION: Staurosporin Biosynthesis Gene Clusters
; FILE REFERENCE: 4-20555/A/PCT
; CURRENT APPLICATION NUMBER: US/09/029,603
; CURRENT FILING DATE: 1998-03-20
; EARLIER APPLICATION NUMBER: PCT/EP96/03643
; EARLIER FILING DATE: 1996-08-19
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 6085
; TYPE: DNA
; ORGANISM: Streptomyces longisporoflavus
; FEATURE:
; NAME/KEY: misc_RNA
; LOCATION: (378)..(1665)
; OTHER INFORMATION: ORF
; FEATURE:
; NAME/KEY: misc_RNA
; LOCATION: (1747)..(2553)
; OTHER INFORMATION: ORF
; FEATURE:
; NAME/KEY: misc_RNA
; LOCATION: (2593)..(4011)
; OTHER INFORMATION: ORF
; FEATURE:
; NAME/KEY: misc_RNA
; LOCATION: (4013)..(4999)
; OTHER INFORMATION: ORF
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; FEATURE:
; NAME/KEY: misc_RNA
; LOCATION: (5071)..(6085)
; OTHER INFORMATION: ORF
; US-09-029-603-4

Query Match      16.9%; Score 35.2; DB 3; Length 6085;
Best Local Similarity 55.8%; Pred. No. 0.85;
Matches 67; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 18 GACCTGCCCCGGTTGGTGTTCATCAAGGTCAACAAGAGCTCGGGTTGCACGCGGTGAG 77
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1017 GAGTGGACCGCGCGCGGCGACGACCGAGCATCTCTCACCTCTCTCTCCGCGGC 1076

QY 78 CCGATCAGCAGCTCGACGCTGACCGAAGAGAGAGTGTGCGCCACCATCGAGTACCTGTC 137
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1077 CGGACACCGGATCACCGCTCAGCGTGGACGGCATCTCGGCCTCCATCTGCTC 1136

RESULT 12
US-09-266-965-76/c
; Sequence 76, Application US/09266965
; Patent No. 6495348
; GENERAL INFORMATION:
; APPLICANT: Sherman, D
; APPLICANT: Mao, Y
; APPLICANT: Varoglu, M
; APPLICANT: He, M
; APPLICANT: Sheldon, P
; TITLE OF INVENTION: Mitomycin biosynthetic gene cluster
; FILE REFERENCE: 600.456US1
; CURRENT APPLICATION NUMBER: US/09/266,965
; CURRENT FILING DATE: 1999-03-12
; EARLIER APPLICATION NUMBER: US 08/624,447
; EARLIER FILING DATE: 1996-08-19
; EARLIER APPLICATION NUMBER: PCT/US94/11279
; EARLIER FILING DATE: 1994-10-06
; EARLIER APPLICATION NUMBER: US 08/133,963
; EARLIER FILING DATE: 1993-10-07
; NUMBER OF SEQ ID NOS: 145
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 76
; LENGTH: 53500
; TYPE: DNA
; ORGANISM: Streptomyces lavendulae
; US-09-266-965-76

Query Match      16.9%; Score 35.2; DB 4; Length 53500;
Best Local Similarity 49.5%; Pred. No. 1.3;
Matches 91; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

QY 23 GSCCCGGTTGTCGTTACAGGTCAACAAGAGCTCGGGTTGCACGCGGTGAGCGCAT 82
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 36346 GCGCGCGTGCCTGGGACAGGTATCCAGAGCGGCGGCGACGCTTTGCACCGCT 36287

QY 83 CACGAGCTCGACGCTGACCGAAGAGAGAGCTCGTGCACCATCTAGTACCTGTCGGCT 142
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 36286 GAGCGGCTCGGCGCGCTTCGTCGCGCGGTCTCTTACTCTCTCGGCGGCTCGGCT 36227

QY 143 GCATGAGGGTCACTCGACGATGACCGTTCAGTTCAGTGGCGGTGCGAGTGGATCTGA 202
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 36226 TCTGTGCGGAAGTACGGGTTCGCGGCGACCATCTGCTGCTGCTGCTGCTGCTG 36167

QY 203 CGAC 206
    ||| |||
Db 36166 CGAC 36163

RESULT 13
US-09-252-991A-13613
; Sequence 13613, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
```

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? GENERAL INFORMATION:
? APPLICANT: Marc J. Rubenfield et al.
? TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONA
? TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
? FILE REFERENCE: 107196.136
? CURRENT APPLICATION NUMBER: US/09/252,991A
? CURRENT FILING DATE: 1999-02-18
? PRIOR APPLICATION NUMBER: US 60/074,788
? PRIOR FILING DATE: 1998-02-18
? PRIOR APPLICATION NUMBER: US 60/094,190
? PRIOR FILING DATE: 1998-07-27
? NUMBER OF SEQ ID NOS: 33142
? SEQ ID NO 13507
? LENGTH: 1641
? TYPE: DNA
? ORGANISM: Pseudomonas aeruginosa
? US-09-252-991A-13507

```

Query Match	16.7%	Score 34.8;	DB 4;	Length 1641;
Best Local Similarity	50.6%;	Pred. No. 0.87;		
Matches	84;	Conservative	0; Mismatches 82;	Indels 0; Gaps 0;
QY	17	CGACCTGGCCCGGGTTGCTGTACAAAGGTCAACAAGATCGGGTTCGACGCGCGGTGA	76	
Db	1333	CGAGCGGCGCACCGAGGCTGGGCGATGGGCGATCCACAGTACCAAGTTGAACGACAGGCG	1392	
QY	77	GCGCATCACAGCTCGACGCTGACCGAAGAGGACGCTGCTGCCACCATCGAGTACCTGGT	136	
Db	1393	CGACTGGATGACGCGGCGCTGCCGACCTGACCCCTGTTGATCAGCCACCAAGACCAAGT	1452	
QY	137	CCGGCTGCATGAGGTCTAGTGCAGATGACCGCTTCCAGGTGGCGTC	182	
Db	1453	CACCCGCGCTGCCGGAACACGCGGGGTGATCGCTTCCAGCGACTTC	1498	

Search completed: September 17, 2003, 23:20:42
Job time : 53.5758 secs

Search completed: September 17, 2003, 23:20:42
Job time : 53.5758 secs

Query Match 80.0%; Score 166.4; DB 10; Length 3519;
Best Local Similarity 87.5%; Pred. No. 4.8e-43;
Matches 182; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 1 TCAGGAGAGCGCTACGACCTGGCCGGGTGGTGTACAAAGTCAACAGAGCTCG 60
DB 884 TCAGGAGAGCGCTACGACCTGGCCGGGTGGTGTACAAAGTCAACAGAGCTCG 943
QY 61 GGTTCACGCGCGGTGACGCGATCAGAGCTCGAGCTGACCGAAGAGAGCTCGTCCGCA 120
DB 944 GGTTCACGCGCGGTGACGCGATCAGAGCTCGAGCTGACCGAAGAGAGCTCGTCCGCA 1003
QY 121 CCATCGATGACCTGTCGCGTGTGATGAGGCTGACGAGTACCGTTCACGAGTGGCG 180
DB 1004 CCATCGATGACCTGTCGCGTGTGATGAGGCTGACGAGTACCGTTCACGAGTGGCG 1063
QY 181 TCGAGGTGCGAGTGGATACGACGACAT 208
DB 1064 TCGAGGTGCGAGTGGATACGACGACAT 1091

RESULT 2
US-09-738-626-547
; Sequence 547, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAT, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OKAZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 547
; LENGTH: 3495
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-547

Query Match 43.1%; Score 89.6; DB 10; Length 3495;
Best Local Similarity 69.0%; Pred. No. 8.8e-19;
Matches 138; Conservative 0; Mismatches 59; Indels 3; Gaps 1;

QY 9 AAGCGCTACGACCTGGCCGGGTGGTGTACAAAGTCAACAGAGCTCGGTTGCAC 68
DB 877 AAGCGCTACGACCTGGCCGGGTGGTGTACAAAGTCAACAGAGCTCGGTTGGT 936
QY 69 GCCGGTACGCGGATCAGAGCTGACGCTGACCGAGAGAGAGCTGCGCCACCATCGAG 128
DB 937 GCCGACACGATGCTGTTGAT---GACTCTTACTGAGAGAGACATCGCAACCATCGAG 993
QY 129 TACCTGTCGCGGTGATGAGGCTGACGCGATGACCGTCCAGGTGGCGTGGAGGTG 188
DB 994 TACCTGTCGCGTGTGACCGAGGTGAGCGGCTGATGACTCTCCAAATGGTGAAGATC 1053
QY 189 CCAGTGGATCTAGCAGACAT 208
DB 1054 CCAGTGGATCTAGCAGACAT 1073

RESULT 3
US-09-984-711-5
; Sequence 5, Application US/09984711
; Patent No. US20020119549A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: STEPHAN, Hans
; APPLICANT: KREUTZER, Caroline
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE rpsL GENE
; FILE REFERENCE: 204209U50
; CURRENT APPLICATION NUMBER: US/09/984,711
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: DE10108230.9
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 5096
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
; OTHER INFORMATION:
US-09-984-711-5

Query Match 43.1%; Score 89.6; DB 10; Length 5096;
Best Local Similarity 69.0%; Pred. No. 9.1e-19;
Matches 138; Conservative 0; Mismatches 59; Indels 3; Gaps 1;

QY 9 AAGCGCTACGACCTGGCCGGGTGGTGTACAAAGTCAACAGAGCTCGGTTGCAC 68
DB 1578 AAGCGCTACGACCTGGCCGGGTGGTGTACAAAGTCAACAGAGCTCGGTTGGT 1637
QY 69 GCCGGTACGCGGATCAGAGCTGACGCTGACCGAGAGAGAGCTGCGCCACCATCGAG 128
DB 1638 GCCGACACGATGCTGTTGAT---GACTCTTACTGAGAGAGACATCGCAACCATCGAG 1694
QY 129 TACCTGTCGCGGTGATGAGGCTGACGCTGACGAGTACCGTCCAGGTGGCGTGGAGGTG 188
DB 1695 TACCTGTCGCTGTCGACCGAGGTGAGCGGCTGATGACTCTCCAAATGGTGAAGATC 1754
QY 189 CCAGTGGATCTAGCAGACAT 208
DB 1755 CCAGTGGATCTAGCAGACAT 1774

RESULT 4
US-09-887-052-1
; Sequence 1, Application US/09887052
; Patent No. US20020119537A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE rpoB GENE
; FILE REFERENCE: 204212U50X
; CURRENT APPLICATION NUMBER: US/09/887,052
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: DE10107229.5
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 5099

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; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
US-09-887-052-1

Query Match      43.1%; Score 89.6; DB 10; Length 5099;
Best Local Similarity 69.0%; Pred. No. 9.1e-19;
Matches 138; Conservative 0; Mismatches 59; Indels 3; Gaps 1;

QY 9 AAGCGCTACGACCTGGCCGGTGGTGTCTTACAGGTCAACAAGAGCTCGGCTGCAC 68
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1578 AAGCGCTACGACCTGGCTGGTGTCTTACAGGTCAACGCGAGCTCGGCTTGGT 1637

QY 69 GCGGTGTAGCGATCAGAGCTCGAGCTGACCGAAGAGAGCTGTCGCCACCATCGAG 128
    || || || || || || || || || || || || || || || || || || || ||
DB 1638 GCGGACCATGATGTTGAT--GACTCTTACTGAAGAGGACATCGCAACCATCGAG 1694

QY 129 TACCTGTCCGGCTGCATGAGGTGCTGTTACAGGTCAACAAGAGCTCGGCTGCAC 188
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1695 TACCTGTCCGGCTGCATGAGGTGCTGTTACAGGTCAACAAGAGCTCGGCTGCAC 1754

QY 189 CCAGTGGATCTAGCAGCAT 208
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1755 CCAGTCGAGACCGATGACAT 1774

RESULT 5
US-09-887-052-3
; Sequence 3, Application US/09887052
; Patent No. US20020119537A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE rpoB GENE
; FILE REFERENCE: 204212USOX
; CURRENT APPLICATION NUMBER: US/09/887,052
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: DE10107229.5
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 5099
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
US-09-887-052-1

Query Match      43.1%; Score 89.6; DB 10; Length 5099;
Best Local Similarity 69.0%; Pred. No. 9.1e-19;
Matches 138; Conservative 0; Mismatches 59; Indels 3; Gaps 1;

QY 9 AAGCGCTACGACCTGGCCGGTGGTGTCTTACAGGTCAACAAGAGCTCGGCTGCAC 68
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1578 AAGCGCTACGACCTGGCTGGTGTCTTACAGGTCAACGCGAGCTCGGCTTGGT 1637

QY 69 GCGGTGTAGCGATCAGAGCTCGAGCTGACCGAAGAGAGCTGTCGCCACCATCGAG 128
    || || || || || || || || || || || || || || || || || || || ||
DB 1638 GCGGACCATGATGTTGAT--GACTCTTACTGAAGAGGACATCGCAACCATCGAG 1694

QY 129 TACCTGTCCGGCTGCATGAGGTGCTGTTACAGGTCAACAAGAGCTCGGCTGCAC 188
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1695 TACCTGTCCGGCTGCATGAGGTGCTGTTACAGGTCAACAAGAGCTCGGCTGCAC 1754

QY 189 CCAGTGGATCTAGCAGCAT 208
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1755 CCAGTCGAGACCGATGACAT 1774

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DB 1755 CCAGTCGAGACCGATGACAT 1774

RESULT 6
US-09-887-052-5
; Sequence 5, Application US/09887052
; Patent No. US20020119537A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE rpoB GENE
; FILE REFERENCE: 204212USOX
; CURRENT APPLICATION NUMBER: US/09/887,052
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: DE10107229.5
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 5099
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
US-09-887-052-5

Query Match      43.1%; Score 89.6; DB 10; Length 5099;
Best Local Similarity 69.0%; Pred. No. 9.1e-19;
Matches 138; Conservative 0; Mismatches 59; Indels 3; Gaps 1;

QY 9 AAGCGCTACGACCTGGCCGGTGGTGTCTTACAGGTCAACAAGAGCTCGGCTGCAC 68
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1578 AAGCGCTACGACCTGGCTGGTGTCTTACAGGTCAACGCGAGCTCGGCTTGGT 1637

QY 69 GCGGTGTAGCGATCAGAGCTCGAGCTGACCGAAGAGAGCTGTCGCCACCATCGAG 128
    || || || || || || || || || || || || || || || || || || || ||
DB 1638 GCGGACCATGATGTTGAT--GACTCTTACTGAAGAGGACATCGCAACCATCGAG 1694

QY 129 TACCTGTCCGGCTGCATGAGGTGCTGTTACAGGTCAACAAGAGCTCGGCTGCAC 188
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1695 TACCTGTCCGGCTGCATGAGGTGCTGTTACAGGTCAACAAGAGCTCGGCTGCAC 1754

QY 189 CCAGTGGATCTAGCAGCAT 208
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1755 CCAGTCGAGACCGATGACAT 1774

RESULT 7
US-10-076-406-1
; Sequence 1, Application US/10076406
; Publication No. US2003016684A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: Nucleotide sequences coding for the rpoB gene
; FILE REFERENCE: 219774USOXIP
; CURRENT APPLICATION NUMBER: US/10/076,406
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: DE 10107229.5
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 09/887052
; PRIOR FILING DATE: 2001-06-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 5099

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; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
; OTHER INFORMATION:
US-10-076-406-1

Query Match      43.1%; Score 89.6; DB 12; Length 5099;
Best Local Similarity 69.0%; Pred. No. 9.le-19;
Matches 138; Conservative 0; Mismatches 59; Indels 3; Gaps 1;

QY 9 AAGCGCTACGACCTGCGCGGTTGGTTCGTTACAAAGTCAACCGCAAGCTCGGCTTGGT 1637
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1578 AAGCGCTACGACCTGCGCGGTTGGTTCGTTACAAAGTCAACCGCAAGCTCGGCTTGGT 1637

QY 69 GCCGGTGAGCCGATCAGAGCTCGAGCTCGACCGTCAACGAGAGAGAGTCTGTCGCCACCATCGAG 128
    ||| | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1638 GCCGACCAACGATGTTTGTAT---GACTCTTACTCAAGAGGACATCGCAACCATCGAG 1694

QY 129 TACCTGTGCGGTCATGAGGTCAGTCGACGATGACCGTTCCAGGTGGGCTGAGGTG 188
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1695 TACCTGTGCGTCTGACGAGTGCAGCGGTGAGCGGTGTCATGACTTCTCCAATGGTGAAGAGATC 1754

QY 189 CCAGTGGATCTAGCAGCAT 208
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1755 CCAGTCGAGACCGATGACAT 1774

RESULT 9
US-10-076-406-5
; Sequence 5, Application US/10076406
; Publication No. US20030166884A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: Nucleotide sequences coding for the rpoB gene
; FILE REFERENCE: 219774US0XCIP
; CURRENT APPLICATION NUMBER: US/10/076,406
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: DE 10107229.5
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 09/887052
; PRIOR FILING DATE: 2001-06-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 5099
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
; OTHER INFORMATION:
; NAME/KEY: mutation
; LOCATION: (2016)..(2016)
; OTHER INFORMATION: Substitution of cytosine by thymine
US-10-076-406-5

Query Match      43.1%; Score 89.6; DB 12; Length 5099;
Best Local Similarity 69.0%; Pred. No. 9.le-19;
Matches 138; Conservative 0; Mismatches 59; Indels 3; Gaps 1;

QY 9 AAGCGCTACGACCTGCGCGGTTGGTTCGTTACAAAGTCAACGAGAGTCTGCGGTTGCAC 68
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1578 AAGCGCTACGACCTGCGCGGTTGGTTCGTTACAAAGTCAACGAGATCAACCGCAAGCTCGGCTTGGT 1637

QY 69 GCCGGTGAGCCGATCAGAGCTCGAGCTCGACCGTCAACGAGAGAGAGTCTGTCGCCACCATCGAG 128
    ||| | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1638 GCCGACCAACGATGTTTGTAT---GACTCTTACTCAAGAGGACATCGCAACCATCGAG 1694

QY 129 TACCTGTGCGGTCATGAGGTCAGTCGACGATGACCGTTCCAGGTGGGCTGAGGTG 188
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1695 TACCTGTGCGTCTGACGAGTGCAGCGGTGAGCGGTGTCATGACTTCTCCAATGGTGAAGAGATC 1754

QY 189 CCAGTGGATCTAGCAGCAT 208
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1755 CCAGTCGAGACCGATGACAT 1774

RESULT 8
US-10-076-406-3
; Sequence 3, Application US/10076406
; Publication No. US20030166884A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: Nucleotide sequences coding for the rpoB gene
; FILE REFERENCE: 219774US0XCIP
; CURRENT APPLICATION NUMBER: US/10/076,406
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: DE 10107229.5
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 09/887052
; PRIOR FILING DATE: 2001-06-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 5099
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
; OTHER INFORMATION:
; NAME/KEY: mutation
; LOCATION: (1987)..(1987)
; OTHER INFORMATION: Substitution of adenine by thymine
; NAME/KEY: (1288)
; LOCATION: (1288)
; OTHER INFORMATION: Substitution of cytosine by thymine
; NAME/KEY: mutation
; LOCATION: (715)..(715)
; OTHER INFORMATION: Substitution of cytosine by thymine
US-10-076-406-3

Query Match      43.1%; Score 89.6; DB 12; Length 5099;
Best Local Similarity 69.0%; Pred. No. 9.le-19;
Matches 138; Conservative 0; Mismatches 59; Indels 3; Gaps 1;

QY 9 AAGCGCTACGACCTGCGCGGTTGGTTCGTTACAAAGTCAACGAGAGTCTGCGGTTGCAC 68
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; Publication No. US2002015557A1
; GENERAL INFORMATION:
; APPLICANT: MCKEL, BETTINA
; APPLICANT: BATHÉ, BRIGITTE
; APPLICANT: HANS, STEFAN
; APPLICANT: KREUTZER, CAROLINE
; APPLICANT: HERMANN, THOMAS
; APPLICANT: PFEFFERLE, WALTER
; APPLICANT: BINDER, MICHAEL
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE rpsL GENE
; FILE REFERENCE: 2184/2USOX
; CURRENT APPLICATION NUMBER: US/10/075,460
; CURRENT FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: DE 10107230.9
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: DE 10162386.0
; PRIOR FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 5099
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
; OTHER INFORMATION:
US-10-075-460-5

Query Match      43.1%; Score 89.6; DB 13; Length 5099;
Best Local Similarity 69.0%; Pred. No. 9.1e-19;
Matches 138; Conservative 0; Mismatches 59; Indels 3; Gaps 1;

QY 9  AAGCGCTACGACCTGCGCGGTTGCTGTACAGGTCAACAGAGAGTCCGGTTCGAC 68
Db 1578 AAGCGCTACGACCTGCGCGGTTGCTGTACAGGTCAACAGAGAGTCCGGTTCG 1637

QY 69  GCGGTGAGCGGATCAGAGCTCGAGCTGACCGAGGAGGACGTCGTGCCACCATCGAG 128
Db 1638 GCGGACACGATGTTGAT---GACTCTTACTGAGAGGACATCGCACCATCGAG 1694

QY 129  TACCTGGTCCGGTGCATGAGGTGATCGACGATGACCGTTCAGGTGCGCTCGAGTG 188
Db 1695 TACCTGGTGGCTGCGACGAGGTGAGCGCGTCATGACTTCTCCAAATGTTGAAGATC 1754

QY 189  CCAGTGGATCTAGCAGCAT 208
Db 1755 CCAGTCGAGACCGATGACAT 1774

RESULT 11
US-09-738-626-1
; Sequence 1, Application US/09738626
; Publication No. US20020197603A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07

; Publication No. US2002015557A1
; GENERAL INFORMATION:
; APPLICANT: MCKEL, BETTINA
; APPLICANT: BATHÉ, BRIGITTE
; APPLICANT: HANS, STEFAN
; APPLICANT: KREUTZER, CAROLINE
; APPLICANT: HERMANN, THOMAS
; APPLICANT: PFEFFERLE, WALTER
; APPLICANT: BINDER, MICHAEL
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE rpsL GENE
; FILE REFERENCE: 2184/2USOX
; CURRENT APPLICATION NUMBER: US/10/075,460
; CURRENT FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: DE 10107230.9
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: DE 10162386.0
; PRIOR FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 5099
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
; OTHER INFORMATION:
US-10-075-460-5

Query Match      43.1%; Score 89.6; DB 13; Length 5099;
Best Local Similarity 69.0%; Pred. No. 9.1e-19;
Matches 138; Conservative 0; Mismatches 59; Indels 3; Gaps 1;

QY 9  AAGCGCTACGACCTGCGCGGTTGCTGTACAGGTCAACAGAGAGTCCGGTTCGAC 68
Db 1578 AAGCGCTACGACCTGCGCGGTTGCTGTACAGGTCAACAGAGAGTCCGGTTCG 1637

QY 69  GCGGTGAGCGGATCAGAGCTCGAGCTGACCGAGGAGGACGTCGTGCCACCATCGAG 128
Db 1638 GCGGACACGATGTTGAT---GACTCTTACTGAGAGGACATCGCACCATCGAG 1694

QY 129  TACCTGGTCCGGTGCATGAGGTGATCGACGATGACCGTTCAGGTGCGCTCGAGTG 188
Db 1695 TACCTGGTGGCTGCGACGAGGTGAGCGCGTCATGACTTCTCCAAATGTTGAAGATC 1754

QY 189  CCAGTGGATCTAGCAGCAT 208
Db 1755 CCAGTCGAGACCGATGACAT 1774

RESULT 11
US-09-738-626-1
; Sequence 1, Application US/09738626
; Publication No. US20020197603A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07

; Publication No. US2002015557A1
; GENERAL INFORMATION:
; APPLICANT: MCKEL, BETTINA
; APPLICANT: BATHÉ, BRIGITTE
; APPLICANT: HANS, STEFAN
; APPLICANT: KREUTZER, CAROLINE
; APPLICANT: HERMANN, THOMAS
; APPLICANT: PFEFFERLE, WALTER
; APPLICANT: BINDER, MICHAEL
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE rpsL GENE
; FILE REFERENCE: 2184/2USOX
; CURRENT APPLICATION NUMBER: US/10/075,460
; CURRENT FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: DE 10107230.9
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: DE 10162386.0
; PRIOR FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 5099
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
; OTHER INFORMATION:
US-10-075-460-5

Query Match      43.1%; Score 89.6; DB 10; Length 3309400;
Best Local Similarity 69.0%; Pred. No. 1.5e-18;
Matches 138; Conservative 0; Mismatches 59; Indels 3; Gaps 1;

QY 9  AAGCGCTACGACCTGCGCGGTTGCTGTACAGGTCAACAGAGAGTCCGGTTCGAC 68
Db 513789 AAGCGCTACGACCTGCGCGTGTGTTTACAAGATCAACCGCAAGTTCGCGCTTGGT 513848

QY 69  GCGGTGAGCGGATCAGAGCTCGAGCTGACCGAGGAGGACGTCGTGCCACCATCGAG 128
Db 513849 GCGGACACGATGTTGAT---GACTCTTACTGAGAGGACATCGCACCATCGAG 513905

QY 129  TACCTGGTCCGGTGCATGAGGTGATCGACGATGACCGTTCAGGTGCGCTCGAGTG 188
Db 513906 TACCTGGTGGCTGCGACGAGGTGAGCGCGTCATGACTTCTCCAAATGTTGAAGATC 513965

QY 189  CCAGTGGATCTAGCAGCAT 208
Db 513966 CCAGTCGAGACCGATGACAT 513985

RESULT 12
US-10-156-761-4898
; Sequence 4898, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIRA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 4898
; LENGTH: 3543
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3543)
US-10-156-761-4898

Query Match      34.8%; Score 72.4; DB 14; Length 3543;
Best Local Similarity 63.0%; Pred. No. 2.4e-13;
Matches 131; Conservative 0; Mismatches 71; Indels 6; Gaps 1;

QY 1  TCAAGGAGAGCGCTACGACCTGCGCGGTTGCTGTACAGGTCAACAGAGAGTGG 60
Db 926  TCAACCCGAGCGCTACGACCTGCGGAGGTGCGCGCTCAAGGTCAACAGAGAGTGG 985

QY 61  GGTTCACCGCGGTGAGCGCGATCAGAGTTCGACCGTCAACGAGAGAGAGTGGTGGCA 120
Db 986  G-----CGCGAGGCGCGCGTGGCGGGATCTGACCGTGGAGGACATCTCTCT 1039
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QY 121 CCATCGAGTACCTGCTCCGGCTGCATGAGGTGACGTGACGATGACCGTTCAGGTGGCG 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1040 CGATCAAGTACCTGGTGAAGCTGACGCGCGTGAGACCGAGACCGCTTGGCGACACGGCA 1099
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 181 TCGAGGTGCCAGTGGATGACGACAT 208
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1100 CCTCGATCGTCTCGAGACCGGACGACAT 1127
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 13
US-10-156-761-1
; Sequence 1, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
; LENGTH: 9025608
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1

Query Match 34.8%; Score 72.4; DB 14; Length 9025608;
Best Local Similarity 63.0%; Pred. No. 4.5e-13;
Matches 131; Conservative 0; Mismatches 71; Indels 6; Gaps 1;

QY 1 TCAAGGAGAGCGCTACGACCTGCGCGGGTTGGTGTACAGGTCAACAAGAGCTCG 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 5970494 TCAACCGAGAGCGCTAGACCTCGCGRAGGTGCGGCTACAGGTCAACAGAGAGCTGG 5970553
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 GGTTCACGCGCGGTGAGCGCATCAGACTCGAGCTGACCGGAGGAGGAGCTGTCGCCA 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 5970554 G-----CGGCGAGGCGCGCTGGAGCGCGGGATCTTGACCGTGCAGGACATCATCTCGT 5970607
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 121 CCATCGAGTACCTGCTCCGGCTGCATGAGGTGACGTGACGATGACCGTTCAGGTGGCG 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 5970608 CGATCAAGTACCTGGTGAAGCTGACGCGCGGTGAGACCGGATGCGGACACGGCA 5970667
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 181 TCGAGGTGCCAGTGGATGACGACAT 208
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 5970668 CCTCGATCGTCTCGAGACCGGACGACAT 5970695
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 14
US-10-156-761-2515/c
; Sequence 2515, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
```

```
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 2515
; LENGTH: 3969
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3969)
US-10-156-761-2515

Query Match 18.7%; Score 38.8; DB 14; Length 3969;
Best Local Similarity 62.2%; Pred. No. 0.01;
Matches 61; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 56 GCTCGGTTTCACGCGGTGAGCGCATCAGAGCTGACGCTGACCGGAGGAGGAGCTCGT 115
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Db 3883 GCCGCGCGCGCACCCGCGGAGCGGTACCCCTCCCGCGGTGCGCGGAGAGGACGACGC 3824
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QY 116 CGCCACCATCGAGTACCTGCTCCGGCTGCATGAGGGTC 153
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 3823 CTTGCGCGCGAGTTCCTTGATGCGCTGCATGAGGGTC 3786
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RESULT 15
US-10-156-761-1/c
; Sequence 1, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
; LENGTH: 9025608
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1

Query Match 18.7%; Score 38.8; DB 14; Length 9025608;
Best Local Similarity 62.2%; Pred. No. 0.018;
Matches 61; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 56 GCTCGGTTTCACGCGGTGAGCGCATCAGAGCTGACGCTGACCGGAGGAGGAGCTCGT 115
    || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 3099006 GCCGCGCGCGCACCCGCGGAGCGGTACCCCTCCCGCGGTGCGCGGAGAGGAGGACGACGC 3098947
    || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 116 CGCCACCATCGAGTACCTGCTCCGGCTGCATGAGGGTC 153
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 3098946 CTTGCGCGCGAGTTCCTTGATGCGCTGCATGAGGGTC 3098909
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Search completed: September 17, 2003, 23:30:20
Job time : 155.97 secs

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OM nucleic - nucleic search, using sw model

Run on: September 17, 2003, 12:31:22 ; Search time 37.5758 Seconds
(without alignments)
2443.269 Million cell updates/sec

Title: US-09-697-123B-24
Perfect score: 208
Sequence: 1 tcaaggaggaagcgctacgac.....ccggtgagacgacgacat 208

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES					Description	
Result No.	Score	Query Match	Length	ID		
1	150.4	72.3	970	1	US-08-250-030-1	Sequence 1, Appli
2	150.4	72.3	970	5	PCT-US95-06790-1	Sequence 1, Appli
3	150.4	72.3	4403765	3	US-09-103-840A-2	Sequence 2, Appli
4	150.4	72.3	4411529	3	US-09-103-840A-1	Sequence 1, Appli
5	134.4	64.6	3447	2	US-08-313-185-57	Sequence 57, Appli
6	134.4	64.6	3447	3	US-09-082-614A-57	Sequence 57, Appli
7	41.2	19.8	2493	4	US-09-252-991A-10571	Sequence 10571, A
8	41.2	19.8	2967	4	US-09-252-991A-10675	Sequence 10675, A
9	39.8	19.1	3027	4	US-09-252-991A-10492	Sequence 10492, A
10	39.8	19.1	1527	4	US-09-252-991A-12552	Sequence 12552, A
11	39.8	19.1	2022	4	US-09-252-991A-12932	Sequence 12932, A
12	39.8	19.1	2289	4	US-09-252-991A-12852	Sequence 12852, A
13	39	18.8	4403765	3	US-09-103-840A-2	Sequence 2, Appli
14	39	18.8	4411529	3	US-09-103-840A-1	Sequence 1, Appli
15	38.2	18.4	1194	4	US-09-252-991A-10286	Sequence 10286, A
16	38	18.3	1415	4	US-09-857-556A-3	Sequence 3, Appli
17	38	18.3	1488	4	US-09-857-556A-19	Sequence 19, Appli
18	37.8	18.2	816	4	US-09-252-991A-1108	Sequence 1108, Ap
19	37.8	18.2	1578	4	US-09-252-991A-935	Sequence 935, App
20	37.8	18.2	1653	4	US-09-252-991A-976	Sequence 976, App
21	37.2	17.9	633	4	US-09-252-991A-488	Sequence 488, App
22	37.2	17.9	879	4	US-09-252-991A-359	Sequence 359, App
23	37.2	17.9	1164	4	US-09-252-991A-385	Sequence 385, App
24	37.2	17.9	1215	4	US-09-266-965-42	Sequence 42, Appli
25	37.2	17.9	1419	4	US-09-252-991A-440	Sequence 440, App
26	37.2	17.9	53500	4	US-09-266-965-76	Sequence 76, Appli
27	37	17.8	855	4	US-09-252-991A-5531	Sequence 5531, Ap

28	37	17.8	2742	4	US-09-252-991A-5556	Sequence 5556, Ap
29	37	17.8	3321	4	US-09-252-991A-5668	Sequence 5668, Ap
30	37	17.8	47981	4	US-09-679-279-1	Sequence 1, Appli
31	36.8	17.7	633	4	US-09-252-991A-6234	Sequence 6234, Ap
32	36.8	17.7	1029	4	US-09-252-991A-6399	Sequence 6399, Ap
33	36.8	17.7	1164	4	US-09-252-991A-6068	Sequence 6068, Ap
34	36.6	17.6	1962	4	US-09-252-991A-231	Sequence 231, App
35	36.6	17.6	77536	4	US-09-410-551B-1	Sequence 1, Appli
36	36.4	17.5	43280	2	US-08-804-227C-1	Sequence 1, Appli
37	36	17.3	785	3	US-08-998-416-748	Sequence 748, App
38	35.6	17.1	885	4	US-09-252-991A-10382	Sequence 10382, A
39	35.6	17.1	2169	4	US-09-252-991A-10268	Sequence 10268, A
40	35.6	17.1	2582	2	US-08-816-105A-2	Sequence 2, Appli
41	35.4	17.0	426	4	US-09-252-991A-9731	Sequence 9731, Ap
42	35.4	17.0	777	3	US-08-998-416-212	Sequence 212, App
43	35.4	17.0	1482	4	US-09-252-991A-9689	Sequence 9689, Ap
44	35.4	17.0	1614	4	US-09-252-991A-9607	Sequence 9607, Ap
45	35.4	17.0	1623	4	US-09-252-991A-9650	Sequence 9650, Ap

ALIGNMENTS

RESULT 1
US-08-250-030-1
; Sequence 1, Application US/08250030
; Patent No. 5643723
; GENERAL INFORMATION:
; APPLICANT: Persing, David H.
; TITLE OF INVENTION: Detection of a Genetic Locus Encoding
; TITLE OF INVENTION: Resistance to Rifampin in Mycobacterial Cultures and in
; TITLE OF INVENTION: Clinical Specimens
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg & Woessner
; STREET: 3500 IDS Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/250,030
; FILING DATE: 26-MAY-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Muehling, Ann M.
; REGISTRATION NUMBER: 33,977
; REFERENCE/DOCKET NUMBER: 150.105US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-339-0331
; TELEFAX: 612-339-3061
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 970 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-250-030-1

Query Match 72.3%; Score 150.4; DB 1; Length 970;
Best Local Similarity 82.7%; Pred. No. 6.2e-30;
Matches 172; Conservative 0; Mismatches 36; Indels 0; Gaps 0;
Oy 1 TCAAGGAGAGCGCTACGACCTGGCCCGGCGTGGCCGCTACAGGTCAACAGAACTCG 60
Db 26 TCAAGGAGAGCGCTACGACCTGGCCCGGCGTGGCCGCTACAGGTCAACAGAACTCG 85

RESULT 3
US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.

```

1  FILE REFERENCE: 24366-20007.00
2  CURRENT APPLICATION NUMBER: US/09/103,840A
3  CURRENT FILING DATE: 1998-06-24
4  NUMBER OF SEQ ID NOS: 2
5  SOFTWARE: PatentIn Ver. 2.1
6  SEQ ID NO 2
7  LENGTH: 4403765
8  TYPE: DNA
9  ORGANISM: Mycobacterium tuberculosis
10 FEATURE:
11 OTHER INFORMATION: CDC 1551
12 OTHER INFORMATION: "n" bases at various positions throughout the sequ
13 OTHER INFORMATION: represent a, t, c or g
14 US-09-103-840A-2

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? GENERAL INFORMATION:
? APPLICANT: FLEISCHMAN, Robert D.
? APPLICANT: WHITE, Owen R.
? APPLICANT: FRASER, Claire M.
? APPLICANT: VENTER, John C.
? TITLE OF INVENTION: DNA SOURCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
? TITLE OF INVENTION: TUBERCULOSIS
? FILE REFERENCE: 24366-20007.00
? CURRENT APPLICATION NUMBER: US/09/103,840A
? CURRENT FILING DATE: 1998-06-24
? NUMBER OF SEQ ID NOS: 2
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 1
? LENGTH: 4411529
? TYPE: DNA
? ORGANISM: Mycobacterium tuberculosis
? OTHER INFORMATION: H37KV
US-09-103-840A-1
Query Match          72.3%   Score 150.4   DB 3;   Length 4411529;

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Best Local Similarity 82.7%; Pred. No. 2.6e-29;
Matches 172; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 1 TCAGAGAGAGCGCTACGACCTGCGCCGGGTGGCGCGCTACAGGTCAACAGAACTCG 60
Db 760688 TCAGAGAGAGCGCTACGACCTGCGCCGGGTGGCGCGCTACAGGTCAACAGAACTCG 760747
QY 61 GGTGTAACACCGAGATGGCGCAACACACCGACCTGACCGAGAGGAGCTGTGGCCA 120
Db 760748 GGTGTAACACCGAGATGGCGCAACACACCGACCTGACCGAGAGGAGCTGTGGCCA 760807
QY 121 CCATCGAATACCTGTGGCTTGCACGAGGGGACCCACGATGAAGTCCCGGTGGCG 180
Db 760808 CCATCGAATACCTGTGGCTTGCACGAGGGGACCCACGATGAAGTCCCGGTGGCG 760867
QY 181 TCGAGGTGCGCGTGGAGCCGACGACAT 208
Db 760868 TCGAGGTGCGCGTGGAGCCGACGACAT 760895

RESULT 5
US-08-313-185-57
; Sequence 57, Application US/08313185
; Patent No. 5851763
; GENERAL INFORMATION:
; APPLICANT: Heym, Beate
; APPLICANT: Cole, Stewart
; APPLICANT: Young, Douglas
; APPLICANT: Zhang, Ying
; APPLICANT: Honore, Nadine
; APPLICANT: Telenti, Amalio
; APPLICANT: Bodmer, Thomas
; TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/313,185
; FILING DATE: 12-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 02356.0068-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3447 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-313-185-57

Query Match 64.6%; Score 134.4; DB 2; Length 3447;
Best Local Similarity 77.9%; Pred. No. 9.3e-26;
Matches 162; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 1 TCAGAGAGAGCGCTACGACCTGCGCCGGGTGGCGCGCTACAGGTCAACAGAACTCG 60
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Db 809 TCAGAGAGAGCGCTACGACCTGCGCCGGGTGGCTGTACAGGTCAACAGAGCTCG 868
QY 61 GGTGTAACACCGAGATGGCGCAACACACCGACCTGACCGAGAGGAGCTGTGGCCA 120
Db 869 GGTGTAACACCGAGATGGCGCAACACACCGACCTGACCGAGAGGAGCTGTGGCCA 928
QY 121 CCATCGAATACCTGTGGCTTGCACGAGGGGACCCACGATGAAGTCCCGGTGGCG 180
Db 929 CCATCGAATACCTGTGGCTTGCATGAGGTGCTGCAATGAGTCCCGAGGTGGGG 988
QY 181 TCGAGGTGCGCGTGGAGCCGACGACAT 208
Db 989 TAGAGTGCCAGTGGAACTGACGATAT 1016

RESULT 6
US-09-082-614A-57
; Sequence 57, Application US/09082614A
; Patent No. 6124098
; GENERAL INFORMATION:
; APPLICANT: Heym, Beate
; APPLICANT: Cole, Stewart
; APPLICANT: Young, Douglas
; APPLICANT: Zhang, Ying
; APPLICANT: Honore, Nadine
; APPLICANT: Telenti, Amalio
; APPLICANT: Bodmer, Thomas
; TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/082.614A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/313,185
; FILING DATE: 12-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 02356.0068-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3447 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-082-614A-57

Query Match 64.6%; Score 134.4; DB 3; Length 3447;
Best Local Similarity 77.9%; Pred. No. 9.3e-26;
Matches 162; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 1 TCAGAGAGAGCGCTACGACCTGCGCCGGGTGGCGCGCTACAGGTCAACAGAACTCG 60
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Db 809 TCAAGAGAAACGCTACGACCTGGCCAGGGTTGGTCTTACAGGTCACCAAGAAAGCTCG 868
QY 61 GCGTGAACACCGAGAATCGCCACCAACCAACGACCTCAGCAGAGAGAGCTCGTCCCA 120
Db 869 GGTTCACCGCGGTGAGTTGATCAGCTCTCCACCTGACCGAAGAGATGCTGCGCCA 928
QY 121 CCATCGAATACCTGGTGGCTTGCACGAGGGGACGCCACGATGAAGGTCCCGGTGGCG 180
Db 929 CCATGAGTACCTGGTGGCTGCTGATGAGGGTCAGTCGACAAATGACTGTCCAGGTGGG 988
QY 181 TCAGGTGCGCGTGGAGACCGACAT 208
Db 989 TAGAGTGCCAGTGGAAACTGACATAT 1016

RESULT 7
US-09-252-991A-10571
; Sequence 10571, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 10571
; LENGTH: 2493
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-10571

Query Match 19.8%; Score 41.2; DB 4; Length 2493;
Best Local Similarity 52.3%; Pred. No. 0.054;
Matches 91; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

QY 1 TCAAGAGAAAGCGCTACGACCTGGCCGGGTGCGCTACAGGTCAACAAAGAACTCG 60
Db 837 TCCTCGAGCATCAGTGCAGCTGCGCGCGCGTGCAGCGGTCTCTGCAATGGCT 896
QY 61 GCGTGAACACCGAGAATCGCCACCAACCAACGACCTCAGCAGAGAGAGCTCGTCCCA 120
Db 897 GCGTGAACAGCTTCCACCACTCCCGGGATGAAGAACTGATGGACCGCGGGTGGTGGCT 956
QY 121 CCATCGAATACCTGGTGGCTTGCACGAGGGGACGCCACGATGAAGGTCCCG 174
Db 957 TCCTCGAAGAAACCGCGCATCAGCGCTGCGGATGCTGCGCAAGGTGAGG 1010

RESULT 8
US-09-252-991A-10675
; Sequence 10675, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 10675
; LENGTH: 2967
; TYPE: DNA

Query Match 19.8%; Score 41.2; DB 4; Length 2967;
Best Local Similarity 52.3%; Pred. No. 0.054;
Matches 91; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

QY 1 TCAAGAGAAAGCGCTACGACCTGGCCGGGTGCGCTACAGGTCAACAAAGAACTCG 60
Db 1811 TCCTCGAGCATCAGTGCAGCTGCGCGCGCGTGCAGCGGTCTCTGCAATGGCT 1752
QY 61 GCGTGAACACCGAGAATCGCCACCAACCAACGACCTCAGCAGAGAGAGCTCGTCCCA 120
Db 1751 GCGTGAACAGCTTCCACCACTCCCGGGATGAAGAACTGATGGACCGCGGGTGGTGGCT 1692
QY 121 CCATCGAATACCTGGTGGCTTGCACGAGGGGACGCCACGATGAAGGTCCCG 174
Db 1691 TCCTCGAAGAAACCGCGCATCAGCGCTGCGGATGCTGCGCAAGGTGAGG 1638

RESULT 9
US-09-252-991A-10492/c
; Sequence 10492, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 10492
; LENGTH: 3027
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-10492

Query Match 19.8%; Score 41.2; DB 4; Length 3027;
Best Local Similarity 52.3%; Pred. No. 0.056;
Matches 91; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

QY 1 TCAAGAGAAAGCGCTACGACCTGGCCGGGTGCGCTACAGGTCAACAAAGAACTCG 60
Db 1811 TCCTCGAGCATCAGTGCAGCTGCGCGCGCGTGCAGCGGTCTCTGCAATGGCT 1752
QY 61 GCGTGAACACCGAGAATCGCCACCAACCAACGACCTCAGCAGAGAGAGCTCGTCCCA 120
Db 1751 GCGTGAACAGCTTCCACCACTCCCGGGATGAAGAACTGATGGACCGCGGGTGGTGGCT 1692
QY 121 CCATCGAATACCTGGTGGCTTGCACGAGGGGACGCCACGATGAAGGTCCCG 174
Db 1691 TCCTCGAAGAAACCGCGCATCAGCGCTGCGGATGCTGCGCAAGGTGAGG 1638

RESULT 10
US-09-252-991A-12552
; Sequence 12552, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 12552
; LENGTH: 2967
; TYPE: DNA

; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-10675

Query Match 19.8%; Score 41.2; DB 4; Length 2967;
Best Local Similarity 52.3%; Pred. No. 0.055;
Matches 91; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

QY 1 TCAAGAGAAAGCGCTACGACCTGGCCGGGTGCGCTACAGGTCAACAAAGAACTCG 60
Db 1412 TCCTCGAGCATCAGTGCAGCTGCGCGCGCGTGCAGCGGTCTCTGCAATGGCT 1471
QY 61 GCGTGAACACCGAGAATCGCCACCAACCAACGACCTCAGCAGAGAGAGCTCGTCCCA 120
Db 1472 GCGTGAACAGCTTCCACCACTCCCGGGATGAAGAACTGATGGACCGCGGGTGGTGGCT 1531
QY 121 CCATCGAATACCTGGTGGCTTGCACGAGGGGACGCCACGATGAAGGTCCCG 174
Db 1532 TCCTCGAAGAAACCGCGCATCAGCGCTGCGGATGCTGCGCAAGGTGAGG 1585

RESULT 9
US-09-252-991A-10492/c
; Sequence 10492, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 10492
; LENGTH: 3027
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-10492

Query Match 19.8%; Score 41.2; DB 4; Length 3027;
Best Local Similarity 52.3%; Pred. No. 0.056;
Matches 91; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

QY 1 TCAAGAGAAAGCGCTACGACCTGGCCGGGTGCGCTACAGGTCAACAAAGAACTCG 60
Db 1811 TCCTCGAGCATCAGTGCAGCTGCGCGCGCGTGCAGCGGTCTCTGCAATGGCT 1752
QY 61 GCGTGAACACCGAGAATCGCCACCAACCAACGACCTCAGCAGAGAGAGCTCGTCCCA 120
Db 1751 GCGTGAACAGCTTCCACCACTCCCGGGATGAAGAACTGATGGACCGCGGGTGGTGGCT 1692
QY 121 CCATCGAATACCTGGTGGCTTGCACGAGGGGACGCCACGATGAAGGTCCCG 174
Db 1691 TCCTCGAAGAAACCGCGCATCAGCGCTGCGGATGCTGCGCAAGGTGAGG 1638

RESULT 10
US-09-252-991A-12552
; Sequence 12552, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 12552
; LENGTH: 2967
; TYPE: DNA

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; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 12552
; LENGTH: 1527
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-12552

Query Match
Best Local Similarity 19.1%; Score 39.8; DB 4; Length 1527;
Matches 98; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

QY 14 CTACGACCTGGCCGGTGGCGCTTACAAAGTCAACAAGAACTCGGCTGAACACCGA 73
Db 312 CTGGGACATCGCTGCAATGCTCGCTGGCTGACTACAGACACACTGGCTGGCGCGGA 371
QY 74 GAATGGCCCAACACCAACCACTGACCGAAGAGAGAGCTGTCGCCACCACTGAATACCT 133
Db 372 GTGGGGCCATCCCTCGGACAACCTCGGGGCATCTCGCGTGGCGGACCACTCTGCA 431
QY 134 GGTGGCTGACAGAGGGGACGCCACGATGAAGTCCCGGTGGGTGGGTGGGTGGGT 193
Db 432 GAAAGCCTGGCCAAAGGGAAGCGCGCTGAGCATGCGCAGGTACTGGAAGCGATGAT 491
QY 194 GGAGACCGACGACAT 208
Db 492 CATGGCCACGAGAT 506

RESULT 11
US-09-252-991A-12932/c
; Sequence 12932, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 12932
; LENGTH: 2022
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-12932

Query Match
Best Local Similarity 19.1%; Score 39.8; DB 4; Length 2022;
Matches 98; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

QY 14 CTACGACCTGGCCGGTGGCGCTTACAAAGTCAACAAGAACTCGGCTGAACACCGA 73
Db 1624 CTGGGACATCGCTGCAATGCTCGCTGGCTGACTACAGACACACTGGCTGGCGCGGA 1565
QY 74 GAATGGCCCAACCAACCACTGACCGAAGAGAGAGCTGTCGCCACCACTGAATACCT 133
Db 1564 GTGGGGCCATCCCTCGGACAACCTCGGGGCATCTCGCGTGGCGGACCACTCTGCA 1505
QY 134 GGTGGCTGACAGAGGGGACGCCACGATGAAGTCCCGGTGGGTGGGTGGGTGGGT 193
Db 1504 GAAAGCCTGGCCAAAGGGAAGCGCGCTGAGCATGCGCAGGTACTGGAAGCGATGAT 1445
QY 194 GGAGACCGACGACAT 208
Db 1444 CATGGCCACGAGAT 1430

RESULT 12
US-09-252-991A-12852
; Sequence 12852, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 12852
; LENGTH: 2289
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-12852

Query Match
Best Local Similarity 19.1%; Score 39.8; DB 4; Length 2289;
Matches 98; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

QY 14 CTACGACCTGGCCGGTGGCGCTTACAAAGTCAACAAGAACTCGGCTGAACACCGA 73
Db 1345 CTGGGACATCGCTGCAATGCTCGCTGGCTGACTACAGACACACTGGCTGGCGCGGA 1404
QY 74 GAATGGCCCAACCAACCACTGACCGAAGAGAGAGCTGTCGCCACCACTGAATACCT 133
Db 1405 GTGGGGCCATCCCTCGGACAACCTCGGGGCATCTCGCGTGGCGGACCACTCTGCA 1464
QY 134 GGTGGCTGACAGAGGGGACGCCACGATGAAGTCCCGGTGGGTGGGTGGGTGGGT 193
Db 1465 GAAAGCCTGGCCAAAGGGAAGCGCGCTGAGCATGCGCAGGTACTGGAAGCGATGAT 1524
QY 194 GGAGACCGACGACAT 208
Db 1525 CATGGCCACGAGAT 1539

RESULT 13
US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match
Best Local Similarity 18.8%; Score 39; DB 3; Length 4403765;
Matches 96; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

QY 14 CTACGACCTGGCCGGTGGCGCTTACAAAGTCAACAAGAACTCGGCTGAACACCGA 73
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Db 3821678 CGACGGCCGCGCGCTGACCGGGCTGATCACCGTCAAGGACTGCTCAAGACCGAGCA 3821619
QY 74 GAATGGCGCAACACACGACCCCTGACCGAAGAGGACGTCGTCGCCACCATCGAATACT 133
Db 3821618 ACACCCGCTGGCCACCAAGGACGACGACGGCGGCTGCTGGTGGGGCGGCCCTCGCGGT 3821559
QY 134 GGTGCGCTTGCACGAGGGGACGACCGACGATGATGTCGCCGCTGCGCTGCGAGTGCCTG 193
Db 3821558 CGGCGCGGATGCTGCTGGTGGCGGCGCATGATGTTGTCGACGCTGGGGTTCGACGCTGCTGT 3821499
QY 194 GGAGACCGGACG 204
Db 3821498 CGTGGACACCG 3821488

RESULT 14

US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Patent No. 6294328

; GENERAL INFORMATION:

; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.

; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM

; TITLE OF INVENTION: TUBERCULOSIS

; FILE REFERENCE: 24366-20007.00

; CURRENT APPLICATION NUMBER: US/09/103,840A

; CURRENT FILING DATE: 1998-06-24

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1

; LENGTH: 4411529

; TYPE: DNA

; ORGANISM: Mycobacterium tuberculosis

; OTHER INFORMATION: H37Rv

US-09-103-840A-1

Query Match 18.8%; Score 39; DB 3; Length 4411529;
Best Local Similarity 50.3%; Pred. No. 0.69;
Matches 96; Conservative 0; Mismatches 95; Indels 0; Gaps 0;
QY 14 CTAGGACCTGGCCGGTGGCGCTACAGGTCAACAGAACTCGGGTGAACACCGA 73
Db 3830853 CGACGGCCGCGCGCTGACCGGGCTGATCACCTCAAGGACTTCGTCAAGACCGACA 3830794
QY 74 GAATGGCGCAACACACGACCCCTGACCGAAGAGGAGTCTGTCGCCACCATCGAATACT 133
Db 3830793 ACACCCGCTGGCCACCAAGGACGACGACGGCGGCTGCTGGTGGGGCGGCCCTCGCGGT 3830734
QY 134 GGTGCGCTTGCACGAGGGGACGACCGACGATGAAGTTCGCCGCTGCGCTGCGAGTGCCTG 193
Db 3830733 CGGCGCGGATGCTGCTGGTGGCGGCGCATGATGTTGTCGACGCTGGGGTTCGACGCTGCTGT 3830674
QY 194 GGAGACCGGACG 204
Db 3830673 CGTGGACACCG 3830663

RESULT 15

US-09-252-991A-10286/c
; Sequence 10286, Application US/09252991A
; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 10286
; LENGTH: 1194
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-10286

Query Match 18.4%; Score 38.2; DB 4; Length 1194;
Best Local Similarity 52.1%; Pred. No. 0.28; Mismatches 78; Indels 0; Gaps 0;
Matches 85; Conservative 0

QY 12 CGCTACGACCTGGCCGGTGGCGCTACAGGTCAACAAGAACTCGGGCTGAACACC 71
Db 1193 CACGTGACGTTGCGCGCGCGCTGCGACCGGCTCTCCAAATGGCTGGCTGAACACG 1134
QY 72 GAGAAATGCGCCAAACCAACCAACGACCTGACCGAAGAGAGCGTGTGCGCCACCATCGAATAC 131
Db 1133 TTCACCACTCCGGGATGAAGAAGCTGATGGACCGCGGCTGGTGGCTTCGTGGAACAG 1074
QY 132 CTGTTGGCTTGCACGAGGGGACGCCACGATGAAGTCCCG 174
Db 1073 AACCGCGCATCACCGCTGCGATGCTGCGCAAGGTGACG 1031

Search completed: September 17, 2003, 23:21:04

Job time : 59.5758 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.
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Run on: September 17, 2003, 13:09:27 ; Search time 128.97 Seconds
(without alignments)
3967.311 Million cell updates/sec
Title: US-09-697-123B-24
Perfect score: 208
Sequence: 1 tcaagagaagcgtacac.....ccggtgagacgacgacat 208
Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 1660708 seqs, 1229959015 residues
Total number of hits satisfying chosen parameters: 3321416
Minimum DB seq length: 0
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Post-processing: Maximum Match 0%
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Listing first 45 summaries

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				2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*			
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				4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*			
				5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*			
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				9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*			
				10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*			
				11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*			
				12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*			
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.							
SUMMARIES							
Result No.	Score	Query Match	Length DB ID	Description			
1	150.4	72.3	3519 10	US-09-712-363-30 Sequence 30, Appl Sequence 547, App			
2	80	38.5	3495 10	US-09-738-626-547 Sequence 5, Appli			
3	80	38.5	5096 10	US-09-984-711-5 Sequence 5, Appli			
4	80	38.5	5099 10	US-09-887-052-1 Sequence 1, Appli			
5	80	38.5	5099 10	US-09-887-052-3 Sequence 3, Appli			
6	80	38.5	5099 10	US-09-887-052-5 Sequence 3, Appli			
7	80	38.5	5099 12	US-10-076-406-1 Sequence 1, Appli			
8	80	38.5	5099 12	US-10-076-406-3 Sequence 3, Appli			
9	80	38.5	5099 12	US-10-076-406-5 Sequence 5, Appli			
10	80	38.5	5099 13	US-10-075-460-5 Sequence 5, Appli			
11	80	38.5	3309400 10	US-09-738-626-1 Sequence 1, Appli			
12	78.8	37.9	3543 14	US-10-156-761-4898 Sequence 4398, Ap			
13	78.8	37.9	9025608 14	US-10-156-761-1 Sequence 1, Appli			
14	42.6	20.5	11058 14	US-10-156-761-3629 Sequence 3629, Ap			
c 15	42.6	20.5	9025608 14	US-10-156-761-1 Sequence 1, Appli			
16	39.2	18.8	6450 12	US-09-930-213-261 Sequence 261, App			

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

17	39	18.8	789	14	US-10-156-761-2971	Sequence 2971, Ap
18	38.6	18.6	774	14	US-10-156-761-6275	Sequence 6275, Ap
19	38.2	18.4	1182	14	US-10-156-761-6832	Sequence 6832, Ap
20	38	18.3	1599	14	US-10-156-761-3074	Sequence 3074, Ap
21	37.6	18.1	825	14	US-10-156-761-6769	Sequence 6769, Ap
22	37.6	18.1	1320	14	US-10-156-761-6285	Sequence 6285, Ap
23	37.6	18.1	1734	14	US-10-156-761-29	Sequence 29, Appl
24	37.4	18.0	687	14	US-10-156-761-2253	Sequence 2253, Ap
25	37.4	18.0	1542	14	US-10-156-761-5967	Sequence 5967, Ap
26	37.2	17.9	447	12	US-10-259-165-688	Sequence 688, Ap
27	37.2	17.9	993	14	US-10-156-761-4673	Sequence 4673, Ap
28	37.2	17.9	1215	12	US-09-953-348-42	Sequence 42, Appl
29	37.2	17.9	1215	14	US-10-267-255-42	Sequence 42, Appl
30	37.2	17.9	2304	14	US-10-156-761-5121	Sequence 5121, Ap
c 31	37.2	17.9	4696	10	US-09-950-335A-8	Sequence 8, Appl
32	37.2	17.9	53500	12	US-09-953-348-76	Sequence 76, Appl
c 33	37.2	17.9	53500	14	US-10-267-255-76	Sequence 76, Appl
34	37	17.8	2622	9	US-09-815-242-7871	Sequence 7871, Ap
35	36.8	17.7	1287	14	US-10-156-761-5314	Sequence 5314, Ap
36	36.8	17.7	1535	12	US-10-159-672-545	Sequence 545, App
37	36.8	17.7	1535	12	US-10-187-749-545	Sequence 545, App
38	36.8	17.7	1535	12	US-10-194-457-545	Sequence 545, App
39	36.8	17.7	1535	12	US-10-184-642-545	Sequence 545, App
40	36.8	17.7	1535	12	US-10-196-747-545	Sequence 545, App
41	36.8	17.7	1535	12	US-10-173-689-545	Sequence 545, App
42	36.8	17.7	1535	12	US-10-173-690-545	Sequence 545, App
43	36.8	17.7	1535	12	US-10-173-691-545	Sequence 545, App
44	36.8	17.7	1535	12	US-10-173-692-545	Sequence 545, App
45	36.8	17.7	1535	12	US-10-173-694-545	Sequence 545, App

ALIGNMENTS

RESULT 1
US-09-712-363-30
; Sequence 30, Application US/09712363
; Patent No. US20020164588A1
; GENERAL INFORMATION:
; APPLICANT: Eisenberg, David
; APPLICANT: Rotstein, Sergio H.
; APPLICANT: Marcotte, Edward M.
; TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND
; FILE REFERENCE: 07419-032001
; CURRENT APPLICATION NUMBER: US/09/712,363
; CURRENT FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: PCT/US00/02246
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,531
; PRIOR FILING DATE: 2000-02-01
; PRIOR APPLICATION NUMBER: 60/117,844
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/118,206,
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: 60/126,593
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/134,093
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/134,092
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/165,124
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/165,086
; PRIOR FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 3519
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-09-712-363-30

Query Match 72.3%; Score 150.4; DB 10; Length 3519;
Best Local Similarity 82.7%; Pred. No. 7.7e-36;
Matches 172; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 1 TCAGAGAGAGCGCTACGACCTGCCCGGCTGGCGCTACAGGTCAACAAGAACTCG 60
DB 884 TCAGAGAGAGCGCTACGACCTGCCCGGCTGGCGCTATAGGTCAACAAGAACTCG 943
QY 61 GGCTGAACACGAGATCGCGCAACACACGACCGCTGACCGAGAGAGGTGTCGCCA 120
DB 944 GGCTGATGTCGGCGAGCCATCATCTGTCGAGCGTGCAGAGAGAGAGTGTGCCA 1003
QY 121 CCATCGAATACCTGGTGGCTGTGCACGAGGGGACCGCCACAGATGAGGTCCCGGTGGG 180
DB 1004 CCATCGAATATCTGCTCCGCTTGCACGAGGTGACAGCAGATGATCCGCGGGG 1063
QY 181 TCAGGTGCGGTGAGAGCCAGACAT 208
DB 1064 TCGAGGTGCGGTGGAACCGACGACAT 1091

RESULT 2
US-09-738-626-547
; Sequence 547, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIALI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09738,626
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 547
; LENGTH: 3495
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-547

Query Match 38.5%; Score 80; DB 10; Length 3495;
Best Local Similarity 66.0%; Pred. No. 1.1e-14;
Matches 132; Conservative 0; Mismatches 65; Indels 3; Gaps 1;

QY 9 AAGCGTACGACCTGGCGGCTGGCGCTACAGGTCAACAAGAACTCGGCTGAAC 68
DB 877 AAGCGTACGACCTGGCGGCTGGCGCTACAGGTCAACAAGAACTCGGCTGGT 936
QY 69 ACCGAGATCGCCACACACCGACCGCTGACCGAGAGAGGTGTCGCCACCATCGAA 128
DB 937 GCGACACCATGCTTTGAT---GACTCTTACTGAAGAGAGATCGCAACCATCGAG 993
QY 129 TACCTGTGGCTTGACAGAGGGGACCGCCACAGATGAGGTCCCGGTGGGTGAGGTG 188
DB 994 TACCTGTGGCTTGACAGAGGGGACCGCCACAGATGAGGTCTCTCCAAATGTTGAAGATC 1053
QY 189 CCGGTGAGAGCCAGACAT 208
DB 1054 CCAGTCGAGACCGATGACAT 1073

RESULT 3
US-09-984-711-5
; Sequence 5, Application US/09984711
; Patent No. US20020119549A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: STEPHAN, Hans
; APPLICANT: KREUTZER, Caroline
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE rpsL GENE
; FILE REFERENCE: 204209U0
; CURRENT APPLICATION NUMBER: US/09/984,711
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: DE10108230.9
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 5096
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
; OTHER INFORMATION:
US-09-984-711-5

Query Match 38.5%; Score 80; DB 10; Length 5096;
Best Local Similarity 66.0%; Pred. No. 1.2e-14;
Matches 132; Conservative 0; Mismatches 65; Indels 3; Gaps 1;

QY 9 AAGCGTACGACCTGGCGGCTGGCGCTACAGGTCAACAAGAACTCGGCTGAAC 68
DB 1578 AAGCGTACGACCTGGCTGGCTTGTGCTTGTACAGATCAACCGAAGCTGGCTTGGT 1637
QY 69 ACCGAGATCGCCACACACCGACCGCTGACCGAGAGAGGTGTCGCCACCATCGAA 128
DB 1638 GCGACACCATGCTTTGAT---GACTCTTACTGAAGAGAGATCGCAACCATCGAG 1694
QY 129 TACCTGTGGCTTGACAGAGGGGACCGCCACAGATGAGGTCCCGGTGGGTGAGGTG 188
DB 1695 TACCTGTGGCTTGACAGAGGGGACCGCCACAGATGAGGTCTCTCCAAATGTTGAAGATC 1754
QY 189 CCGGTGAGAGCCAGACAT 208
DB 1755 CCAGTCGAGACCGATGACAT 1774

RESULT 4
US-09-887-052-1
; Sequence 1, Application US/09887052
; Patent No. US20020119537A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE rpoB GENE
; FILE REFERENCE: 204212U0X
; CURRENT APPLICATION NUMBER: US/09/887,052
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: DE10107229.5
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 5099

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RESULT 7
US-10-076-406-1
; Sequence 1, Application US/10076406
; Publication NO. US2003016684A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: Nucleotide sequences coding for the rpoB gene
; FILE REFERENCE: 219774USOXCIP
; CURRENT APPLICATION NUMBER: US/10/076, 406
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: DE 10107229.5
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 09/887052
; PRIOR FILING DATE: 2001-06-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent version 3.1
; SEQ ID NO 1
; LENGTH: 5099

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; Publication No. US2002015557A1
; GENERAL INFORMATION:
; APPLICANT: MCKEL, BETTINA
; APPLICANT: BATHE, BRIGITTE
; APPLICANT: HANS, STEFAN
; APPLICANT: KREUTZER, CAROLINE
; APPLICANT: HERMANN, THOMAS
; APPLICANT: PFEFFERLE, WALTER
; APPLICANT: BINDER, MICHAEL
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE IPSL GENE
; FILE REFERENCE: 218472USOX
; CURRENT APPLICATION NUMBER: US/10/075,460
; CURRENT FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: DE 10107230.9
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: DE 10162386.0
; PRIOR FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 5099
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
; OTHER INFORMATION:
;
US-10-075-460-5

Query Match      38.5%; Score 80; DB 13; Length 5099;
Best Local Similarity 66.0%; Pred. No. 1.2e-14;
Matches 132; Conservative 0; Mismatches 65; Indels 3; Gaps 1;

QY      9 AAGCGCTACGACCTGGCCGGTGGCGCTACAAAGTCAACAAGAACTCGGGCTGAAC 68
        |||||
DB      1578 AAGCGCTACGACCTGGCGTGGTGGTGTACAAAGTCAACAAGAACTCGGGCTGGT 1637
        |||||

QY      69 ACCGAGATGCGCCAAACCACCGACCTGACCGAGGAGGAGCGTGTGCCACCATCGAA 128
        |||||
DB      1638 GCGACACACATGGTTGAT---GACTCTTACTGAAGAGGACATCGCAACCATCGAG 1694
        |||||

QY      129 TACCTGGTGGCTGTGACGAGGGGCGACCGCATGAAGTCCCGGTGGCGTGAAGTG 188
        |||||
DB      1695 TACCTGGTGGCTGTGACGAGGAGTGTGCGGTGATGCTTCTCCAAATGGTGAAGAGATC 1754
        |||||

QY      189 CCGGTGAGACCGACGACAT 208
        |||||
DB      1755 CCACTCGAGACCGATGACAT 1774
        |||||

RESULT 11
US-09-738-626-1
; Sequence 1, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIALI, KEIHO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07

; Publication No. US2002015557A1
; GENERAL INFORMATION:
; APPLICANT: MCKEL, BETTINA
; APPLICANT: BATHE, BRIGITTE
; APPLICANT: HANS, STEFAN
; APPLICANT: KREUTZER, CAROLINE
; APPLICANT: HERMANN, THOMAS
; APPLICANT: PFEFFERLE, WALTER
; APPLICANT: BINDER, MICHAEL
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE IPSL GENE
; FILE REFERENCE: 218472USOX
; CURRENT APPLICATION NUMBER: US/10/075,460
; CURRENT FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: DE 10107230.9
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: DE 10162386.0
; PRIOR FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 5099
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
; OTHER INFORMATION:
;
US-10-075-460-5

Query Match      38.5%; Score 80; DB 13; Length 5099;
Best Local Similarity 66.0%; Pred. No. 1.2e-14;
Matches 132; Conservative 0; Mismatches 65; Indels 3; Gaps 1;

QY      9 AAGCGCTACGACCTGGCCGGTGGCGCTACAAAGTCAACAAGAACTCGGGCTGAAC 68
        |||||
DB      1578 AAGCGCTACGACCTGGCGTGGTGGTGTACAAAGTCAACAAGAACTCGGGCTGGT 1637
        |||||

QY      69 ACCGAGATGCGCCAAACCACCGACCTGACCGAGGAGGAGCGTGTGCCACCATCGAA 128
        |||||
DB      1638 GCGACACACATGGTTGAT---GACTCTTACTGAAGAGGACATCGCAACCATCGAG 1694
        |||||

QY      129 TACCTGGTGGCTGTGACGAGGGGCGACCGCATGAAGTCCCGGTGGCGTGAAGTG 188
        |||||
DB      1695 TACCTGGTGGCTGTGACGAGGAGTGTGCGGTGATGCTTCTCCAAATGGTGAAGAGATC 1754
        |||||

QY      189 CCGGTGAGACCGACGACAT 208
        |||||
DB      1755 CCACTCGAGACCGATGACAT 1774
        |||||

RESULT 12
US-10-156-761-4898
; Sequence 4898, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 4898
; LENGTH: 3543
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3543)
;
US-10-156-761-4898

Query Match      37.9%; Score 78.8; DB 14; Length 3543;
Best Local Similarity 64.9%; Pred. No. 2.6e-14;
Matches 135; Conservative 0; Mismatches 67; Indels 6; Gaps 1;

QY      1 TCAAGGAGAGCGCTACGACCTGGCCCGGTGGCGCTACAAAGTCAACAAGAACTCG 60
        |||||
DB      926 TCAACCCGAGAGCGCTACGACCTGGCGAGGTGGCGCGCTACAAAGGTCAACAAGAGCTGG 985
        |||||

QY      61 GCGTGAACCGAGAGATGGCCCAACCAACCAAGACCACTGACCGGAGGAGGAGCTGTCGCCA 120
        |||||
DB      986 G-----CGGCGAGGCGCGCTGGAGCGCGGATCTCTGACCGCGAGGACATCATCTCGT 1099
        |||||
```

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OY 121 CCATCAATACCTGGTGGCTGCTACAGAGGGCCACGACGAGTCCCGGTGGCG 180
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1040 CGATCAAGTACCTGGTGAAGCTGCACGCGGTGAGACCGAGACCGTTGGCGACAGCGCA 1099
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 181 TCGAGTGGCGGTGGAGACGAGACAT 208
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1100 CCTCGATGCTGCTGAGACCGAGGACAT 1127
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 13
US-10-156-761-1
; Sequence 1, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
; LENGTH: 9025608
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1

Query Match 37.9%; Score 78.8; DB 14; Length 9025608;
Best Local Similarity 64.9%; Pred. No. 4.4e-14;
Matches 135; Conservative 0; Mismatches 67; Indels 6; Gaps 1;

OY 1 TCAAGGAGAAGCGGTAGCACTGGCCCGGGTGGCGGCTACAGGTCAACAAGAACTCG 60
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5970494 TCAACCGAAGCGGTAGCACTGCGGAAGTGGCGGCTACAGGTCAACAAGACCTGG 5970553
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 61 GCGTGNACACCGAGAATGCCGCCAACCAACACGACCTGACCGAGAGGAGCTGTCGCCA 120
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5970554 G-----CGGCGAGGCGCGGCTGGAGCGCGGGATCTCTGACGTCGAGGACATCTCGT 5970607
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 121 CCATCAATACCTGGTGGCTGCTACAGAGGGCCACGACGATGAAGTCCCGGTGGCG 180
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5970608 CGATCAAGTACCTGGTGAAGCTGCACGCGGTGAGACCGAGACCGTGGCGACAGCGCA 5970667
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 181 TCGAGTGGCGGTGGAGACGAGACAT 208
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5970668 CCTCGATGCTGCTGAGACCGAGGACAT 5970695
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 14
US-10-156-761-3629
; Sequence 3629, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
```

```
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 3629
; LENGTH: 11058
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(11058)
US-10-156-761-3629

Query Match 20.5%; Score 42.6; DB 14; Length 11058;
Best Local Similarity 51.3%; Pred. No. 0.0021;
Matches 99; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

OY 11 GCGCTACGACCTGGCCCGGGTGGCGGCTACAGGTCAACAAGAACTCGGCTGAACAC 70
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 225 GCGCGGCGCCCTCGACACACGAGGCGCTCGACAAGCGCTGGCACCACTGCTGGAGCGCA 284
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 71 CGAATATGGCCCAACACACGACGACCTGACCGAGGAGACGCTGCGCCACCATGAATA 130
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 285 CGAATCTGCGCACCGCTACGCTGAGCGGCGACGCGCCGCTCCAGATCATCGAGCG 344
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 131 CTTGTGCGCTTGCACGAGGGGCACCGCACGATGAAGTCCCGGTGGCGTGAAGTGGC 190
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 345 GCGCGCGCCCTGCGCCCTGGACCGGTCCGGGCGCGGACGACGCGTCCGCGCCCT 404
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 191 GTGAGAGCCGAC 203
      ||| ||| ||| |||
Db 405 GTCGAGGCGGAC 417
      ||| ||| ||| |||

RESULT 15
US-10-156-761-1/c
; Sequence 1, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
; LENGTH: 9025608
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1

Query Match 20.5%; Score 42.6; DB 14; Length 9025608;
Best Local Similarity 51.3%; Pred. No. 0.0034;
Matches 99; Conservative 0; Mismatches 94; Indels 0; Gaps 0;
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QY      11 GGGCTACACCTGGCCCGGGTGGCGGCTACAGGTCAACAAGAACTCGGCGCTGAACAC 70
Db      4510921 GCGCGGCGCCCTCGACACCGAGGCGCCCTCGACAGGCGCTGGCACCACCACTGCTGGAGCGGCA 4510862
QY      71 CGAGGATCGGCAACCAACCAACGACCTGACCGAAGAGGAGCGTGTGCGCCACCATCGAATA 130
Db      4510861 CGAGATCCTGGGCACCGCTACGCCCTGGACGGCGACGAGCCGTCAGATCATCGAGCG 4510802
QY      131 CCTGTGTGCGCTTGCACGAGGGGACGCCACGATGAAGGTCCCCGGTGGCGTCGAGGTGCC 190
Db      4510801 GCGCGGCGCCCTGCGCCCTGGACCGGTCCGGGGCGCGGACGACGCGGTCCGGCGCCT 4510742
QY      191 GGTGAGACCGAC 203
Db      4510741 GGTGAGGCGGAC 4510729

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Search completed: September 17, 2003, 23:30:46
 Job time : 154.97 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 17, 2003, 12:31:22 ; Search time 3.61305 Seconds
(without alignments)
2443.269 Million cell updates/sec

Title: US-09-697-123B-26

Perfect score: 20

Sequence: 1 ggatgttcagcagggtctgc 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_NA.*

- 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/PTUS_COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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c 2	20	100.0	254	4	US-08-750-088A-37
c 3	20	100.0	306	3	US-09-147-935A-1
c 4	20	100.0	306	3	US-09-147-935A-3
c 5	20	100.0	306	3	US-09-147-935A-4
c 6	20	100.0	306	3	US-09-147-935A-5
c 7	20	100.0	306	3	US-09-147-935A-8
c 8	20	100.0	306	3	US-09-147-935A-9
c 9	20	100.0	306	3	US-09-147-935A-10
c 10	20	100.0	306	3	US-09-147-935A-11
c 11	20	100.0	306	3	US-09-147-935A-12
c 12	20	100.0	306	3	US-09-147-935A-13
c 13	20	100.0	306	3	US-09-147-935A-14
c 14	20	100.0	306	3	US-09-147-935A-15
c 15	20	100.0	306	3	US-09-147-935A-17
c 16	20	100.0	306	3	US-09-147-935A-18
c 17	20	100.0	306	3	US-09-147-935A-22
c 18	20	100.0	306	3	US-09-147-935A-27
c 19	20	100.0	306	3	US-09-147-935A-28
c 20	20	100.0	306	3	US-09-147-935A-29
c 21	20	100.0	306	3	US-09-147-935A-31
c 22	20	100.0	306	3	US-09-147-935A-31
c 23	20	100.0	306	3	US-09-147-935A-32
c 24	20	100.0	306	3	US-09-147-935A-33
c 25	20	100.0	306	3	US-09-147-935A-35
c 26	20	100.0	306	3	US-09-147-935A-36
c 27	20	100.0	306	3	US-09-147-935A-37

c 28	20	100.0	306	3	US-09-147-935A-38
c 29	20	100.0	306	3	US-09-147-935A-39
c 30	20	100.0	306	3	US-09-147-935A-40
c 31	20	100.0	306	3	US-09-147-935A-43
c 32	20	100.0	306	3	US-09-147-935A-46
c 33	20	100.0	306	3	US-09-147-935A-47
c 34	20	100.0	319	4	US-08-750-088A-35
c 35	20	100.0	324	4	US-08-750-088A-36
c 36	18.4	92.0	306	3	US-09-147-935A-20
c 37	18.4	92.0	306	3	US-09-147-935A-21
c 38	18.4	92.0	306	3	US-09-147-935A-23
c 39	18.4	92.0	306	3	US-09-147-935A-25
c 40	18.4	92.0	306	3	US-09-147-935A-26
c 41	18.4	92.0	306	3	US-09-147-935A-34
c 42	18.4	92.0	306	3	US-09-147-935A-42
c 43	18.4	92.0	306	3	US-09-147-935A-44
c 44	16.8	84.0	306	3	US-09-147-935A-2
c 45	16.8	84.0	306	3	US-09-147-935A-6

ALIGNMENTS

RESULT 1
US-08-750-088A-69/c
; Sequence 69, Application US/08750088A
; Patent No. 6329138
; GENERAL INFORMATION:
; APPLICANT: DE BEENHOUWER, HANS
; APPLICANT: PORTAELS, FRAN OISE
; APPLICANT: MACHTELINCKX, LIEVE
; APPLICANT: JANNES, GEERT
; APPLICANT: ROSSAU, RUDI
; TITLE OF INVENTION: METHOD FOR DETECTION OF THE ANTIBIOTIC
; TITLE OF INVENTION: RESISTANCE SPECTRUM OF MYCOBACTERIUM SPECIES
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: US
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/750,088A
; FILING DATE: 21-FEB-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: GOLDSTEIN, JORGE A.
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 1657.0010000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 228 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-750-088A-69

Query Match 100.0%; Score 20; DB 4; Length 228;

Best Local Similarity 100.0%; Pred. No. 1.4; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

QY 1 GGATGTTGATCAGGTCGTCG 20

Db 88 GGATGTTGATCAGGGTCTGC 69
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RESULT 2

US-08-750-088A-37/c
; Sequence 37, Application US/08750088A
; Patent No. 6329138
; GENERAL INFORMATION:
; APPLICANT: DE BEENHOWER, HANS
; APPLICANT: PORTAELS, FRAN OISE
; APPLICANT: MACHTELINCKX, LIEVE
; APPLICANT: JANNES, GEERT
; APPLICANT: ROSSAU, RUDI
; TITLE OF INVENTION: METHOD FOR DETECTION OF THE ANTIBIOTIC
; TITLE OF INVENTION: RESISTANCE SPECTRUM OF MYCOBACTERIUM SPECIES
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: US
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/750,088A
; FILING DATE: 21-FEB-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: GOLDSTEIN, JORGE A.
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 1657.0010000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 254 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-750-088A-37

Query Match 100.0%; Score 20; DB 4; Length 254;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATGTTGATCAGGGTCTGC 20
Db 94 GGATGTTGATCAGGGTCTGC 75
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RESULT 3

US-09-147-935A-1/c
; Sequence 1, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
; APPLICANT: KOOK, Yoon-Hoh
; APPLICANT: KIM, Bum-Joon
; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
; FILE REFERENCE: 0136/0F425
; CURRENT APPLICATION NUMBER: US/09/147,935A
; CURRENT FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/KR98/00228
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 50

; SOFTWARE: KOPATIN 1.0
; SEQ ID NO 1
; LENGTH: 306
; TYPE: DNA
; ORGANISM: Mycobacterium abscessus
US-09-147-935A-1

Query Match 100.0%; Score 20; DB 3; Length 306;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATGTTGATCAGGGTCTGC 20
Db 129 GGATGTTGATCAGGGTCTGC 110
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RESULT 4

US-09-147-935A-3/c
; Sequence 3, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
; APPLICANT: KOOK, Yoon-Hoh
; APPLICANT: KIM, Bum-Joon
; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
; FILE REFERENCE: 0136/0F425
; CURRENT APPLICATION NUMBER: US/09/147,935A
; CURRENT FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/KR98/00228
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: KOPATIN 1.0
; SEQ ID NO 3
; LENGTH: 306
; TYPE: DNA
; ORGANISM: Mycobacterium asiaticum
US-09-147-935A-3

Query Match 100.0%; Score 20; DB 3; Length 306;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATGTTGATCAGGGTCTGC 20
Db 129 GGATGTTGATCAGGGTCTGC 110
|||||

RESULT 5

US-09-147-935A-4/c
; Sequence 4, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
; APPLICANT: KOOK, Yoon-Hoh
; APPLICANT: KIM, Bum-Joon
; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
; FILE REFERENCE: 0136/0F425
; CURRENT APPLICATION NUMBER: US/09/147,935A
; CURRENT FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/KR98/00228
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: KOPATIN 1.0
; SEQ ID NO 4
; LENGTH: 306
; TYPE: DNA
; ORGANISM: Mycobacterium aurum
US-09-147-935A-4

Query Match 100.0%; Score 20; DB 3; Length 306;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATGTTGATCAGGGTCTGC 20
|||||
Db 129 GGATGTTGATCAGGGTCTGC 110

RESULT 6

US-09-147-935A-5/c
; Sequence 5, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
; APPLICANT: KOOK, Yoon-Hoh
; APPLICANT: KIM, Bum-Joon
; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
; TITLE OF INVENTION: COMPARATIVE SEQUENCE ANALYSIS OF rpoB GENE
; FILE REFERENCE: 0136/OF425
; CURRENT APPLICATION NUMBER: US/09/147,935A
; CURRENT FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/KR98/00228
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: KOPATIN 1.0
; SEQ ID NO 5
; LENGTH: 306
; TYPE: DNA
; ORGANISM: Mycobacterium avium
US-09-147-935A-5

Query Match 100.0%; Score 20; DB 3; Length 306;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATGTTGATCAGGGTCTGC 20
|||||
Db 129 GGATGTTGATCAGGGTCTGC 110

RESULT 7

US-09-147-935A-8/c
; Sequence 8, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
; APPLICANT: KOOK, Yoon-Hoh
; APPLICANT: KIM, Bum-Joon
; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
; TITLE OF INVENTION: COMPARATIVE SEQUENCE ANALYSIS OF rpoB GENE
; FILE REFERENCE: 0136/OF425
; CURRENT APPLICATION NUMBER: US/09/147,935A
; CURRENT FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/KR98/00228
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: KOPATIN 1.0
; SEQ ID NO 8
; LENGTH: 306
; TYPE: DNA
; ORGANISM: Mycobacterium celatum Type1
US-09-147-935A-8

Query Match 100.0%; Score 20; DB 3; Length 306;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATGTTGATCAGGGTCTGC 20
|||||
Db 129 GGATGTTGATCAGGGTCTGC 110

RESULT 8

US-09-147-935A-9/c
; Sequence 9, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
; APPLICANT: KOOK, Yoon-Hoh

; APPLICANT: KIM, Bum-Joon
; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
; TITLE OF INVENTION: COMPARATIVE SEQUENCE ANALYSIS OF rpoB GENE
; FILE REFERENCE: 0136/OF425
; CURRENT APPLICATION NUMBER: US/09/147,935A
; CURRENT FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/KR98/00228
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: KOPATIN 1.0
; SEQ ID NO 9
; LENGTH: 306
; TYPE: DNA
; ORGANISM: Mycobacterium celatum Type2
US-09-147-935A-9

Query Match 100.0%; Score 20; DB 3; Length 306;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATGTTGATCAGGGTCTGC 20
|||||
Db 129 GGATGTTGATCAGGGTCTGC 110

RESULT 9

US-09-147-935A-10/c
; Sequence 10, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
; APPLICANT: KOOK, Yoon-Hoh
; APPLICANT: KIM, Bum-Joon
; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
; TITLE OF INVENTION: COMPARATIVE SEQUENCE ANALYSIS OF rpoB GENE
; FILE REFERENCE: 0136/OF425
; CURRENT APPLICATION NUMBER: US/09/147,935A
; CURRENT FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/KR98/00228
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: KOPATIN 1.0
; SEQ ID NO 10
; LENGTH: 306
; TYPE: DNA
; ORGANISM: Mycobacterium chelonae
US-09-147-935A-10

Query Match 100.0%; Score 20; DB 3; Length 306;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATGTTGATCAGGGTCTGC 20
|||||
Db 129 GGATGTTGATCAGGGTCTGC 110

RESULT 10

US-09-147-935A-11/c
; Sequence 11, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
; APPLICANT: KOOK, Yoon-Hoh
; APPLICANT: KIM, Bum-Joon
; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
; TITLE OF INVENTION: COMPARATIVE SEQUENCE ANALYSIS OF rpoB GENE
; FILE REFERENCE: 0136/OF425
; CURRENT APPLICATION NUMBER: US/09/147,935A
; CURRENT FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/KR98/00228
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: KOPATIN 1.0
; SEQ ID NO 11

; LENGTH: 306
; TYPE: DNA
; ORGANISM: Mycobacterium chitae
US-09-147-935A-11

Query Match 100.0%; Score 20; DB 3; Length 306;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATGTTGATCAGGGTCTGC 20
|||||

Db 129 GGATGTTGATCAGGGTCTGC 110

RESULT 11

US-09-147-935A-12/c
; Sequence 12, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
; APPLICANT: KOOK, Yoon-Hoh
; APPLICANT: KIM, Bum-Joon
; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
; FILE REFERENCE: 0136/0F425
; CURRENT APPLICATION NUMBER: US/09/147,935A
; CURRENT FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/KR98/00228
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: KOPATIN 1.0
; SEQ ID NO 12
; LENGTH: 306
; TYPE: DNA
; ORGANISM: Mycobacterium fallax
US-09-147-935A-12

Query Match 100.0%; Score 20; DB 3; Length 306;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATGTTGATCAGGGTCTGC 20
|||||

Db 129 GGATGTTGATCAGGGTCTGC 110

RESULT 12

US-09-147-935A-13/c
; Sequence 13, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
; APPLICANT: KOOK, Yoon-Hoh
; APPLICANT: KIM, Bum-Joon
; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
; FILE REFERENCE: 0136/0F425
; CURRENT APPLICATION NUMBER: US/09/147,935A
; CURRENT FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/KR98/00228
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: KOPATIN 1.0
; SEQ ID NO 13
; LENGTH: 306
; TYPE: DNA
; ORGANISM: Mycobacterium flavescens
US-09-147-935A-13

Query Match 100.0%; Score 20; DB 3; Length 306;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATGTTGATCAGGGTCTGC 20
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Db 129 GGATGTTGATCAGGGTCTGC 110

RESULT 13

US-09-147-935A-14/c
; Sequence 14, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
; APPLICANT: KOOK, Yoon-Hoh
; APPLICANT: KIM, Bum-Joon
; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
; FILE REFERENCE: 0136/0F425
; CURRENT APPLICATION NUMBER: US/09/147,935A
; CURRENT FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/KR98/00228
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: KOPATIN 1.0
; SEQ ID NO 14
; LENGTH: 306
; TYPE: DNA
; ORGANISM: Mycobacterium fortuitum
US-09-147-935A-14

Query Match 100.0%; Score 20; DB 3; Length 306;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATGTTGATCAGGGTCTGC 20
|||||

Db 129 GGATGTTGATCAGGGTCTGC 110

RESULT 14

US-09-147-935A-15/c
; Sequence 15, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
; APPLICANT: KOOK, Yoon-Hoh
; APPLICANT: KIM, Bum-Joon
; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
; FILE REFERENCE: 0136/0F425
; CURRENT APPLICATION NUMBER: US/09/147,935A
; CURRENT FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/KR98/00228
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: KOPATIN 1.0
; SEQ ID NO 15
; LENGTH: 306
; TYPE: DNA
; ORGANISM: Mycobacterium fortuitum 49403
US-09-147-935A-15

Query Match 100.0%; Score 20; DB 3; Length 306;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATGTTGATCAGGGTCTGC 20
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Db 129 GGATGTTGATCAGGGTCTGC 110

RESULT 15

US-09-147-935A-17/c
; Sequence 17, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
; APPLICANT: KOOK, Yoon-Hoh
; APPLICANT: KIM, Bum-Joon
; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY

; TITLE OF INVENTION: COMPARATIVE SEQUENCE ANALYSIS OF rpoB GENE
; FILE REFERENCE: 0136/0F425
; CURRENT APPLICATION NUMBER: US/09/147,935A
; CURRENT FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/KR98/00228
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: KOPATIN 1.0
; SEQ ID NO 17
; LENGTH: 306
; TYPE: DNA
; ORGANISM: Mycobacterium genavense
US-09-147-935A-17

Query Match 100.0%; Score 20; DB 3; Length 306;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGATGTTGATCAGGCTGTC 20
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Db 129 GGATGTTGATCAGGCTGTC 110

Search completed: September 17, 2003, 23:21:04
Job time : 3.61305 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 17, 2003, 13:09:27 ; Search time 12.4009 Seconds
(without alignments)
3967.311 Million cell updates/sec

Title: US-09-697-123B-26

Perfect score: 20

Sequence: 1 ggatgttgatcagggtctgc 20

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Gapop 10.0 , Gapext 1.0

Searched: 1660708 seqs, 122959015 residues

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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c 3	20	100.0	319	12	US-10-339-604-35
c 4	20	100.0	324	12	US-10-339-604-36
c 5	20	100.0	652	10	US-09-285-306-30
c 6	20	100.0	652	10	US-09-285-306-38
c 7	20	100.0	687	10	US-09-285-306-18
c 8	20	100.0	687	10	US-09-285-306-19
c 9	20	100.0	687	10	US-09-285-306-20
c 10	20	100.0	687	10	US-09-285-306-21
c 11	20	100.0	687	10	US-09-285-306-22
c 12	20	100.0	687	10	US-09-285-306-23
c 13	20	100.0	687	10	US-09-285-306-25
c 14	20	100.0	687	10	US-09-285-306-26
c 15	20	100.0	687	10	US-09-285-306-27
c 16	20	100.0	687	10	US-09-285-306-48

c 17	20	100.0	687	10	US-09-285-306-49
c 18	20	100.0	687	10	US-09-285-306-50
c 19	20	100.0	687	10	US-09-285-306-58
c 20	20	100.0	687	10	US-09-285-306-59
c 21	20	100.0	687	10	US-09-285-306-60
c 22	20	100.0	687	10	US-09-285-306-61
c 23	20	100.0	687	10	US-09-285-306-62
c 24	20	100.0	687	10	US-09-285-306-63
c 25	20	100.0	687	10	US-09-285-306-80
c 26	20	100.0	687	10	US-09-285-306-81
c 27	20	100.0	687	10	US-09-285-306-82
c 28	20	100.0	687	10	US-09-285-306-97
c 29	20	100.0	687	10	US-09-285-306-98
c 30	20	100.0	687	10	US-09-285-306-99
c 31	20	100.0	687	10	US-09-285-306-100
c 32	20	100.0	687	10	US-09-285-306-137
c 33	20	100.0	687	10	US-09-285-306-138
c 34	20	100.0	687	10	US-09-285-306-139
c 35	20	100.0	687	10	US-09-285-306-140
c 36	20	100.0	687	10	US-09-285-306-141
c 37	20	100.0	687	10	US-09-285-306-142
c 38	20	100.0	687	10	US-09-285-306-145
c 39	20	100.0	687	10	US-09-285-306-146
c 40	20	100.0	687	10	US-09-285-306-148
c 41	20	100.0	687	10	US-09-285-306-149
c 42	20	100.0	687	10	US-09-285-306-150
c 43	20	100.0	687	10	US-09-285-306-151
c 44	20	100.0	687	10	US-09-285-306-152
c 45	20	100.0	687	10	US-09-285-306-158

ALIGNMENTS

RESULT 1

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US-10-339-604-69/c
; Sequence 69, Application US/10339604
; Publication No. US20030152982A1
; GENERAL INFORMATION:
; APPLICANT: DE BEENHOUWER, HANS
; APPLICANT: PORTIELS, FRANCOISE
; APPLICANT: MACHTELINCKX, LIEVE
; APPLICANT: JANNES, GEERT
; APPLICANT: ROSSAU, RUDI
; TITLE OF INVENTION: Oligonucleotide Molecules for Use in Detection of Mycobacter
; FILE REFERENCE: 1657.0010001
; CURRENT APPLICATION NUMBER: US/10/339,604
; CURRENT FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: US/09/722,319
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 08/750,088
; PRIOR FILING DATE: 1996-12-06
; PRIOR APPLICATION NUMBER: PCT/EP95/02230
; PRIOR FILING DATE: 1995-06-09
; PRIOR APPLICATION NUMBER: EP 94870093.5
; PRIOR FILING DATE: 1994-06-09
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 69
; LENGTH: 228
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe
; NAME/KEY: misc_feature
; LOCATION: (8)..(8)
; OTHER INFORMATION: n can be any nucleotide
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (33)..(33)
; OTHER INFORMATION: n can be any nucleotide
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RESULT 9
US-09-285-306-20/c
; Sequence 20, Application US/09285306A
; Publication No. US20020187467A1
; GENERAL INFORMATION:
; APPLICANT: Gingeras, Thomas
; APPLICANT: Drenkow, Jorg
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Mycobacterial rpoB Sequences
; FILE REFERENCE: 018547-018570US
; CURRENT APPLICATION NUMBER: US/09/285,306A
; CURRENT FILING DATE: 1999-04-02
; EARLIER APPLICATION NUMBER: US 60/080,616
; EARLIER FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 181
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 687
; TYPE: DNA
; ORGANISM: Mycobacterium avium
US-09-285-306-20

Query Match      100.0%; Score 20; DB 10; Length 687;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATGTTGATCAGGGTCTGC 20
   |||||||||||||||||||
Db 35 GGATGTTGATCAGGGTCTGC 16

RESULT 10
US-09-285-306-21/c
; Sequence 21, Application US/09285306A
; Publication No. US20020187467A1
; GENERAL INFORMATION:
; APPLICANT: Gingeras, Thomas
; APPLICANT: Drenkow, Jorg
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Mycobacterial rpoB Sequences
; FILE REFERENCE: 018547-018570US
; CURRENT APPLICATION NUMBER: US/09/285,306A
; CURRENT FILING DATE: 1999-04-02
; EARLIER APPLICATION NUMBER: US 60/080,616
; EARLIER FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 181
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 687
; TYPE: DNA
; ORGANISM: Mycobacterium avium
US-09-285-306-21

Query Match      100.0%; Score 20; DB 10; Length 687;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATGTTGATCAGGGTCTGC 20
   |||||||||||||||||||
Db 35 GGATGTTGATCAGGGTCTGC 16

RESULT 11
US-09-285-306-22/c
; Sequence 22, Application US/09285306A
; Publication No. US20020187467A1
; GENERAL INFORMATION:
; APPLICANT: Gingeras, Thomas
; APPLICANT: Drenkow, Jorg
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Mycobacterial rpoB Sequences
; FILE REFERENCE: 018547-018570US
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; CURRENT APPLICATION NUMBER: US/09/285,306A
; CURRENT FILING DATE: 1999-04-02
; EARLIER APPLICATION NUMBER: US 60/080,616
; EARLIER FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 181
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 687
; TYPE: DNA
; ORGANISM: Mycobacterium avium
US-09-285-306-22

Query Match      100.0%; Score 20; DB 10; Length 687;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATGTTGATCAGGGTCTGC 20
   |||||||||||||||||||
Db 35 GGATGTTGATCAGGGTCTGC 16

RESULT 12
US-09-285-306-23/c
; Sequence 23, Application US/09285306A
; Publication No. US20020187467A1
; GENERAL INFORMATION:
; APPLICANT: Gingeras, Thomas
; APPLICANT: Drenkow, Jorg
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Mycobacterial rpoB Sequences
; FILE REFERENCE: 018547-018570US
; CURRENT APPLICATION NUMBER: US/09/285,306A
; CURRENT FILING DATE: 1999-04-02
; EARLIER APPLICATION NUMBER: US 60/080,616
; EARLIER FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 181
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 687
; TYPE: DNA
; ORGANISM: Mycobacterium avium
US-09-285-306-23

Query Match      100.0%; Score 20; DB 10; Length 687;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATGTTGATCAGGGTCTGC 20
   |||||||||||||||||||
Db 35 GGATGTTGATCAGGGTCTGC 16

RESULT 13
US-09-285-306-25/c
; Sequence 25, Application US/09285306A
; Publication No. US20020187467A1
; GENERAL INFORMATION:
; APPLICANT: Gingeras, Thomas
; APPLICANT: Drenkow, Jorg
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Mycobacterial rpoB Sequences
; FILE REFERENCE: 018547-018570US
; CURRENT APPLICATION NUMBER: US/09/285,306A
; CURRENT FILING DATE: 1999-04-02
; EARLIER APPLICATION NUMBER: US 60/080,616
; EARLIER FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 181
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 687
; TYPE: DNA
; ORGANISM: Mycobacterium avium
US-09-285-306-25
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Job time : 12.4009 secs

Query Match 100.0%; Score 20; DB 10; Length 687;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATGTTGATCAGGGTCTGC 20
|||||
Db 35 GGATGTTGATCAGGGTCTGC 16

RESULT 14
US-09-285-306-26/c
; Sequence 26, Application US/09285306A
; Publication No. US20020187467A1
; GENERAL INFORMATION:
; APPLICANT: Gingeras, Thomas
; APPLICANT: Drenkow, Jorg
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Mycobacterial rpoB Sequences
; FILE REFERENCE: 018547-018570US
; CURRENT APPLICATION NUMBER: US/09/285,306A
; CURRENT FILING DATE: 1999-04-02
; EARLIER APPLICATION NUMBER: US 60/080,616
; EARLIER FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 181
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 687
; TYPE: DNA
; ORGANISM: Mycobacterium avium
US-09-285-306-26

Query Match 100.0%; Score 20; DB 10; Length 687;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATGTTGATCAGGGTCTGC 20
|||||
Db 35 GGATGTTGATCAGGGTCTGC 16

RESULT 15
US-09-285-306-27/c
; Sequence 27, Application US/09285306A
; Publication No. US20020187467A1
; GENERAL INFORMATION:
; APPLICANT: Gingeras, Thomas
; APPLICANT: Drenkow, Jorg
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Mycobacterial rpoB Sequences
; FILE REFERENCE: 018547-018570US
; CURRENT APPLICATION NUMBER: US/09/285,306A
; CURRENT FILING DATE: 1999-04-02
; EARLIER APPLICATION NUMBER: US 60/080,616
; EARLIER FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 181
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 687
; TYPE: DNA
; ORGANISM: Mycobacterium avium complex (MAC)
US-09-285-306-27

Query Match 100.0%; Score 20; DB 10; Length 687;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATGTTGATCAGGGTCTGC 20
|||||
Db 35 GGATGTTGATCAGGGTCTGC 16

Search completed: September 17, 2003, 23:30:46

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OM nucleic - nucleic search, using sw model

Run on: September 17, 2003, 11:54:34 ; Search time 30.1105 Seconds
(without alignments)
3049.028 Million cell updates/sec

Title: US-09-697-123B-3

Perfect score: 208

Sequence: 1 tcaagagaagcgctacagc.....ccggtggagaccgacacat 208

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents.NA.*

- 1: /cgn2_6/ptodata/1/ina/5A.COMB.seq.*
- 2: /cgn2_6/ptodata/1/ina/5B.COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A.COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B.COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/PCRUS.COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	171.2	82.3	970	1 US-08-250-030-1	Sequence 1, Appli
2	171.2	82.3	970	5 PCT-US95-06790-1	Sequence 1, Appli
3	171.2	82.3	4403765	3 US-09-103-840A-2	Sequence 2, Appli
4	171.2	82.3	4411529	3 US-09-103-840A-1	Sequence 1, Appli
5	144	69.2	3447	2 US-08-313-185-57	Sequence 57, Appli
6	144	69.2	3447	3 US-09-082-614A-57	Sequence 57, Appli
7	45.4	22.3	6085	3 US-09-028-603-4	Sequence 4, Appli
8	43.4	20.9	924	4 US-09-252-991A-969	Sequence 969, App
9	43.4	20.9	939	4 US-09-252-991A-925	Sequence 925, App
c 10	43	20.7	276	4 US-09-252-991A-8365	Sequence 8365, Ap
c 11	43	20.7	768	4 US-09-252-991A-1114	Sequence 1114, Ap
c 12	43	20.7	1731	4 US-09-252-991A-8512	Sequence 8512, Ap
c 13	40.6	19.5	4403765	3 US-09-103-840A-2	Sequence 2, Appli
c 14	40.2	19.3	4411529	3 US-09-103-840A-1	Sequence 1, Appli
c 15	39.8	19.1	1414	4 US-09-501-115-5	Sequence 5, Appli
c 16	39.6	19.0	1089	4 US-09-252-991A-14778	Sequence 14778, A
c 17	39.6	19.0	1347	4 US-09-252-991A-14972	Sequence 14972, A
c 18	39.6	19.0	1482	4 US-09-252-991A-14656	Sequence 14656, A
c 19	39.2	18.8	1074	4 US-09-252-991A-5833	Sequence 5833, Ap
c 20	39.2	18.8	1275	4 US-09-252-991A-5813	Sequence 5813, Ap
c 21	39.2	18.8	1554	4 US-09-252-991A-5777	Sequence 5777, Ap
c 22	39.2	18.8	5046	4 US-09-548-938A-5	Sequence 5, Appli
c 23	38.8	18.7	2244	1 US-08-476-519-10	Sequence 10, Appli
c 24	38.8	18.7	2244	5 PCT-US95-09323-10	Sequence 10, Appli
c 25	38.8	18.7	2334	1 US-08-476-519-1	Sequence 1, Appli
c 26	38.8	18.7	2334	5 PCT-US95-09323-1	Sequence 1, Appli
c 27	38.6	18.6	1014	4 US-09-252-991A-2663	Sequence 2663, Ap

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28 38.6 18.6 1155 4 US-09-252-991A-2762 Sequence 2762, Ap
c 29 38.6 18.6 1233 4 US-09-252-991A-3203 Sequence 3203, Ap
c 30 38 18.3 657 4 US-09-252-991A-13503 Sequence 13503, A
31 38 18.3 981 4 US-09-252-991A-5092 Sequence 5092, Ap
32 38 18.3 1050 4 US-09-252-991A-13134 Sequence 13134, A
33 38 18.3 1149 4 US-09-252-991A-5033 Sequence 5033, Ap
c 34 38 18.3 1707 4 US-09-252-991A-12666 Sequence 12666, A
35 38 18.3 1836 4 US-09-252-991A-13295 Sequence 13295, A
36 37.6 18.1 12588 2 US-08-387-942C-1 Sequence 1, Appli
37 37.4 18.0 792 4 US-09-252-991A-10944 Sequence 10944, A
c 38 37.4 18.0 1209 4 US-09-252-991A-11118 Sequence 11118, A
39 37.4 18.0 1632 4 US-09-252-991A-11079 Sequence 11079, A
40 37 17.8 20235 1 US-07-642-734C-3 Sequence 3, Appli
41 37 17.8 20235 3 US-08-439-009A-3 Sequence 3, Appli
c 42 37 17.8 44377 2 US-08-804-227C-7 Sequence 7, Appli
c 43 37 17.8 44377 2 US-08-804-198-1 Sequence 1, Appli
c 44 36.8 17.7 969 4 US-09-252-991A-12911 Sequence 12911, A
45 36.8 17.7 1257 4 US-09-252-991A-12881 Sequence 12881, A

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ALIGNMENTS

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RESULT 1
US-08-250-030-1
; Sequence 1, Application US/08250030
; Patent No. 5643723
; GENERAL INFORMATION:
; APPLICANT: Persing, David H.
; TITLE OF INVENTION: Detection of a Genetic Locus Encoding
; TITLE OF INVENTION: Resistance to Rifampin in Mycobacterial Cultures and in
; TITLE OF INVENTION: Clinical Specimens
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Schweigman, Lundberg & Woessner
; STREET: 3500 IDS Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/250,030
; FILING DATE: 26-MAY-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Muetting, Ann M.
; REGISTRATION NUMBER: 33,977
; REFERENCE/DOCKET NUMBER: 150.105US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-339-0331
; TELEFAX: 612-339-3061
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 970 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-250-030-1

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Query Match 82.3%; Score 171.2; DB 1; Length 970;
Best Local Similarity 88.9%; Pred. No. 3.2e-34;
Matches 185; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 1 TCAAGAGAAGCGCTAGACCTGGCCCGTGGCCGCTACAAAGTCAACAAGAGCTCG 60

DB 26 TCAAGAGAAGCGCTAGACCTGGCCCGTGGCCGCTACAAAGTCAACAAGAGCTCG 85

Best Local Similarity 88.9%; Pred. No. 9.5e-34;
Matches 185; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 1 TCAAGAGAGAGCGTAGGACCTGGCCCGTGTGCGCGCTACAGGTCACACAGAGCTCG 60
DB 760688 TCAAGGAGAGCGTAGGACCTGGCCCGTGTGCGCGCTACAGGTCACACAGAGCTCG 760747
QY 61 GCGTCAGCTCGGGGATCCGATCACACAGCTCCAGCTGACCGAAGAGAGCTCGTCGCGCA 120
DB 760748 GCGTCAGCTCGGGGAGCCCATCACGTCGTGAGAGCTGACCGAAGAGAGCTCGTCGCGCA 760807
QY 121 CCATCGAGTACTGGTCCGCTCTGCGAGGGTTCAGCACAGATGACCGTTCGCGGCGCA 180
DB 760808 CCATCGAATATCTGTCGCTTGCACAGGGTTCAGACACAGATGACCGTTCGCGGCGCG 760867
QY 181 CCGAGGTCGCGGTGGAGACCGAGCAT 208
DB 760868 TCGAGGTCCGCGTGGAAACCGAGCAT 760895

RESULT 5

US-08-313-185-57
; Sequence 57, Application US/08313185
; Patent No. 5851763
; GENERAL INFORMATION:
; APPLICANT: Heym, Beate
; APPLICANT: Cole, Stewart
; APPLICANT: Young, Douglas
; APPLICANT: Zhang, Ying
; APPLICANT: Honore, Nadine
; APPLICANT: Telenti, Amalio
; APPLICANT: Bodmer, Thomas
; TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
; TITLE OF INVENTION: in Mycobacterium Tuberculosis
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/313,185
; FILING DATE: 12-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 02356.0068-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4400
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3447 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-313-185-57

Query Match 69.2%; Score 144; DB 2; Length 3447;
Best Local Similarity 80.8%; Pred. No. 2.2e-27;
Matches 168; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 1 TCAAGGAGAGCGCTACGACCTGGCCGCTGTGCGCGCTACAGGTCACACAGAGCTCG 60

DB 809 TCAAGGAGAAACGCTAGGACCTGGCCAGGGTGGTTCGTTTCAAGGTCAACAAGCTCG 868
QY 61 GCGTCAGCTCGGGGATCCGATCACACAGTCCAGCTGACCGGAGAGAGCTCGTCGCGCA 120
DB 869 GGTTCAGCGCGGTGAGTTGATCACTGTCACGCTGACCGAAGAGAGTGTGTCGCGCA 928
QY 121 CCATCGAGTACTGGTCCGCTCTGCGAGGGTTCAGCACAGATGACCGTTCGCGGCGCA 180
DB 929 CCATAGAGTACTGGTTCGCTCTGATGAGGGTTCAGTGGGTCAGTGTCCAGAGTGGGG 988
QY 181 CCGAGGTCGCGGTGGAGACCGAGCAT 208
DB 989 TAGAAGTCCAGTGGAAACTGACGATAT 1016

RESULT 6

US-09-082-614A-57
; Sequence 57, Application US/09082614A
; Patent No. 6124098
; GENERAL INFORMATION:
; APPLICANT: Heym, Beate
; APPLICANT: Cole, Stewart
; APPLICANT: Young, Douglas
; APPLICANT: Zhang, Ying
; APPLICANT: Honore, Nadine
; APPLICANT: Telenti, Amalio
; APPLICANT: Bodmer, Thomas
; TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
; TITLE OF INVENTION: in Mycobacterium Tuberculosis
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/082,614A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/313,185
; FILING DATE: 12-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 02356.0068-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4400
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3447 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-082-614A-57

Query Match 69.2%; Score 144; DB 3; Length 3447;
Best Local Similarity 80.8%; Pred. No. 2.2e-27;
Matches 168; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 1 TCAAGGAGAGCGCTACGACCTGGCCGCTGTGCGCGCTACAGGTCACACAGAGCTCG 60

Db 809 TCAGGAGAAACGCTACGACTGCGCCAGGTTGGTGTACAAAGGTCAACAAGAACTCG 868
QY 61 GCCTGCACGTCGCGCATCGATCACAGCTCCACGCTGACCGAAGAGACGTGTCGCCA 120
Db 869 GGTTCACCGCGGTGAGTTGATCAGCTCTCCAGCTGACCGAAGAGAGTGTGTCGCCA 928
QY 121 CCATCGAGTACCTGTCGCTGTCACGAGGTCAGACACAGATGACCGTTCGCGGCGGCA 180
Db 929 CCATAGAGTACCTGTCGCTGTCATGAGGTCAGTCGACAAATGACTTCCACAGGTGGG 988
QY 181 CCGAGTTCGCTGCGAGCCGACGACAT 208
Db 989 TAGAAGTCCAGTGGAAACTGACGATAT 1016

RESULT 7

US-09-029-603-4
; Sequence 4, Application US/09029603
; Patent No. 6210935
; GENERAL INFORMATION:
; APPLICANT: Schupp, Thomas
; APPLICANT: Engel, Natalie
; APPLICANT: Bietenhader, Jurg
; APPLICANT: Toupet, Christine
; APPLICANT: Pospiech, Andreas
; TITLE OF INVENTION: Staurosporin Biosynthesis Gene Clusters
; FILE REFERENCE: 4-20555/A/PCT
; CURRENT APPLICATION NUMBER: US/09/029,603
; CURRENT FILING DATE: 1998-03-20
; EARLIER APPLICATION NUMBER: PCT/EP96/03643
; EARLIER FILING DATE: 1996-08-19
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 6085
; TYPE: DNA
; ORGANISM: Streptomyces longisporoflavus
; FEATURE:
; NAME/KEY: misc_RNA
; LOCATION: (378)..(1665)
; OTHER INFORMATION: ORF
; FEATURE:
; NAME/KEY: misc_RNA
; LOCATION: (1747)..(2553)
; OTHER INFORMATION: ORF
; FEATURE:
; NAME/KEY: misc_RNA
; LOCATION: (2593)..(4011)
; OTHER INFORMATION: ORF
; FEATURE:
; NAME/KEY: misc_RNA
; LOCATION: (4013)..(4999)
; OTHER INFORMATION: ORF
; FEATURE:
; NAME/KEY: misc_RNA
; LOCATION: (5071)..(6085)
; OTHER INFORMATION: ORF
US-09-029-603-4

Query Match 22.3%; Score 46.4; DB 3; Length 6085;
Best Local Similarity 61.7%; Pred. No. 0.0044;
Matches 74; Conservative 0; Mismatches 46; Indels 0; Gaps 0;
QY 18 GACCTGGCCGCTGTCGCGCTGCTACAAAGTCAACAAGAGCTGGGCTGCACTGCGGAT 77
Db 1017 GAGTGGACCGCGCGCGCGGACGACCGGACGAGCTGCTCACCTCTCTGTCGCGGCC 1076
QY 78 CCGATCACAGTCCACGCTGACCGAAGAGACGCTGTCGCCACCATCGATCTGCTC 137
Db 1077 CGGACACCGGATCAACGCTCAGCTGACGCGCATGCTGGCACCTGGCTCCATCTGCTC 1136

RESULT 8

Query Match 22.3%; Score 46.4; DB 3; Length 6085;
Best Local Similarity 61.7%; Pred. No. 0.0044;
Matches 74; Conservative 0; Mismatches 46; Indels 0; Gaps 0;
QY 18 GACCTGGCCGCTGTCGCGCTGCTACAAAGTCAACAAGAGCTGGGCTGCACTGCGGAT 77
Db 1017 GAGTGGACCGCGCGCGCGGACGACCGGACGAGCTGCTCACCTCTCTGTCGCGGCC 1076
QY 78 CCGATCACAGTCCACGCTGACCGAAGAGACGCTGTCGCCACCATCGATCTGCTC 137
Db 1077 CGGACACCGGATCAACGCTCAGCTGACGCGCATGCTGGCACCTGGCTCCATCTGCTC 1136

US-09-252-991A-969
; Sequence 969, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONA;
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 969
; LENGTH: 924
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-969

Query Match 20.9%; Score 43.4; DB 4; Length 924;
Best Local Similarity 53.2%; Pred. No. 0.019;
Matches 92; Conservative 0; Mismatches 81; Indels 0; Gaps 0;
QY 17 CGACCTGGCCGCTGTCGCGCTGCTACAAAGTCAACAAGAGCTGCGCTGACGTCGCGCA 76
Db 597 CGACCGCTGCGCTGCTGTCGCGACCGCGCGGCGGTGGCGCGCGACCTGGTGAG 656
QY 77 TCCGATCACAGCTCCACGCTGACCGAGAGAGAGCTGTCGCCACCATCGAGTACCTGGT 136
Db 657 CACCGACGTGTGGCTCGATGGCCAGGAGAGCGCGCGCGCATCGCCCTGTT 716
QY 137 CCGTCTGCACGAGGTCACGACGATGACCGTTCGCGCGCGCGAGGTTTC 189
Db 717 CCGTCCCTACAGGTGACGCGCGGTGCTCGATGGCGCGCGAGTGTAC 769

RESULT 9

US-09-252-991A-925
; Sequence 925, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONA;
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 925
; LENGTH: 939
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-925

Query Match 20.9%; Score 43.4; DB 4; Length 939;
Best Local Similarity 53.2%; Pred. No. 0.019;
Matches 92; Conservative 0; Mismatches 81; Indels 0; Gaps 0;
QY 17 CGACCTGGCCGCTGTCGCGCTGCTACAAAGTCAACAAGAGCTGCGCTGACGTCGCGCA 76
Db 604 CGACCGCTGCGCTGCTGTCGCGACCGCGCGGCGGTGGCGCGCGACCTGGTGAG 663
QY 77 TCCGATCACAGCTCCACGCTGACCGAAGAGAGAGCTGTCGCCACCATCGAGTACCTGGT 136
Db 664 CACCGACGTGTGGCTCGATGGCCAGGAGAGCGCGCGCGCATCGCCCTGTT 723
QY 137 CCGTCTGCACGAGGTCACGACGATGACCGTTCGCGCGCGCGAGGTTTC 189


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; APPLICANT: Rafalski, Antoni
; TITLE OF INVENTION: Plant Cinnamyl-Alcohol Dehydrogenase Homologs
; FILE REFERENCE: BB1328 US NA
; CURRENT APPLICATION NUMBER: US/09/501,115
; CURRENT FILING DATE: 2000-02-09
; EARLIER APPLICATION NUMBER: 60/119,585
; EARLIER FILING DATE: 1999-February-10
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 5
; LENGTH: 1414
; TYPE: DNA
; ORGANISM: Triticum aestivum
; US-09-501-115-5

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	Query Match	19.1%;	Score 39.8;	DB 4;	Length 1414;
	Best Local Similarity	59.1%;	Pred. No. 0.16;		
	Matches 68;	Conservative	Mismatches 47;	Indels 0;	Gaps 0;
QY	14	CTAGACCTGGCCCGCTGTGTCGCCGCTACAAAGTCTCAAGAAGCTCGCGCTGCACGTGG	73		
Db	385	CTCTGCGCGAGCTCGGACAGCTTCACAAAGGGGTACGAGAGCTACTGCCCCGAGCTGCT	444		
QY	74	CGATCGGATCACCAAGCTCCAGCTGTACCGAAGAAGACGCTCTGCGCCACCATCGAG	128		
Db	445	GGAGAGCTTCAACGGCGTGAAGCTTGGACACAGATGACGGCGCGCCACCAACAAG	499		

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Job time : 52.1605 secs

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RESULT 15
US-09-501-115-5
; Sequence 5, Application US/09501115
; Patent No. 6552249
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Fader, Gary M.

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 17, 2003, 11:54:34 : Search time 108.259 Seconds
(without alignments)
4726.283 Million cell updates/sec

Title: US-09-697-123B-3
Perfect score: 208
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1660708 seqs, 122959015 residues

Total number of hits satisfying chosen parameters: 3321416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_NA:
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4: /cgn2.6/ptodata/1/pubpna/US06_PUBCOMB.seq:
5: /cgn2.6/ptodata/1/pubpna/US07_NEW_PUB.seq:
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10: /cgn2.6/ptodata/1/pubpna/US09_PUBCOMB.seq:
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12: /cgn2.6/ptodata/1/pubpna/US09_NEW_PUB.seq:
13: /cgn2.6/ptodata/1/pubpna/US10A_PUBCOMB.seq:
14: /cgn2.6/ptodata/1/pubpna/US10B_PUBCOMB.seq:
15: /cgn2.6/ptodata/1/pubpna/US10_NEW_PUB.seq:
16: /cgn2.6/ptodata/1/pubpna/US60_NEW_PUB.seq:
17: /cgn2.6/ptodata/1/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	171.2	82.3	3519	10	US-09-712-363-30
2	89.6	43.1	3495	10	US-09-738-626-547
3	89.6	43.1	5096	10	US-09-984-711-5
4	89.6	43.1	5099	10	US-09-887-052-1
5	89.6	43.1	5099	10	US-09-887-052-3
6	89.6	43.1	5099	10	US-09-887-052-5
7	89.6	43.1	5099	12	US-10-076-406-1
8	89.6	43.1	5099	12	US-10-076-406-3
9	89.6	43.1	5099	12	US-10-076-406-5
10	89.6	43.1	5099	13	US-10-075-460-5
11	89.6	43.1	3309400	10	US-09-738-626-1
12	80.4	38.7	3543	14	US-10-156-761-4898
13	80.4	38.7	9025608	14	US-10-156-761-1
14	43.6	21.0	1596	14	US-10-156-761-4136
15	42.8	20.6	2329	10	US-09-816-828-9
16	41.8	20.1	63158	12	US-10-292-198-1

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Sequence 5, Appli
Sequence 3052, Ap
Sequence 5314, Ap
Sequence 4, Appli
Sequence 1, Appli
Sequence 4634, Ap
Sequence 5027, Ap
Sequence 2303, Ap
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Sequence 1568, Ap
Sequence 5959, Ap
Sequence 2136, Ap
Sequence 6155, Ap
Sequence 3330, Ap
Sequence 2540, Ap
Sequence 608, App
Sequence 12478, A
Sequence 139, App
Sequence 139, App
Sequence 3597, Ap
Sequence 4238, Ap
Sequence 5692, Ap
Sequence 5, Appli
Sequence 5464, Ap
Sequence 1901, Ap
Sequence 2561, Ap

17 40.4 19.4 2730 14 US-10-156-761-3553
c 18 40.4 19.4 9025608 14 US-10-156-761-1
19 39.8 19.1 1316 12 US-10-361-460-30
20 39.8 19.1 1414 12 US-10-357-886-5
21 39.8 19.1 1674 14 US-10-156-761-3052
22 39.4 18.9 1287 14 US-10-156-761-5314
23 39.4 18.9 1317 14 US-10-028-245-4
24 39.4 18.9 1826 14 US-10-028-245-1
25 39.2 18.8 1458 14 US-10-156-761-4634
26 38.8 18.7 3675 14 US-10-156-761-5027
27 38.4 18.5 825 14 US-10-156-761-2303
28 38.4 18.5 88421 10 US-09-976-059-1
29 38.2 18.4 603 14 US-10-156-761-1568
30 38.2 18.4 5418 14 US-10-156-761-5959
c 31 38 1290 14 US-10-156-761-2136
32 37.6 18.1 831 14 US-10-156-761-6155
33 37.6 18.1 1629 14 US-10-156-761-3330
34 37.4 18.0 984 14 US-10-156-761-2540
35 37.4 18.0 1857 14 US-10-225-567A-608
36 37.4 18.0 2156 14 US-10-198-846-12478
37 37.2 17.9 843 10 US-09-712-363-139
38 37.2 17.9 1215 14 US-10-156-761-2811
39 37 17.8 402 14 US-10-156-761-3597
40 37 17.8 921 14 US-10-156-761-4238
41 37 17.8 3942 14 US-10-156-761-5692
42 36.8 17.7 1514 14 US-10-289-743-5
43 36.8 17.7 1800 14 US-10-156-761-5464
44 36.8 17.7 2046 14 US-10-156-761-1901
45 36.8 17.7 2217 14 US-10-156-761-2561

ALIGNMENTS

RESULT 1
US-09-712-363-30
; Sequence 30, Application US/09712363
; Patent No. US20020164588A1
; GENERAL INFORMATION:
; APPLICANT: Eisenberg, David
; APPLICANT: Roestlein, Sergio H.
; APPLICANT: Marcotte, Edward M.
; TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND
; TITLE OF INVENTION: INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS
; FILE REFERENCE: 07419-032001
; CURRENT APPLICATION NUMBER: US/09/712.363
; CURRENT FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: PCT/US00/02246
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,531
; PRIOR FILING DATE: 2000-02-01
; PRIOR APPLICATION NUMBER: 60/117,844
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/118,206,
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: 60/126,593
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/134,093
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/134,092
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/165,124
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/165,086
; PRIOR FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 3519
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-09-712-363-30

Query Match 82.3%; Score 171.2; DB 10; Length 3519;
Best Local Similarity 88.9%; Pred. No. 1.3e-41;
Matches 185; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 1 TCAAGAGAACCGCTAGACCTGGCCCGTGTGCGCCGCTACAGGTCAACAGAGACTCG 60
DB 884 TCARGGAGAACGCTAGACCTGGCCCGTGTGCGCCGCTATAAGGTCAACAGAGACTCG 943
QY 61 GCGTCAGCTCGGCGATCCGATCACACAGCTCCAGCTGACCGAGAGAGCGTCGCGCA 120
DB 944 GCTGCACTGCGGAGCCCATACAGCTGCTGAGCGCTGACCGAGAGAGCTGTCGCCA 1003
QY 121 CCATCGAGTACTGGTCCGCTGTCAGAGAGGTCAACAGATGACCGTTCGGCGCGCA 180
DB 1004 CCATGGAATATCTGTCGCTGTCAGAGGGTCAACAGGATGACCGTTCGGCGCGCG 1063
QY 181 CGAGGTTCGCTGAGACCGAGCAT 208
DB 1064 TCGAGGTGCGGTGGAACCGAGGACAT 1091

RESULT 2
US-09-738-626-547
; Sequence 547, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 547
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-547

Query Match 43.1%; Score 89.6; DB 10; Length 3495;
Best Local Similarity 69.0%; Pred. No. 2.3e-17;
Matches 138; Conservative 0; Mismatches 59; Indels 3; Gaps 1;

QY 9 AAGCGCTACGACCTGGCCCGTGTGCGCCGCTACAGGTCAACAGAGCTCGGCTGCAC 68
DB 877 AAGCGCTACGACCTGGCCCGTGTGCTGCTTACAGATCAACCGAAGCTCGGCTT--- 933
QY 69 GTCGGCGATCCGATCACCAGCTCCAGCTGACCGAGAGAGCTGCTCGCCACCATCGAG 128
DB 934 GGTGGCGACCGATGTTGATGACTCTTACTGAGAGGACATCCCAACCATCGAG 993
QY 129 TACCTGTGCTGTCAGAGGTGTCAGACAGATGACCGTTCGGGCGGCGACCGAGTT 188
DB 994 TACCTGGTGGCTGTCAGCGAGGTGAGCGCGCTCATGACTTCTCCAAATGTTGAAGATC 1053
QY 189 CCGGTGGAGACCGAGCAT 208
DB 1054 CCAGTCGAGACCGATGACAT 1073

US-09-984-711-5
; Sequence 5, Application US/09984711
; Patent No. US20020119549A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: STEPHAN, Hans
; APPLICANT: KREUTZER, Caroline
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE rpsL GENE
; FILE REFERENCE: 204209US0
; CURRENT APPLICATION NUMBER: US/09/984,711
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: DE10108230.9
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 5096
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
; OTHER INFORMATION:
US-09-984-711-5

Query Match 43.1%; Score 89.6; DB 10; Length 5096;
Best Local Similarity 69.0%; Pred. No. 2.3e-17;
Matches 138; Conservative 0; Mismatches 59; Indels 3; Gaps 1;

QY 9 AAGCGCTACGACCTGGCCCGTGTGCGCCGCTACAGGTCAACAGAGCTCGGCTGCAC 68
DB 1578 AAGCGCTACGACCTGGCTCGCTGCTTACAGATCAACCGCAAGCTCGGCTT--- 1634
QY 69 GTCGGGATCCGATCACCAGCTCCAGCTGACCGAGAGAGCTGCTCGCCACCATCGAG 128
DB 1635 GGTGGCGACCGATGTTGATGACTTCTGAGAGGAGACATCGCAACCATCGAG 1694
QY 129 TACCTGTGCTGTCAGAGGTGTCAGACAGATGACCGTTCGGGCGGCGACCGAGTT 188
DB 1695 TACCTGTGCTGTCAGCGAGGTGAGCGCGCTCATGACTTCTCCAAATGTTGAAGATC 1754
QY 189 CCGGTGGAGACCGAGCAT 208
DB 1755 CCAGTCGAGACCGATGACAT 1774

RESULT 4
US-09-887-052-1
; Sequence 1, Application US/09887052
; Patent No. US20020119537A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE rpoB GENE
; FILE REFERENCE: 204212US0X
; CURRENT APPLICATION NUMBER: US/09/887,052
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: DE10107229.5
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 5099

[illegible]

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; LENGTH: 5099
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; LENGTH: 5099
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; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
; OTHER INFORMATION:
US-10-076-406-1

Query Match 43.1%; Score 89.6; DB 12; Length 5099;
Best Local Similarity 69.0%; Pred. No. 2.3e-17;
Matches 138; Conservative 0; Mismatches 59; Indels 3; Gaps 1;

QY 9 AAGCGCTACGACCTGGCCGCTGTGCGCCGCTACAAAGTCAACGAAGCTCGGCTGCAC 68
Db 1578 AAGCGCTACGACCTGGCCGCTGTGCGCCGCTACAAAGTCAACGAAGCTCGGCTGCAC 1634

QY 69 GTCGGCATCCGATCACAGCTCCACGCTGACCGTGCACGAGAGAGAGAGTGTGTCGCCACCATCGAG 128
Db 1635 GTCGGCATCCGATCACAGCTCCACGCTGACCGTGCACGAGAGAGAGAGTGTGTCGCCACCATCGAG 1694

QY 129 TACCTGTGCGTGTGTCACGAGGTCAGCACACGATGACCGTTCGCGGGCGCACCGAGTT 188
Db 1695 TACCTGTGCGTGTGTCACGAGGTCAGCACACGATGACCGTTCGCGGGCGCACCGAGTT 188

QY 1695 TACCTGTGCGTGTGTCACGAGGTCAGCACACGATGACCGTTCGCGGGCGCACCGAGTT 1754
Db 1755 CCAGTCGAGACCGATGACAT 1774

QY 189 CCGGTGGAGACCGACGACAT 208
Db 1755 CCAGTCGAGACCGATGACAT 1774

RESULT 8
US-10-076-406-3
; Sequence 3, Application US/10076406
; Publication No. US20030166884A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: Nucleotide sequences coding for the rpoB gene
; FILE REFERENCE: 219774USOXCIP
; CURRENT APPLICATION NUMBER: US/10/076,406
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: DE 10107229.5
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 09/887052
; PRIOR FILING DATE: 2001-06-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
; OTHER INFORMATION:
; NAME/KEY: mutation
; LOCATION: (1987)..(1987)
; OTHER INFORMATION: Substitution of adenine by thymine
; NAME/KEY: mutation
; LOCATION: (1288)..(1288)
; OTHER INFORMATION: Substitution of cytosine by thymine
; NAME/KEY: mutation
; LOCATION: (715)..(715)
; OTHER INFORMATION: Substitution of cytosine by thymine
US-10-076-406-3

Query Match 43.1%; Score 89.6; DB 12; Length 5099;
Best Local Similarity 69.0%; Pred. No. 2.3e-17;
Matches 138; Conservative 0; Mismatches 59; Indels 3; Gaps 1;

QY 9 AAGCGCTACGACCTGGCCGCTGTGCGCCGCTACAAAGTCAACGAAGCTCGGCTGCAC 68
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Db 1578 AAGCGCTACGACCTGGCCGCTGTGCGCCGCTACAAAGTCAACGAAGCTCGGCTGCAC 1634

QY 69 GTCGGCATCCGATCACAGCTCCACGCTGACCGTGCACGAGAGAGAGTGTGTCGCCACCATCGAG 128
Db 1635 GTCGGCATCCGATCACAGCTCCACGCTGACCGTGCACGAGAGAGAGTGTGTCGCCACCATCGAG 1694

QY 129 TACCTGTGCGTGTGTCACGAGGTCAGCACACGATGACCGTTCGCGGGCGCACCGAGTT 188
Db 1695 TACCTGTGCGTGTGTCACGAGGTCAGCACACGATGACCGTTCGCGGGCGCACCGAGTT 188

QY 1695 TACCTGTGCGTGTGTCACGAGGTCAGCACACGATGACCGTTCGCGGGCGCACCGAGTT 1754
Db 1755 CCAGTCGAGACCGATGACAT 1774

QY 189 CCGGTGGAGACCGACGACAT 208
Db 1755 CCAGTCGAGACCGATGACAT 1774

RESULT 9
US-10-076-406-5
; Sequence 5, Application US/10076406
; Publication No. US20030166884A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: Nucleotide sequences coding for the rpoB gene
; FILE REFERENCE: 219774USOXCIP
; CURRENT APPLICATION NUMBER: US/10/076,406
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: DE 10107229.5
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 09/887052
; PRIOR FILING DATE: 2001-06-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
; OTHER INFORMATION:
; NAME/KEY: mutation
; LOCATION: (2016)..(2016)
; OTHER INFORMATION: Substitution of cytosine by thymine
US-10-076-406-5

Query Match 43.1%; Score 89.6; DB 12; Length 5099;
Best Local Similarity 69.0%; Pred. No. 2.3e-17;
Matches 138; Conservative 0; Mismatches 59; Indels 3; Gaps 1;

QY 9 AAGCGCTACGACCTGGCCGCTGTGCGCCGCTACAAAGTCAACGAAGCTCGGCTGCAC 68
Db 1578 AAGCGCTACGACCTGGCCGCTGTGCGCCGCTACAAAGTCAACGAAGCTCGGCTGCAC 1634

QY 69 GTCGGCATCCGATCACAGCTCCACGCTGACCGTGCACGAGAGAGAGTGTGTCGCCACCATCGAG 128
Db 1635 GTCGGCATCCGATCACAGCTCCACGCTGACCGTGCACGAGAGAGAGTGTGTCGCCACCATCGAG 1694

QY 129 TACCTGTGCGTGTGTCACGAGGTCAGCACACGATGACCGTTCGCGGGCGCACCGAGTT 188
Db 1695 TACCTGTGCGTGTGTCACGAGGTCAGCACACGATGACCGTTCGCGGGCGCACCGAGTT 188

QY 1695 TACCTGTGCGTGTGTCACGAGGTCAGCACACGATGACCGTTCGCGGGCGCACCGAGTT 1754
Db 1755 CCAGTCGAGACCGATGACAT 1774

QY 189 CCGGTGGAGACCGACGACAT 208
Db 1755 CCAGTCGAGACCGATGACAT 1774

RESULT 10
US-10-075-460-5
; Sequence 5, Application US/10075460
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```
; Publication No. US2002015557A1
; GENERAL INFORMATION:
; APPLICANT: MCKEL, BETTINA
; APPLICANT: BATHE, BRIGITTE
; APPLICANT: HANS, STEFAN
; APPLICANT: KREUTZER, CAROLINE
; APPLICANT: HERMANN, THOMAS
; APPLICANT: PEPPERLE, WALTER
; APPLICANT: BLINDER, MICHAEL
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE rpsL GENE
; FILE REFERENCE: 218472USX
; CURRENT APPLICATION NUMBER: US/10/075,460
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: DE 10107230.9
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: DE 10162386.0
; PRIOR FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 5099
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
; OTHER INFORMATION:
US-09-075-460-5

Query Match 43.1%; Score 89.6; DB 13; Length 5099;
Best Local Similarity 69.0%; Pred. No. 2.3e-17;
Matches 138; Conservative 0; Mismatches 59; Indels 3; Gaps 1;

QY 9 AAGCGTAGACCTGGCCGCTGCGCGCTACAGGTCACAGAAGCTCGCCCTGCAC 68
DB 1578 AAGCGTAGACCTGGCTGCGGTGCTTACAGATCAACCCGAAGCTCGCCCT--- 1634
QY 69 GTGCGGATCCGATCACCAGCTCCAGCTGACCGAGGAGAGAGCTGTCGCCACCATCGAG 128
DB 1635 GTGCGGACCCAGATGGTTGATGACTCTTACTGAGAGGACATCGCAACCATCGAG 1694
QY 129 TACCTGGTCCGCTGTCAGAGGCTACAGACAGATGACCGTTCCGGCGGCGCACCGAGGTT 188
DB 1695 TACCTGGTCCGCTGTCAGAGGCTGAGCGGCTCATGACTTCTCCAAATGGTGAAGAGATC 1754
QY 189 CCGGTGAGACCGAGCAT 208
DB 1755 CCAAGTCGAGACCGATGACAT 1774

RESULT 11
US-09-738-626-1
; Sequence 1, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIO
; APPLICANT: OKHAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OKAZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
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; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 1
; LENGTH: 3309400
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-1

Query Match 43.1%; Score 89.6; DB 10; Length 3309400;
Best Local Similarity 69.0%; Pred. No. 2.7e-17;
Matches 138; Conservative 0; Mismatches 59; Indels 3; Gaps 1;

QY 9 AAGCGTAGACCTGGCCGCTGCGCGCTACAGGTCACAGAAGCTCGCCCTGCAC 68
DB 513789 AAGCGTAGACCTGGCTGCGGTGCTTACAGATCAACCCGAAGCTCGCCCT--- 513845
QY 69 GTGCGGATCCGATCACCAGCTCCAGCTGACCGAGGAGAGAGCTGTCGCCACCATCGAG 128
DB 513846 GTGCGGACCCAGATGGTTGATGACTCTTACTGAGAGGACATCGCAACCATCGAG 513905
QY 129 TACCTGGTCCGCTGTCAGAGGCTACAGACAGATGACCGTTCCGGCGGCGCACCGAGGTT 188
DB 513906 TACCTGGTCCGCTGTCAGAGGCTGAGCGGCTCATGACTTCTCCAAATGGTGAAGAGATC 513965
QY 189 CCGGTGAGACCGAGCAT 208
DB 513966 CCAAGTCGAGACCGATGACAT 513985

RESULT 12
US-10-156-761-4898
; Sequence 4898, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 4898
; LENGTH: 3543
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3543)
US-10-156-761-4898

Query Match 38.7%; Score 80.4; DB 14; Length 3543;
Best Local Similarity 65.4%; Pred. No. 1.2e-14;
Matches 136; Conservative 0; Mismatches 66; Indels 6; Gaps 1;
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QY 1 TCACGAGGAGAGCTGACGACCTGCGCGCTGCGCGCTACAGGTCACAGAAGCTCG 60
DB 956 TCACCGGAGGCGCTACGACCTCGCGAGGCTCGCGCTGCGCGCTACAGGTCACAGAAGCTCG 985
QY 61 GCCTGACGCTCGCGGATCCGATCACCAGTCCAGCTCCACCGAGAGAGAGAGCTGTCGCCA 120
DB 986 G-----CGCGAGGCGCGCTGGACGCGGATCCTGACCGCTCGAGGACATCATCTCST 1039
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; LOCATION: (1612)..(2211)
US-09-816-828-9

Query Match	20.6%	Score 42.8;	DB 10;	Length 2329;
Best Local Similarity	54.4%	Pred. No. 0.0018;		
Matches 86;	Conservative 0;	Mismatches 72;	Indels 0;	Gaps 0;

QY	51	AAAGAGCTCGGCTTCACGTCGGCGATCCGATCACCAAGCTCCACGCTGACCGAAGAGAC	110
Db	1924	AAAGGCCACGGCAAGAGGTGGCCGACGCGCTGACCAACGCCCTGGCGCACGTGGACGAC	1983
QY	111	GTGCTCGCCACCATCGAGTACCTGTGCTGTGTCGACGAGGTCAGCACACGATGACCGTT	170
Db	1984	ATGCCCAAGCGCTGGCGCACGTGGACGACATGCCCAACGCGCTGTCCGCCCTGAGCGAC	2043
QY	171	CCGGCGCGCACCGAGGTTCCGGTGGAGACCGACACAT	208
Db	2044	CTGCACGGCACAAAGCTTCGGGTGGACCGCGTCAACTT	2081

Search completed: September 17, 2003, 13:02:59
Job time : 128.259 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Run on: September 17, 2003, 11:54:34 ; Search time 29.9657 Seconds
        (without alignments)
        3049.028 Million cell updates/sec
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Title: US-09-697-123B-4
 Perfect score: 207
 Sequence: 1 tcaagagagagccgtacgac.....ccgtggagaccgacgacat 207

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6pdataca/1/ina/5B_COMB.seq: *
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6: /cgn2_6pdataca/1/ina/backfiles1.seq: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query			ID	Description
	Score	Match	Length		
1	157.6	76.1	970	1	US-08-250-030-1
2	157.6	76.1	970	5	PCT-US95-06790-1
3	157.6	76.1	4403765	3	US-09-103-840A-2
4	157.6	76.1	4411529	3	US-09-103-840A-1
5	128.8	62.2	3447	2	US-08-313-185-57
6	128.8	62.2	3447	3	US-09-082-614A-57
7	43.4	21.0	6085	3	US-09-029-603-4
8	39.6	19.2	1414	4	US-09-501-115-5
9	39.6	19.1	1841	4	US-09-252-991A-5092
10	39.6	19.1	1149	4	US-09-252-991A-5033
c 11	39.6	19.1	4403765	3	US-09-103-840A-2
c 12	39.6	19.1	4411529	3	US-09-103-840A-1
13	38.6	18.6	1014	4	US-09-252-991A-2663
14	38.6	18.6	1155	4	US-09-252-991A-2762
c 15	38.6	18.6	1233	4	US-09-252-991A-3203
16	38.2	18.5	829	3	US-09-313-300-7
17	38	18.4	2244	1	US-08-476-519-10
18	38	18.4	2244	5	PCT-US95-09323-10
19	38	18.4	2334	1	US-08-476-519-1
20	38	18.4	2334	5	PCT-US95-09323-1
21	37.8	18.3	2043	4	US-09-252-991A-995
c 22	37.8	18.3	3138	4	US-09-252-991A-1090
c 23	37.4	18.1	594	4	US-09-252-991A-13801
c 24	37.4	18.1	1494	4	US-09-252-991A-13441
25	37.4	18.1	2298	4	US-09-252-991A-13540
c 26	37.4	18.1	2412	4	US-09-252-991A-13908
27	37	17.9	1626	4	US-09-252-991A-8639

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Query Match 76.13; Score 157.6; DB 1; Length 970;
Best Local Similarity 88.03; Pred. No. 1.2e-31;
Matches 183; Conservative 24; Indels 1; Gaps 1;

QY 1 TC AAGGAAAGCGCTACGACTGGCCCGCTGTGCGCGCTCAAGGTCACAAAGACTGG 60
26 TC AAGGAAAGCGCTACGACTGGCCCGCTGTGCGCTCAAGGTCACAAAGACTGG 85

QY	61	GCCTGCAGTCTCGCGCATCGATACCAACAGCTCGACGCTGCAGCGCTGCAGAAAGAGAGAGCTGCTCGCCA	120
Db	86	GGCTGCATGTCTCGCGAGAGCCATACAGCTGCTGCAGCTGCACCGTACCGAAAGAGAGAGCTGCTGCGCCA	145
QY	121	CCATCGAGTACCTGTGTCGCCCTCCACGAGGGTCCAGCACACGATGA-CGTTCCGGGGGGGA	179
Db	146	CCATCGAATATCTGTGTCGCTTTCACGAGGGTTCAGACACGATGACCGTTCCGGGGCGCG	205
QY	180	CCGAGGTTCCGGTGGAGACCGACACAT	207
Db	206	TCGAGGTGCCGGTGGAAACCCAGACAT	233

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RESULT 2
PCI-US95-06790-1
; Sequence 1, Application PC/TUS9506790
; GENERAL INFORMATION:
; APPLICANT: Mayo Foundation for Medical Education and Research
; APPLICANT: and Hoffmann-La Roche Inc.
; TITLE OF INVENTION: Detection of a Genetic Locus Encoding
; TITLE OF INVENTION: Resistance to Rifampin
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg & Woessner
; STREET: 3500 IDS Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:

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Query Match	76.1%	Score 157.6	DB 5	Length 970
Best Local Similarity	88.0%	Prod. No. 1.2e-31		
Matches 183	Conservative 0	Mismatches 24	Indels 1	Gaps 1
Qy	1	TCAGGAGAGCGCCTACGACCTGGCCCGCTGTCGGCGCTACAAAGTCAACAAGAAAGCTGG	60	
Db	26	TCAGGAGAGCGCTACGACCTGGCCCGCTGCTATAGGTCAACAAGAACTCG	85	
Qy	61	GCCTGCGATGTCGGCGATCCGATACCAAGCTTCGACGCTACCGAGAGAGAGCTGCTGCCCA	120	
Db	86	GGCTGCGATGTCGGCGAGCCCATCAAGTCTGTCGACGCTGCCGAAGAGACGCTGCTGCCCA	145	
Qy	121	CCATCGAGTACCTGTCGCGCTCCACGAGGCTCAGCACACGATGA-CGTTCCGGCGCGGA	179	
Db	146	CCATCGATATCTGGTCCGCTTCACGAGGGTCAACACACGATGACCGTCCGGCGCGGG	205	
Qy	180	CCGAGGTTCCGGTGGAGACCGACGACAT	207	
Db	206	TCGAGGTCGCGGTGGAAACCGACGACAT	233	

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RESULT 3
US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

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Query Match	76.1%	Score 157.6	DB 3	Length 440365
Best Local Similarity	88.0%	Prod. No. 3.5e-31		
Matches 183	Conservative 0	Mismatches 24	Indels 1	Gaps 1
Qy	1	TCAGGAGAGCGCTACGACCTGGCCCGCTGTGGCCGCTACAGGCTACACAGAGCTGG	60	
Db	762648	TCAGGAGAGCGCTACGACCTGGCCCGCTGTGGCTATAGGTCACAGAGCTCG	762707	
Qy	61	GCGTCGATGTCGGGATTCGATCACACGCTCGAGCTGACCGAGAGACGCTTCGCCA	120	
Db	762708	GCGTCGATGTCGGCGAGCCCATCAGCTGTCGAGGCTGACCGAAGAAGACGCTCGCCA	762767	
Qy	121	CCATCGAGTACTGTCGCGCTCCAGAGGTCAGCACAGATGA-CGTCGGCGCGGGA	179	
Db	762768	CCATCGAATATCTGGTCCGCTTGACAGAGGTCAGACCAGATACCGTTCGGCGCGCG	762827	
Qy	180	CGAGGTTCCGGTGGAGCCGACGACAT	207	
Db	762828	TCGAGGTCGCGGTGGAAACCGACGACAT	762855	

```

RESULT 4
US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R. M.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-200007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

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Query Match 76.18; Score 157.6; DB 3; Length 4411529;

Db 809 TCAGGAGAAACGCTACGACCTGCCAGGTTGGTCTTACAGGTCAACAAGAGCTCG 868
QY 61 GCTGTGATGTCGGCGATCGATCACAGCTGACGCTGACCGAAGAGAGCTGTCGCCA 120
Db 869 GGTTCACCGCGGTGAGTTGATCATGCTCCACGCTGACCGAAGAGATGCTGCCCA 928
QY 121 CCAFCGAGTACCTGTCGCTCCACGAGGTCAGCACAGTAC-GTCCCGGGGGGA 179
Db 929 CCAATAGTACCTGTCGCTGTCATGAGGTCAGTCCGCAATGACTGCCAGGTGGG 988
QY 180 CCGAGTTCGGTGGAGACCGACGACAT 207
Db 989 TAGAAGTCGAGTGGAAACTGACGATAT 1016

RESULT 7
US-09-029-603-4
; Sequence 4, Application US/09029603
; Patent No. 6210935
; GENERAL INFORMATION:
; APPLICANT: Schupp, Thomas
; APPLICANT: Engel, Natalie
; APPLICANT: Bietenhader, Jurg
; APPLICANT: Toupet, Christine
; APPLICANT: Pospiech, Andreas
; TITLE OF INVENTION: Staurosporin Biosynthesis Gene Clusters
; FILE REFERENCE: 4-20555/A/PCT
; CURRENT APPLICATION NUMBER: US/09/029,603
; CURRENT FILING DATE: 1998-03-20
; EARLIER APPLICATION NUMBER: PCT/EP96/03643
; EARLIER FILING DATE: 1996-08-19
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 6085
; TYPE: DNA
; ORGANISM: Streptomyces longisporoflavus
; FEATURE:
; NAME/KEY: misc_RNA
; LOCATION: (378)..(1665)
; OTHER INFORMATION: ORF
; FEATURE:
; NAME/KEY: misc_RNA
; LOCATION: (1747)..(2553)
; OTHER INFORMATION: ORF
; FEATURE:
; NAME/KEY: misc_RNA
; LOCATION: (2593)..(4011)
; OTHER INFORMATION: ORF
; FEATURE:
; NAME/KEY: misc_RNA
; LOCATION: (4013)..(4999)
; OTHER INFORMATION: ORF
; FEATURE:
; NAME/KEY: misc_RNA
; LOCATION: (5071)..(6085)
; OTHER INFORMATION: ORF
US-09-029-603-4

Query Match 21.0%; Score 43.4; DB 3; Length 6085;
Best Local Similarity 57.9%; Pred. No. 0.016;
Matches 77; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 18 GACCTGGCCCGTTCGCGCCGCTACAGGTCAACAAGAGCTGGCGCTGATGCGCGAT 77
Db 1017 GAGGTGGACCGCGCGCGCGACGACCGCGACGATCTGCTACCCCTCTCGTCGGGCC 1076
QY 78 CGATCACCAGCTCGACGTGACCGAAGAGAGCTCTCCACCATGAGTACCTGCTC 137
Db 1077 CGGGACACCGGATCACCGCTCAGCGTGGACGCGCATCTCGGCACCTGCTCATCTGTC 1136
QY 138 CGCCTCCACGAGG 150

Db 1137 ACCCGCGGCCACG 1149

RESULT 8
US-09-501-115-5
; Sequence 5, Application US/09501115
; Patent No. 6552249
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Fader, Gary M.
; APPLICANT: Rafalski, Antoni
; TITLE OF INVENTION: Plant Cinnamyl-Alcohol Dehydrogenase Homologs
; FILE REFERENCE: BB1328 US NA
; CURRENT APPLICATION NUMBER: US/09/501,115
; CURRENT FILING DATE: 2000-02-09
; EARLIER APPLICATION NUMBER: 60/119,585
; EARLIER FILING DATE: 1999-February-10
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 5
; LENGTH: 1414
; TYPE: DNA
; ORGANISM: Triticum aestivum
US-09-501-115-5

Query Match 19.2%; Score 39.8; DB 4; Length 1414;
Best Local Similarity 59.1%; Pred. No. 0.11;
Matches 68; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 14 CTACGACCTGGCCCGTGTCTGCGCGCTACAAAGTCAACAAGAGCTGGCGCTGCATGTCGG 73
Db 385 CTCTGCGCGAGTCTGCGACAGCTGCAGCAAGGGGTACGAGAGCTACTGCCCGCAGCTCGT 444
QY 74 CGATCCGATCACCAGCTCGACGCTGACCGAAGAGAGAGCTGTCGCCACCATCGAG 128
Db 445 GGAGAGCTCCACGCGCTGAGCTGAGAGAGATGACGCGCGCGCACCAAG 499

RESULT 9
US-09-252-991A-5092
; Sequence 5092, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONA
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 5092
; LENGTH: 981
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-5092

Query Match 19.1%; Score 39.6; DB 4; Length 981;
Best Local Similarity 53.2%; Pred. No. 0.11;
Matches 84; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

QY 2 CAAGGAGAAGCGTTACGACCTGCGCCGCTGTCGGCGCTCAAGGTCAACAAGAGCTGGG 61
Db 388 CGACGAGAGAACAATCAAGCGGCGCTGGAGTTCTTCGCAAGATGCGCAAGAGGCGG 447
QY 62 CTTGATGTCGGGATCCGATCCAGCTCGACGCTGACCGAAGAGAGAGCTGTCGCCAC 121
Db 448 CTTGTCGTGACCAACCCCGGTGATCGCACCTCGCAAAAGGGCGAGGTGGAATGGCAT 507
QY 122 CATCGATGTAACCTGGTCCGCTCCACAGGGTCAAGCACA 159

: PRIORITY DATE: 1998-07-27

Query Match 76.18; Score 157.6; DB 10; Length 3519;

Best Local Similarity 88.08; Pred. No. 7e-38;
Matches 183; Conservative 0; Mismatches 24; Indels 1; Gaps 1;

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QY 1 TCAAGGAGAAGCGTAGACCTGGCCGCTGTCGGCCGTACAAGGTCACACAGAGCTGG 60
DB 884 TCAGGAGAAGCGTAGACCTGGCCGCTGTCGGCCGTATAGGTCACACAGAGCTGG 943
QY 61 GCGTCAGTGGGAGTCCGATCCAGCTGACGCTGACCGAGAGAGGACGTCGTCGCCA 120
DB 944 GCGTCAGTGGGAGGACCCATCACTGCTGACGCTGACCGAGAGAGGCTGTCGGCCA 1003
QY 121 CCATGAGTACTGCTGCTGCTCCAGAGGTCACACAGATGA-CGTTCCGGCGGGGA 179
DB 1004 CCATCGAATATCTGCTGCTGCTCCAGAGGTCAGACCACTGACCGTTCCGGCGGG 1063
QY 180 CCAGGTTCCGCTGAGACGAGGACAT 207
DB 1064 TCAGGTGCGGTGGAACCGAGCAT 1091
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RESULT 2

US-09-738-626-547

; Sequence 547, Application US/09738626

; Publication No. US20020197605A1

; GENERAL INFORMATION:

; APPLICANT: NAKAGAWA, SATOSHI

; APPLICANT: MIZOGUCHI, HIROSHI

; APPLICANT: ANDO, SEIKO

; APPLICANT: HAYASHI, MIKIRO

; APPLICANT: OCHIALI, KEIKO

; APPLICANT: YOKOI, HARUHIKO

; APPLICANT: TATEISHI, NAOKO

; APPLICANT: SENOH, AKIHIRO

; APPLICANT: IKEDA, MASATO

; APPLICANT: OZAKI, AKIO

; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES

; FILE REFERENCE: 249-125

; CURRENT APPLICATION NUMBER: US/09/738,626

; CURRENT FILING DATE: 2000-12-18

; PRIOR APPLICATION NUMBER: JP 99/377484

; PRIOR FILING DATE: 1999-12-16

; PRIOR APPLICATION NUMBER: JP 00/159162

; PRIOR FILING DATE: 2000-04-07

; PRIOR APPLICATION NUMBER: JP 00/280988

; PRIOR FILING DATE: 2000-08-03

; NUMBER OF SEQ ID NOS: 7059

; SOFTWARE: PatentIn ver. 3.0

; SEQ ID NO 547

; LENGTH: 3495

; TYPE: DNA

; ORGANISM: Corynebacterium glutamicum

US-09-738-626-547

Query Match 39.08; Score 80.8; DB 10; Length 3495;

Best Local Similarity 69.58; Pred. No. 6.6e-15;
Matches 139; Conservative 0; Mismatches 57; Indels 4; Gaps 2;

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QY 9 AAGCGTAGACCTGGCCGCTGTCGGCCGTACAAGGTCACACAGAGCTGGCCCTGCAT 68
DB 877 AAGCGTAGACCTGGCCGCTGTCGGCCGTACAAGGTCACACAGAGCTGGCCCT--T 933
QY 69 GTGCGGATCCGATCACCAGCTGACGCTGACCGAGAGGAGCTGTCGCCACCATCGAG 128
DB 934 GTGCGGACCGAGATGTTTGTGACTCTTACTGAGAGGACATCGCAACCATCGAG 993
QY 129 TACTGTGTCGCTCCAGAGGTCACACAGATGACGT-TCCGGCGGGACCGAGGTT 187
DB 994 TACTGTGTCGCTCCAGAGGTCACACAGATGACGTCTCTCCAAATGTAAGAGATC 1053
QY 188 CCGGTGGAGACCGAGCAT 207
DB 1054 CCACTGAGACCGAGCAT 1073
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RESULT 3

US-09-984-711-5

; Sequence 5, Application US/09984711

; Patent No. US20020119549A1

; GENERAL INFORMATION:

; APPLICANT: MOECKEL, Bettina

; APPLICANT: BATHE, Brigitte

; APPLICANT: STEPHAN, Hans

; APPLICANT: KREUTZER, Caroline

; APPLICANT: HERMANN, Thomas

; APPLICANT: PFEFFERLE, Walter

; APPLICANT: BINDER, Michael

; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE rpsL GENE

; FILE REFERENCE: 204209US0

; CURRENT APPLICATION NUMBER: US/09/984,711

; CURRENT FILING DATE: 2001-10-31

; PRIOR APPLICATION NUMBER: DE10108230.9

; PRIOR FILING DATE: 2001-02-16

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 5

; LENGTH: 5096

; TYPE: DNA

; ORGANISM: Corynebacterium glutamicum

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (702)..(4196)

; OTHER INFORMATION:

US-09-984-711-5

Query Match 39.08; Score 80.8; DB 10; Length 5096;
Best Local Similarity 69.58; Pred. No. 6.6e-15;
Matches 139; Conservative 0; Mismatches 57; Indels 4; Gaps 2;

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QY 9 AAGCGTAGACCTGGCCGCTGTCGGCCGTACAAGGTCACACAGAGCTGGCCCTGCAT 68
DB 1578 AAGCGTAGACCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1634
QY 69 GTGCGGATCCGATCACCAGCTGACGCTGACCGAGAGGAGCTGTCGCCACCATCGAG 128
DB 1635 GTGCGGACCGAGTGGTTGATGACTTACTGAGAGGACATCGCAACCATCGAG 1694
QY 129 TACTGTGTCGCTCCAGAGGTCACACAGATGACGT-TCCGGCGGGACCGAGGTT 187
DB 1695 TACTGTGTCGCTCCAGAGGTCAGCGCTGATGACTTCTCCAAATGTAAGAGATC 1754
QY 188 CCGGTGGAGACCGAGCAT 207
DB 1755 CCAGTCGAGACCGATGACAT 1774
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RESULT 4

US-09-887-052-1

; Sequence 1, Application US/09887052

; Patent No. US20020119537A1

; GENERAL INFORMATION:

; APPLICANT: MOECKEL, Bettina

; APPLICANT: BATHE, Brigitte

; APPLICANT: HERMANN, Thomas

; APPLICANT: PFEFFERLE, Walter

; APPLICANT: BINDER, Michael

; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE rpoB GENE

; FILE REFERENCE: 204212US0X

; CURRENT APPLICATION NUMBER: US/09/887,052

; CURRENT FILING DATE: 2001-06-25

; PRIOR APPLICATION NUMBER: DE10107229.5

; PRIOR FILING DATE: 2001-02-16

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 1

; LENGTH: 5099

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; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
US-09-887-052-1

Query Match      39.0%; Score 80.8; DB 10; Length 5099;
Best Local Similarity 69.5%; Pred. No. 6.6e-15;
Matches 139; Conservative 0; Mismatches 57; Indels 4; Gaps 2;

QY 9 AAGCGCTACGACCTGCGCGCTGTCGGCGCTACAGGTCACAAAGAGCTGGCGCTGCAT 68
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1578 AAGCGCTACGACCTGCGCGCTGTCGGCGCTACAGGTCACAAAGAGCTGGCGCT---T 1634

QY 69 GTCGGCGATCCGATCACCAGCTCGACGCTGACCGAGAGAGAGCTGTCGCCACCATCGAG 128
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1635 GGTGGCCACCAACGATGGTTGATGACTCTTACTGAAGAGAGACATCGCAACCATCGAG 1694

QY 129 TACCTGTGCGCTCCACGAGGTCAGACACAGATGACGT-TCCGGGGGGGACCGAGGTT 187
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1695 TACCTGTGCGCTCGACGAGGTCAGCGCGCTGATGACTCTTCCAAATGGTGAAGAGATC 1754

QY 188 CCGGTGGAGACCGAGACAT 207
    || || || || || || || || || || || || || || || || || || || || ||
Db 1755 CCAGTCGAGACCGATGACAT 1774

RESULT 5
US-09-887-052-3
; Sequence 3, Application US/09887052
; Patent No. US20020119537A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE rpoB GENE
; CURRENT APPLICATION NUMBER: US/09/887,052
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: DE10107229.5
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 5099
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
US-09-887-052-5

Query Match      39.0%; Score 80.8; DB 10; Length 5099;
Best Local Similarity 69.5%; Pred. No. 6.6e-15;
Matches 139; Conservative 0; Mismatches 57; Indels 4; Gaps 2;

QY 9 AAGCGCTACGACCTGCGCGCTGTCGGCGCTACAGGTCACAAAGAGCTGGCGCTGCAT 68
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1578 AAGCGCTACGACCTGCGCGCTGTCGGCGCTACAGGTCACAAAGAGCTGGCGCT---T 1634

QY 69 GTCGGCGATCCGATCACCAGCTCGACGCTGACCGAGAGAGAGCTGTCGCCACCATCGAG 128
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1635 GGTGGCCACCAACGATGGTTGATGACTCTTACTGAAGAGAGACATCGCAACCATCGAG 1694

QY 129 TACCTGTGCGCTCCACGAGGTCAGACACAGATGACGT-TCCGGGGGGGACCGAGGTT 187
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1695 TACCTGTGCGCTCGACGAGGTCAGCGCGCTGATGACTCTTCCAAATGGTGAAGAGATC 1754

QY 188 CCGGTGGAGACCGAGACAT 207
    || || || || || || || || || || || || || || || || || || || || ||
Db 1755 CCAGTCGAGACCGATGACAT 1774

RESULT 6
US-09-887-052-5
; Sequence 5, Application US/09887052
; Patent No. US20020119537A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE rpoB GENE
; CURRENT APPLICATION NUMBER: US/09/887,052
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: DE10107229.5
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 5099
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
US-09-887-052-5

Query Match      39.0%; Score 80.8; DB 10; Length 5099;
Best Local Similarity 69.5%; Pred. No. 6.6e-15;
Matches 139; Conservative 0; Mismatches 57; Indels 4; Gaps 2;

QY 9 AAGCGCTACGACCTGCGCGCTGTCGGCGCTACAGGTCACAAAGAGCTGGCGCTGCAT 68
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1578 AAGCGCTACGACCTGCGCGCTGTCGGCGCTACAGGTCACAAAGAGCTGGCGCT---T 1634

QY 69 GTCGGCGATCCGATCACCAGCTCGACGCTGACCGAGAGAGAGCTGTCGCCACCATCGAG 128
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1635 GGTGGCCACCAACGATGGTTGATGACTCTTACTGAAGAGAGACATCGCAACCATCGAG 1694

QY 129 TACCTGTGCGCTCCACGAGGTCAGACACAGATGACGT-TCCGGGGGGGACCGAGGTT 187
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1695 TACCTGTGCGCTCGACGAGGTCAGCGCGCTGATGACTCTTCCAAATGGTGAAGAGATC 1754

QY 188 CCGGTGGAGACCGAGACAT 207
    || || || || || || || || || || || || || || || || || || || || ||
Db 1755 CCAGTCGAGACCGATGACAT 1774

RESULT 7
US-10-076-406-1
; Sequence 1, Application US/10076406
; Publication No. US20030166884A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: Nucleotide sequences coding for the rpoB gene
; FILE REFERENCE: 219774US0XCIP
; CURRENT APPLICATION NUMBER: US/10/076,406
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: DE 10107229.5
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 09/887052
; PRIOR FILING DATE: 2001-06-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 5099
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Db 1755 CCAGTCGAGACCGATGACAT 1774

RESULT 6
US-09-887-052-5
; Sequence 5, Application US/09887052
; Patent No. US20020119537A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE rpoB GENE
; CURRENT APPLICATION NUMBER: US/09/887,052
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: DE10107229.5
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 5099
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
US-09-887-052-5

Query Match      39.0%; Score 80.8; DB 10; Length 5099;
Best Local Similarity 69.5%; Pred. No. 6.6e-15;
Matches 139; Conservative 0; Mismatches 57; Indels 4; Gaps 2;

QY 9 AAGCGCTACGACCTGCGCGCTGTCGGCGCTACAGGTCACAAAGAGCTGGCGCTGCAT 68
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1578 AAGCGCTACGACCTGCGCGCTGTCGGCGCTACAGGTCACAAAGAGCTGGCGCT---T 1634

QY 69 GTCGGCGATCCGATCACCAGCTCGACGCTGACCGAGAGAGAGCTGTCGCCACCATCGAG 128
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1635 GGTGGCCACCAACGATGGTTGATGACTCTTACTGAAGAGAGACATCGCAACCATCGAG 1694

QY 129 TACCTGTGCGCTCCACGAGGTCAGACACAGATGACGT-TCCGGGGGGGACCGAGGTT 187
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1695 TACCTGTGCGCTCGACGAGGTCAGCGCGCTGATGACTCTTCCAAATGGTGAAGAGATC 1754

QY 188 CCGGTGGAGACCGAGACAT 207
    || || || || || || || || || || || || || || || || || || || || ||
Db 1755 CCAGTCGAGACCGATGACAT 1774

RESULT 7
US-10-076-406-1
; Sequence 1, Application US/10076406
; Publication No. US20030166884A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: Nucleotide sequences coding for the rpoB gene
; FILE REFERENCE: 219774US0XCIP
; CURRENT APPLICATION NUMBER: US/10/076,406
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: DE 10107229.5
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 09/887052
; PRIOR FILING DATE: 2001-06-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 5099
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; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
; OTHER INFORMATION:
US-10-076-406-1

Query Match          39.0%; Score 80.8; DB 12; Length 5099;
Best Local Similarity 69.5%; Pred. No. 6.6e-15;
Matches 139; Conservative 0; Mismatches 57; Indels 4; Gaps 2;

QY 9 AAGCGCTACGACCTGGCCCTGTGCGCGCTACAAAGGTCACAAAGAGTGGGCGCTGCAT 68
    |||||
Db 1578 AAGCGCTACGACCTGGCTGCTGTGCTTACAAAGATCAACCAAGCTCGGCCT--T 1634
    |||||

QY 69 GTGCGGATCCGATCACCAGCTGCAGCGCTGACCGAGAGGACGTCGTCGCCACCATCGAG 128
    |||||
Db 1635 GTGCGGACCCAGATGTTGATGACTCTTACTGAAGAGGACATCGCAACCCATCGAG 1694
    |||||

QY 129 TACCTGGTCCGCTCCACGAGGCTCAGACACGATGACGT-TCCGGGCGGACCGAGGTT 187
    |||||
Db 1695 TACCTGGTCCGCTCTCCACGAGGCTGAGCGCGTCATGACTTCCAAATGTTGAAGATC 1754
    |||||

QY 188 CCGGTGGAGACCGAGGACAT 207
    |||||
Db 1755 CCAGTCGAGACCGATGACAT 1774

RESULT 8
US-10-076-406-3
; Sequence 3, Application US/10076406
; Publication No. US2003016684A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: Nucleotide sequences coding for the rpoB gene
; FILE REFERENCE: 219774USOXCP
; CURRENT APPLICATION NUMBER: US/10/076,406
; PRIOR FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: DE 10107229.5
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 09/887052
; PRIOR FILING DATE: 2001-06-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 3
; LENGTH: 5099
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
; OTHER INFORMATION:
; NAME/KEY: mutation
; LOCATION: (1987)..(1987)
; OTHER INFORMATION: Substitution of adenine by thymine
; NAME/KEY: mutation
; LOCATION: (1288)
; OTHER INFORMATION: Substitution of cytosine by thymine
; NAME/KEY: mutation
; LOCATION: (715)..(715)
; OTHER INFORMATION: Substitution of cytosine by thymine
US-10-076-406-3

Query Match          39.0%; Score 80.8; DB 12; Length 5099;
Best Local Similarity 69.5%; Pred. No. 6.6e-15;
Matches 139; Conservative 0; Mismatches 57; Indels 4; Gaps 2;

QY 9 AAGCGCTACGACCTGGCCCTGTGCGCGCTACAAAGGTCACAAAGAGTGGGCGCTGCAT 68
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Db 1578 AAGCGCTACGACCTGGCTGCTGTGCTTACAAAGATCAACCAAGCTCGGCCT--T 1634
    |||||
QY 69 GTGCGGATCCGATCACCAGCTGCAGCGCTGACCGAGAGGACGTCGTCGCCACCATCGAG 128
    |||||
Db 1635 GTGCGGACCCAGATGTTGATGACTCTTACTGAAGAGGACATCGCAACCCATCGAG 1694
    |||||
QY 129 TACCTGGTCCGCTCCACGAGGCTCAGACACGATGACGT-TCCGGGCGGACCGAGGTT 187
    |||||
Db 1695 TACCTGGTCCGCTCTCCACGAGGCTGAGCGCGTCATGACTTCCAAATGTTGAAGATC 1754
    |||||
QY 188 CCGGTGGAGACCGAGGACAT 207
    |||||
Db 1755 CCAGTCGAGACCGATGACAT 1774

RESULT 9
US-10-076-406-5
; Sequence 5, Application US/10076406
; Publication No. US2003016684A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: Nucleotide sequences coding for the rpoB gene
; FILE REFERENCE: 219774USOXCP
; CURRENT APPLICATION NUMBER: US/10/076,406
; PRIOR FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: DE 10107229.5
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 09/887052
; PRIOR FILING DATE: 2001-06-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 5
; LENGTH: 5099
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
; OTHER INFORMATION:
; NAME/KEY: mutation
; LOCATION: (2016)..(2016)
; OTHER INFORMATION: Substitution of cytosine by thymine
US-10-076-406-5

Query Match          39.0%; Score 80.8; DB 12; Length 5099;
Best Local Similarity 69.5%; Pred. No. 6.6e-15;
Matches 139; Conservative 0; Mismatches 57; Indels 4; Gaps 2;

QY 9 AAGCGCTACGACCTGGCCCTGTGCGCGCTACAAAGGTCACAAAGAGTGGGCGCTGCAT 68
    |||||
Db 1578 AAGCGCTACGACCTGGCTGCTGTGCTTACAAAGATCAACCAAGCTCGGCCT--T 1634
    |||||
QY 69 GTGCGGATCCGATCACCAGCTGCAGCGCTGACCGAGAGGACGTCGTCGCCACCATCGAG 128
    |||||
Db 1635 GTGCGGACCCAGATGTTGATGACTCTTACTGAAGAGGACATCGCAACCCATCGAG 1694
    |||||
QY 129 TACCTGGTCCGCTCCACGAGGCTCAGACACGATGACGT-TCCGGGCGGACCGAGGTT 187
    |||||
Db 1695 TACCTGGTCCGCTCTCCACGAGGCTGAGCGCGTCATGACTTCCAAATGTTGAAGATC 1754
    |||||
QY 188 CCGGTGGAGACCGAGGACAT 207
    |||||
Db 1755 CCAGTCGAGACCGATGACAT 1774

RESULT 10
US-10-075-460-5
; Sequence 5, Application US/10075460
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; Publication No. US2002015557A1
; GENERAL INFORMATION:
; APPLICANT: MCKEL, BETTINA
; APPLICANT: BATHE, BRIGITTE
; APPLICANT: HANS, STEFAN
; APPLICANT: KREUTZER, CAROLINE
; APPLICANT: HERMANN, THOMAS
; APPLICANT: PFEFFERLE, WALTER
; APPLICANT: BINDER, MICHAEL
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE rpsL GENE
; FILE REFERENCE: 218472USOX
; CURRENT APPLICATION NUMBER: US/10/075,460
; CURRENT FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: DE 10107230.9
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: DE 10162386.0
; PRIOR FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 5099
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
; OTHER INFORMATION:
US-10-075-460-5

Query Match          39.0%; Score 80.8; DB 13; Length 5099;
Best Local Similarity 69.5%; Pred. No. 6.6e-15;
Matches 139; Conservative 0; Mismatches 57; Indels 4; Gaps 2;

QY      9  AAGCGCTACGACCTGGCCCGTGTCCGCGCTACAAAGTCAACAGAGAGTGGGCTGCAT 68
Db      1578  AAGCGCTACGACCTGGCTCGCTGTGTGCTTACAAAGTCAACCGCAAGCTCGGCT--T 1634
QY      69  GTCCGCGATCCGATCACCAGCTCGACGTCGACGGAAGAGGACGCTCGTCCGCCACCATCGAG 128
Db      1635  GTGCGGACACGAGTGTGTGACTCTTACTGAGAGGACATCGCAACACCATCGAG 1694
QY      129  TACCTGTGCCCTCCACGAGGTGACACAGATGAGCT-TCCGGGCGGGACCGAGGTT 187
Db      1695  TACCTGTGGCTCTGCACGAGGTGAGCGCGTCTGCTTCCAAATGTTGAAGAGATC 1754
QY      188  CCGGTGGAGACCGAGCAT 207
Db      1755  CCAGTCGAGACCGATGACAT 1774

RESULT 11
US-09-738-626-1
; Sequence 1, Application US/09738626
; Publication No. US20020197603A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
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; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 1
; LENGTH: 3309400
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-1

Query Match          39.0%; Score 80.8; DB 10; Length 3309400;
Best Local Similarity 69.5%; Pred. No. 7.7e-15;
Matches 139; Conservative 0; Mismatches 57; Indels 4; Gaps 2;

QY      9  AAGCGCTACGACCTGGCCCGTGTCCGCGCTACAAAGTCAACAGAGAGTGGGCTGCAT 68
Db      513789  AAGCGCTACGACCTGGCTCGCTGTGTGCTTACAAAGTCAACCGCAAGCTCGGCT--T 513845
QY      69  GTCCGCGATCCGATCACCAGCTCGACGTCGACGGAAGAGGACGCTCGTCCGCCACCATCGAG 128
Db      513846  GGTGCGGACACGAGTGTGTGACTCTTACTGAGAGGACATCGCAACACCATCGAG 513905
QY      129  TACCTGTGCCCTCCACGAGGTGACACAGATGAGCT-TCCGGGCGGGACCGAGGTT 187
Db      513906  TACCTGTGGCTCTGCACGAGGTGAGCGCGTCTGCTTCCAAATGTTGAAGAGATC 513965
QY      188  CCGGTGGAGACCGAGCAT 207
Db      513966  CCAGTCGAGACCGATGACAT 513985

RESULT 12
US-10-156-761-4898
; Sequence 4898, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 4898
; LENGTH: 3543
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3543)
US-10-156-761-4898

Query Match          35.4%; Score 73.2; DB 14; Length 3543;
Best Local Similarity 66.3%; Pred. No. 1.2e-12;
Matches 138; Conservative 0; Mismatches 63; Indels 7; Gaps 2;

QY      1  TCAAGAGAGCGGTACGACCTGGCCCGTGTCCGCGCTACAAAGTCAACAGAGAGCTGG 60
Db      926  TCAACCGGAAGCGGTACGACCTGGCAAGGTGGCGGCTACAAAGGTCAACAGAGCTGG 985
QY      61  GCCTGCATGTCGGCGATCCGATCACCAGCTCGACGCTGACCGAGAGAGAGCTGTCGCCA 120
Db      986  GC-----GGCGAGGCGCGCGTGGCGGGATCCTGACCGTCGAGGACATCATCTGCT 1039
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Query Match      19.8%; Score 41; DB 14; Length 1287;
Best Local Similarity 56.2%; Pred. No. 0.0052;
Matches 77; Conservative 0; Mismatches 60; Indels 0; Gaps 0;
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Qy	1	TCAAGGAGAAGCGCTACGACTGGCCCGGTGTCGCCGCCTACAAGTCAACAAAGAGCTGG	60
Db	614	TCGGCGCAGACTACGACTGGACCGGTGCTCTCCGGCTCGACAAGCTGTGA	673
Qy	61	GCTTGATGTCGGGATCCGATCACAGCTGCAGCTGACCAGAGAGAGCTGTCGCCA	120
Db	674	TTCTGCACGCGACGACGACGAACTGTTGTGCTACTCCACCGTGGCTGTGTCGGCTGCTG	733

RESULT 14
US-10-292-198-1
; Sequence 1, Application US/10292198
; Publication NO. US20030157654A1
; GENERAL INFORMATION:
; APPLICANT: SHEN, Ben
; APPLICANT: LIU, Wen
; TITLE OF INVENTION: BIOSYNTHESIS OF ENEDIYNE COMPOUNDS BY MANIPULATION OF C-1027 GENE
; TITLE OF INVENTION: PATHWAY
; FILE REFERENCE: 054030-0007
; CURRENT APPLICATION NUMBER: US/10/292,198
; CURRENT FILING DATE: 2003-03-14

QY 121 CCATCGAGTACCTGGTC 137
| | | | | | | |
Db 734 CGCAGGCGACATGTTT 750

Search completed: September 17, 2003, 13:03:15
Job time : 123.739 secs

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OM nucleic - nucleic search, using sw model

Run on: September 17, 2003, 11:54:34 ; Search time 30.1105 Seconds
(without alignments)
3049.028 Million cell updates/sec

Title: US-09-697-123B-5
Perfect score: 208
Sequence: 1 tcaaggagaagcgctacgac.....ccgggtggaacccgacgacat 208

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_NA.*
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2: /cgn2.6/ptodata/1/ina/5B_COMB.seq.*
3: /cgn2.6/ptodata/1/ina/6A_COMB.seq.*
4: /cgn2.6/ptodata/1/ina/6B_COMB.seq.*
5: /cgn2.6/ptodata/1/ina/PCRUS_COMB.seq.*
6: /cgn2.6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	208	100.0	970	1	US-08-250-030-1
2	208	100.0	970	5	PCT-US95-06790-1
3	208	100.0	4403765	3	US-09-103-840A-2
4	208	100.0	4411529	3	US-09-103-840A-1
5	148.8	71.5	3447	2	US-08-313-185-57
6	148.8	71.5	3447	3	US-09-082-614B-57
7	38.6	18.6	924	4	US-09-252-991A-969
8	38.6	18.6	939	4	US-09-252-991A-925
c 9	38.2	18.4	768	4	US-09-252-991A-1114
c 10	37.2	17.9	1412	1	US-08-097-831-1
c 11	37.2	17.9	1452	4	US-09-252-991A-13650
c 12	37.2	17.9	1980	4	US-09-252-991A-13782
13	37	17.8	6085	3	US-09-029-603-4
c 14	36.4	17.5	258	4	US-09-252-991A-13457
15	36.4	17.5	615	4	US-09-252-991A-13899
16	36.4	17.5	1695	4	US-09-252-991A-13695
17	36	17.3	870	4	US-09-252-991A-7157
c 18	36	17.3	2415	4	US-09-252-991A-7480
19	36	17.3	2657	4	US-09-252-991A-7216
20	35.2	16.9	1326	4	US-09-252-991A-10931
c 21	35.2	16.9	2211	4	US-09-252-991A-11256
22	35.2	16.9	2289	4	US-09-252-991A-10995
23	34.6	16.6	1621	1	US-08-722-001-13
24	34.6	16.6	1766	1	US-08-722-001-29
25	34.6	16.6	2002	4	US-09-016-434-1172
26	34.6	16.6	2140	1	US-08-334-698-1
27	34.6	16.6	2140	1	US-08-228-932-1

28 34.6 16.6 2140 1 US-08-468-939-1 Sequence 1, Appli
29 34.6 16.6 2140 2 US-08-406-855A-1 Sequence 1, Appli
30 34.6 16.6 2140 2 US-08-722-190-1 Sequence 1, Appli
31 34.6 16.6 2140 3 US-08-244-354-1 Sequence 1, Appli
32 34.6 16.6 2140 3 US-09-206-899-1 Sequence 1, Appli
33 34.6 16.6 2140 4 US-09-444-783-1 Sequence 1, Appli
34 34.6 16.6 2140 4 US-09-688-415-1 Sequence 1, Appli
35 34.6 16.6 2140 5 PCT-US95-04203-1 Sequence 1, Appli
36 34.4 16.5 1894 3 US-09-329-350-32 Sequence 32, Appli
37 34.4 16.5 30001 1 US-08-125-468-1 Sequence 1, Appli
38 34.4 16.5 30001 2 US-08-474-933-1 Sequence 1, Appli
39 34 16.3 680 4 US-09-556-877-267 Sequence 267, App
40 34 16.3 680 4 US-09-620-412C-267 Sequence 267, App
41 34 16.3 680 4 US-09-598-419-267 Sequence 267, App
42 34 16.3 1716 4 US-09-252-991A-1306 Sequence 1306, Ap
43 34 16.3 1788 4 US-09-252-991A-1395 Sequence 1395, Ap
c 44 34 16.3 1980 4 US-09-252-991A-1160 Sequence 1160, Ap
c 45 33.8 16.2 894 4 US-09-252-991A-10907 Sequence 10907, A

ALIGNMENTS

RESULT 1
US-08-250-030-1
; Sequence 1, Application US/08250030
; Patent No. 5643723
; GENERAL INFORMATION:
; APPLICANT: Persing, David H.
; TITLE OF INVENTION: Detection of a Genetic Locus Encoding
; TITLE OF INVENTION: Resistance to Rifampin in Mycobacterial Cultures and in
; TITLE OF INVENTION: Clinical Specimens
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg & Woessner
; STREET: 3500 IDS Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/250,030
; FILING DATE: 26-MAY-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Muetting, Ann M.
; REGISTRATION NUMBER: 33,977
; REFERENCE/DOCKET NUMBER: 150.105US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-339-0331
; TELEFAX: 612-339-3061
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 970 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-250-030-1

Query Match 100.0%; Score 208; DB 1; Length 970;
Best Local Similarity 100.0%; Pred. No. 3.6e-48;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAGGAGAGCGCTACGACCTGCGCGCTGCTATAGCTCAACAGAGCTCG 60

Db 26 TCAAGGAGAGCGCTACGACCTGCGCGCTGCTATAGCTCAACAGAGCTCG 85

QY 61 GCGTCATGTCGGCGAGCCCATCAGCTGCTGAGCTGACCGAAGAGAGCTGCTGGCCA 120
Db 86 GCGTCATGTCGGCGAGCCCATCAGCTGCTGAGCTGACCGAAGAGAGCTGCTGGCCA 145
QY 121 CCATCGAATATCTGTCGGTTCGACGAGGTCAGACCATGACGATGACCGTTCGGGCGGCG 180
Db 146 CCATCGAATATCTGTCGGTTCGACGAGGTCAGACCATGACGATGACCGTTCGGGCGGCG 205
QY 181 TCGAGGTGCGGGTGGAAACCGAGACAT 208
Db 206 TCGAGGTGCGGGTGGAAACCGAGACAT 233

RESULT 2

PCT-US95-06790-1
; Sequence 1, Application PC/TUS9506790
; GENERAL INFORMATION:
; APPLICANT: Mayo Foundation for Medical Education and Research
; APPLICANT: and Hoffmann-La Roche Inc.
; TITLE OF INVENTION: Detection of a Genetic Locus Encoding
; TITLE OF INVENTION: Resistance to Rifampin
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Schwesman, Lundberg & Woessner
; STREET: 3500 IDS Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06790
FILING DATE: 26-MAY-1995

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Raasch, Kevin W.
REGISTRATION NUMBER: 35,651
REFERENCE/DOCKET NUMBER: 150.150501
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-0331
TELEFAX: 612-339-3061
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 970 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
PCT-US95-06790-1

Query Match 100.0%; Score 208; DB 5; Length 970;
Best Local Similarity 100.0%; Pred. No. 3.6e-48;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCAAGGAGAAGCGCTACGACCTGGCCCGCTGCTGCTATTAAGGTCAACAAGAGCTCG 60
Db 26 TCAAGGAGAAGCGCTACGACCTGGCCCGCTGCTGCTATTAAGGTCAACAAGAGCTCG 85
QY 61 GCGTCATGTCGGCGAGCCCATCAGCTGCTGAGCTGACCGAAGAGAGCTGCTGGCCA 120
Db 86 GCGTCATGTCGGCGAGCCCATCAGCTGCTGAGCTGACCGAAGAGAGCTGCTGGCCA 145
QY 121 CCATCGAATATCTGTCGGTTCGACGAGGTCAGACCATGACGATGACCGTTCGGGCGGCG 180
Db 146 CCATCGAATATCTGTCGGTTCGACGAGGTCAGACCATGACGATGACCGTTCGGGCGGCG 205
QY 181 TCGAGGTGCGGGTGGAAACCGAGACAT 208
Db 206 TCGAGGTGCGGGTGGAAACCGAGACAT 233

RESULT 3

US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: FRASER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match 100.0%; Score 208; DB 3; Length 4403765;
Best Local Similarity 100.0%; Pred. No. 1.5e-47;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCAAGGAGAAGCGCTACGACCTGGCCCGCTGCTGCTATTAAGGTCAACAAGAGCTCG 60
Db 762648 TCAAGGAGAAGCGCTACGACCTGGCCCGCTGCTGCTATTAAGGTCAACAAGAGCTCG 762707
QY 61 GCGTCATGTCGGCGAGCCCATCAGCTGCTGAGCTGACCGAAGAGAGCTGCTGGCCA 120
Db 762708 GCGTCATGTCGGCGAGCCCATCAGCTGCTGAGCTGACCGAAGAGAGCTGCTGGCCA 762767
QY 121 CCATCGAATATCTGTCGGTTCGACGAGGTCAGACCATGACGATGACCGTTCGGGCGGCG 180
Db 762768 CCATCGAATATCTGTCGGTTCGACGAGGTCAGACCATGACGATGACCGTTCGGGCGGCG 762827
QY 181 TCGAGGTGCGGGTGGAAACCGAGACAT 208
Db 762828 TCGAGGTGCGGGTGGAAACCGAGACAT 762855

RESULT 4

US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: FRASER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match 100.0%; Score 208; DB 3; Length 4411529;

Best Local Similarity 100.0%; Pred. No. 1.5e-47;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAGGAGAGAGCCTACGACCTGGCCCGCTCGCTATAGGTCAACAGAGCTCG 60
Db 760688 TCAGGAGAGAGCCTACGACCTGGCCCGCTCGCTATAGGTCAACAGAGCTCG 760747
QY 61 GCGTCGATGTCGCGAGGCCATCACGTCGTCGACGCTGACCGAAGAGAGCTCGTGCCCA 120
Db 760748 GCGTCGATGTCGCGAGGCCATCACGTCGTCGACGCTGACCGAAGAGAGCTCGTGCCCA 760807
QY 121 CCATCGAATATCTGTCGCTTGCACGAGGCTCAGACCGATGACCGTCCGGGCGCG 180
Db 760808 CCATCGAATATCTGTCGCTTGCACGAGGCTCAGACCGATGACCGTCCGGGCGCG 180
QY 181 TCGAGGTGCGGTGGAAACCGACGACAT 208
Db 760868 TCGAGGTGCGGTGGAAACCGACGACAT 760895

RESULT 5

US-08-313-185-57
; Sequence 57, Application US/08313185
; Patent No. 5851763
; GENERAL INFORMATION:
; APPLICANT: Heym, Beate
; APPLICANT: Cole, Stewart
; APPLICANT: Young, Douglas
; APPLICANT: Zhang, Ying
; APPLICANT: Honore, Nadine
; APPLICANT: Telenti, Amalio
; APPLICANT: Bodmer, Thomas
; TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
; TITLE OF INVENTION: in Mycobacterium Tuberculosis
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/313,185
; FILING DATE: 12-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 02356.0068-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3447 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-313-185-57

Query Match 71.5%; Score 148.8; DB 2; Length 3447;
Best Local Similarity 82.2%; Pred. No. 6.4e-32;
Matches 171; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 1 TCAGGAGAGAGCCTACGACCTGGCCCGCTCGCTATAGGTCAACAGAGCTCG 60

Db 809 TCAGGAGAGAGCCTACGACCTGGCCCGCTCGCTATAGGTCAACAGAGCTCG 868
QY 61 GCGTCGATGTCGCGAGGCCATCACGTCGTCGACGCTGACCGAAGAGAGCTCGTGCCCA 120
Db 869 GGTTCACGCGGTGAGTTGATCACGTCGTCACGCTGACCGAAGAGAGTATCGTCGCCCA 928
QY 121 CCATCGAATATCTGTCGCTTGCACGAGGCTCAGACCGATGACCGTCCGGGCGCG 180
Db 929 CCATGAGTACCTGGTTCGCTGATGAGGCTCAGTCGACATGACTGTCGCCAGGTGGG 988
QY 181 TCGAGGTGCGGTGGAAACCGACGACAT 208
Db 989 TAGAGTGCACGTGGAACTGACGATAT 1015

RESULT 6

US-09-082-614A-57
; Sequence 57, Application US/09082614A
; Patent No. 6124098
; GENERAL INFORMATION:
; APPLICANT: Heym, Beate
; APPLICANT: Cole, Stewart
; APPLICANT: Young, Douglas
; APPLICANT: Zhang, Ying
; APPLICANT: Honore, Nadine
; APPLICANT: Telenti, Amalio
; APPLICANT: Bodmer, Thomas
; TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
; TITLE OF INVENTION: in Mycobacterium Tuberculosis
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/082,614A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/313,185
; FILING DATE: 12-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 02356.0068-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3447 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-082-614A-57

Query Match 71.5%; Score 148.8; DB 3; Length 3447;
Best Local Similarity 82.2%; Pred. No. 6.4e-32;
Matches 171; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 1 TCAGGAGAGAGCCTACGACCTGGCCCGCTCGCTATAGGTCAACAGAGCTCG 60

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Db      809 TCAAGGAGAAACCTACGACCTGGCCAGGGTTGGTCTTACAGGTCACACAGAGCTCG 868
QY      61 GGTGTCATTCGGCAGACCCATCAGCTGTCGACGCTACCGAAGAGAGCTGCTGGCCA 120
Db      869 GGTGTCACCGCGGTGAGTGTATCAGCTGCTCCACGCTGACCGAAGAGGATGCTGTCGCCA 928
QY      121 CCATCGAATATCTGCTCGCTTGCAGAGGGTCAAGACACGATGACGCTGCGGGCGCG 180
Db      929 CCATAGAGTACTGGTTCGCTGCAATGAGGGTCACTGACAACTACTGTCCTCCAGGTGGG 988
QY      181 TCGAGTGGCGGTGGAACACGACGACAT 208
Db      989 TAGAGTGCAGTGGAAACTGACGATAT 1016

RESULT 7
US-09-252-991A-969
; Sequence 969, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 969
; LENGTH: 924
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-969

Query Match      18.6%; Score 38.6; DB 4; Length 924;
Best Local Similarity 51.4%; Pred. No. 0.061;
Matches 89; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY      17 CGACCTGGCCGCGCTGCTGCTATAGGTCAACAGAGCTCGGGCTGATGTCGGCGA 76
Db      597 CGACCCCTGCGCTGCTGCTGCGACCGCGCGAGGCGTGGCCGCGCACTGTGTAG 656
QY      77 GCCATCAGCTGCTCGAGCTGACCGAAGAGAGCTGCTGGCCACCATCGAATATCTGT 136
Db      657 CACCGACGCTGGGCTCGATGGGCCAGAGAACGCGCGCGCATCGCCCTGTT 716
QY      137 CCCTTTGCAGAGGTGACGACGATGACCGTTCGGGGCGGCTCGAGTGC 189
Db      717 CCCTCCCTACCAGGTGAACGCGCTTGTCTGATGGGCGCGCGACGATGTAC 769

RESULT 8
US-09-252-991A-925
; Sequence 925, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 925
; LENGTH: 939
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-925

Query Match      18.6%; Score 38.6; DB 4; Length 939;
Best Local Similarity 51.4%; Pred. No. 0.061;
Matches 89; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY      17 CGACCTGGCCGCGCTGCTGCTATAGGTCAACAGAGCTCGGGCTGATGTCGGCGA 76
Db      597 CGACCCCTGCGCTGCTGCTGCGACCGCGCGAGGCGTGGCCGCGCACTGTGTAG 656
QY      77 GCCATCAGCTGCTCGAGCTGACCGAAGAGAGCTGCTGGCCACCATCGAATATCTGT 136
Db      657 CACCGACGCTGGGCTCGATGGGCCAGAGAACGCGCGCGCATCGCCCTGTT 716
QY      137 CCCTTTGCAGAGGTGACGACGATGACCGTTCGGGGCGGCTCGAGTGC 189
Db      717 CCCTCCCTACCAGGTGAACGCGCTTGTCTGATGGGCGCGCGACGATGTAC 769
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-925

Query Match      18.6%; Score 38.6; DB 4; Length 939;
Best Local Similarity 51.4%; Pred. No. 0.061;
Matches 89; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY      17 CGACCTGGCCGCGCTGCTGCTATAGGTCAACAGAGCTCGGGCTGATGTCGGCGA 76
Db      604 CGACCGCTTGCCTGCTGCTGCGACCGCGCGAGCGGTGGCGGCGCGACCTGTGTAG 663
QY      77 GCCATCAGCTGCTCGAGCTGACCGAAGAGAGCTGCTGGCCACCATCGAATATCTGT 136
Db      664 CACCGACGCTGGGCTCGATGGGCCAGAGAACGCGCGCGCATCGCCCTGTT 723
QY      137 CCCTTTGCAGAGGTGACGACGATGACCGTTCGGGGCGGCTCGAGTGC 189
Db      724 CCCTCCCTACCAGGTGAACGCGCTTGTCTGATGGGCGCGCGACGATGTAC 776

RESULT 9
US-09-252-991A-1114/c
; Sequence 1114, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 1114
; LENGTH: 768
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1114

Query Match      18.4%; Score 38.2; DB 4; Length 768;
Best Local Similarity 51.5%; Pred. No. 0.076;
Matches 88; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

QY      17 CGACCTGGCCGCGCTGCTGCTATAGGTCAACAGAGCTCGGGCTGATGTCGGCGA 76
Db      172 CGACCGCTTGCCTGCTGCTGCGACCGCGCGAGCGGTGGCGCGCGACCTGTGTAG 113
QY      77 GCCATCAGCTGCTGAGCTGACCGAAGAGAGCTGCTGGCCACCATCGAATATCTGT 136
Db      112 CACCGACGCTGGGCTCGATGGGCCAGAGAACGCGCGCGCATCGCCCTGTT 53
QY      137 CCCTTTGCAGAGGTGACGACGATGACCGTTCGGGGCGGCTCGAGT 187
Db      52 CCCTCCCTACCAGGTGAACGCGCTTGTCTGATGGGCGCGCGACGATGT 2

RESULT 10
US-08-097-831-1
; Sequence 1, Application US/08097831
; Patent No. 5510473
; GENERAL INFORMATION:
; APPLICANT: Camerini-Otero, Rafael D.
; APPLICANT: Angov, Evangelina
; TITLE OF INVENTION: Cloning and Expression of Taq recA
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KNOBBE, MARTENS, OLSON AND BEAR
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
```

COUNTRY: USA
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/097,831
FILING DATE: 19930726
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E.
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: NIH066.001A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
TELEFAX: 714-760-9502
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1412 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: gDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: Taq reca
FEATURE:
NAME/KEY: CDS
LOCATION: 62..1082
US-08-097-831-1

Query Match 17.9%; Score 37.2; DB 1; Length 1412;
Best Local Similarity 53.4%; Pred. No. 0.16;
Matches 78; Conservative 0; Mismatches 68; Indels 0; Gaps 0;
QY 50 CAAGAAGTCGGGTGCTATGTCGGGAGCCCATCATCAGTCGTCGACGTCGACCGAAGAAGA 109
DB 370 CAAGAAGTCGGGTGCTATGTCGGGAGCCCATCATCAGTCGTCGACGTCGACCGAAGAAGA 429
QY 110 CBTGTCGCGCCACCATCAATATCTGTTCGCGTTCGACGAGGTCGACGACGATGACCGT 169
DB 430 GCGTTTGAGATCTGAGAGCTTCTGCGCGCTCGGGGCGGTGGACGTGATGCTGTGTTGA 489
QY 170 TCGGGCGCGTCGAGTGGTCCGGTGG 195
DB 490 TCGGTGGCGCGTTTGGTGGCCCAAGG 515

RESULT 11
US-09-252-991A-13650/C
; Sequence 13650, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 13650
; LENGTH: 1452
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13650

Query Match 17.9%; Score 37.2; DB 4; Length 1452;
Best Local Similarity 56.6%; Pred. No. 0.16;
Matches 69; Conservative 0; Mismatches 53; Indels 0; Gaps 0;
QY 13 GGTAGCACTGGCCCGGCTGCTGCTATAGGTCAACAAGAAGCTGGGCTGCATGTCG 72
DB 806 GCGCCTACTGTGCTTGAAGGCTTCGAGAGATGCCCAATACTGCCCATGAGG 747
QY 73 GCGAGCCCATCACTGCTGCGACGCTGACGAGAGAGAGCTGGGCCACCATCGAATATC 132
DB 746 ACAGACAGCCGACGAGGAGCGCTGGCGCCATGTGACGTGGCGCCCTGGAAAGC 687
QY 133 TG 134
DB 686 AG 685

RESULT 12
US-09-252-991A-13782
; Sequence 13782, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 13782
; LENGTH: 1980
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13782

Query Match 17.9%; Score 37.2; DB 4; Length 1980;
Best Local Similarity 56.6%; Pred. No. 0.17; Mismatches 53; Indels 0; Gaps 0;
Matches 69; Conservative 0; Mismatches 53; Indels 0; Gaps 0;
QY 13 GCTAGCACTGGCCCGGCTGCTGCTATAGGTCAACAAGAAGCTGGGCTGCATGTCG 72
DB 1340 GCGCCTACTGTGCTTGAAGGCTTCGAGAGATGCCCAATACTGCCCATGAGG 1399
QY 73 GCGAGCCCATCACTGCTGCGACGCTGACGAGAGAGAGCTGGGCCACCATCGAATATC 132
DB 1400 ACAGACAGCCGACGAGGAGCGCTGGCGCCATGTGACGTGGCGCCCTGGAAAGC 1459
QY 133 TG 134
DB 1460 AG 1461

RESULT 13
US-09-029-603-4
; Sequence 4, Application US/09029603
; Patent No. 6210935
; GENERAL INFORMATION:
; APPLICANT: Schupp, Thomas
; APPLICANT: Engel, Natalie
; APPLICANT: Bietenhader, Jurg
; APPLICANT: Toupet, Christine
; APPLICANT: Pospiech, Andreas
; TITLE OF INVENTION: Staurosporin Biosynthesis Gene Clusters
; FILE REFERENCE: 4-20555/A/PCT
; CURRENT APPLICATION NUMBER: US/09/029,603
; CURRENT FILING DATE: 1998-03-20
; EARLIER APPLICATION NUMBER: PCT/EP96/03643
; EARLIER FILING DATE: 1996-08-19
; NUMBER OF SEQ ID NOS: 11

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 6085
; TYPE: DNA
; ORGANISM: Streptomyces longisporoflavus
; FEATURE:
; NAME/KEY: misc_RNA
; LOCATION: (378)..(1665)
; OTHER INFORMATION: ORF
; FEATURE:
; NAME/KEY: misc_RNA
; LOCATION: (1747)..(2553)
; OTHER INFORMATION: ORF
; FEATURE:
; NAME/KEY: misc_RNA
; LOCATION: (2593)..(4011)
; OTHER INFORMATION: ORF
; FEATURE:
; NAME/KEY: misc_RNA
; LOCATION: (4013)..(4999)
; OTHER INFORMATION: ORF
; FEATURE:
; NAME/KEY: misc_RNA
; LOCATION: (5071)..(6085)
; OTHER INFORMATION: ORF
; US-09-029-603-4

Query Match      17.8%; Score 37; DB 3; Length 6085;
Best Local Similarity 51.5%; Pred. No. 0.23; Indels 0; Gaps 0;
Matches 85; Conservative 0; Mismatches 80;

QY 18 GACCTGCGCGCGTGGTGGTATAGGTCAACAGAGAGCTCGGCTGCATGTGGCGAG 77
Db 1017 GAGGTGACCGCGCGCGGCGGAGCAGCGGAGCATCTCTCACCTCTCTGTCGGCGC 1076

QY 78 CCCATCAGCTGCTGCGTACGACGCTGACGAGAGAGCTGTGGCCACCATGCAATATCTGGTC 137
Db 1077 CGGACACCGGATCACCCTGAGCTGAGCGGAGGATCGTGGCAGCATCTGCTCATCTGCTC 1136

QY 138 CGCTGTCACGAGGTGACGACGATGACCGTTCGCGGCGGGGTC 182
Db 1137 ACCGCGGCCACGAGCACCACCACTGCTGCCAGGGCGGTC 1181

RESULT 14
US-09-252-991A-13457/c
; Sequence 13457, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 13457
; LENGTH: 258
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-13457

Query Match      17.5%; Score 36.4; DB 4; Length 258;
Best Local Similarity 56.8%; Pred. No. 0.2; Indels 0; Gaps 0;
Matches 67; Conservative 0; Mismatches 51;

QY 17 CGACCTGCGCGGCTGGTGGTATAGGTCAACAGAGAGCTCGGCTGCATGTGGCGGA 76
Db 258 CTACCTGTGCTCGAGGCTTCGAGAGATCGGCCCAAAATACCTGCCCATGACGAGA 199

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 6085
; TYPE: DNA
; ORGANISM: Streptomyces longisporoflavus
; FEATURE:
; NAME/KEY: misc_RNA
; LOCATION: (378)..(1665)
; OTHER INFORMATION: ORF
; FEATURE:
; NAME/KEY: misc_RNA
; LOCATION: (1747)..(2553)
; OTHER INFORMATION: ORF
; FEATURE:
; NAME/KEY: misc_RNA
; LOCATION: (2593)..(4011)
; OTHER INFORMATION: ORF
; FEATURE:
; NAME/KEY: misc_RNA
; LOCATION: (4013)..(4999)
; OTHER INFORMATION: ORF
; FEATURE:
; NAME/KEY: misc_RNA
; LOCATION: (5071)..(6085)
; OTHER INFORMATION: ORF
; US-09-029-603-4

Query Match      17.5%; Score 36.4; DB 4; Length 615;
Best Local Similarity 51.9%; Pred. No. 0.23; Indels 0; Gaps 0;
Matches 82; Conservative 0; Mismatches 76;

QY 6 GAGAGAGCGCTACGACCTGGCCCGGCTGGTGGTATAGGTCAACAGAGAGCTCGGCTG 65
Db 311 GCGAGTTCTACGAGTCTCCCTCGCGGCGAGCTCGGCGGCGAGCCAGCTCGGCGAG 370

QY 66 CATGTGGGAGGCCATACGTGCTGCGAGCTGACCGAGAGAGAGCTGCTGGCCACCATC 125
Db 371 ATCTCGGCGCGCTTCGCTTCGCGGAGGAGAGATGCGGAGCTGATCGACAGATCATCCAG 430

QY 126 GAATATCTGTGGCTGCGCTGCGAGGAGGTGAGACACCAT 163
Db 431 GTCTACGTGAGACGCGCGGAGGAGAGACCCCTTCAT 468

Search completed: September 17, 2003, 12:26:59
Job time : 42.1605 secs

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; TYPE: DNA
; ORGANISM: Streptomyces longisporoflavus
; FEATURE:
; NAME/KEY: misc_RNA
; LOCATION: (378)..(1665)
; OTHER INFORMATION: ORF
; FEATURE:
; NAME/KEY: misc_RNA
; LOCATION: (1747)..(2553)
; OTHER INFORMATION: ORF
; FEATURE:
; NAME/KEY: misc_RNA
; LOCATION: (2593)..(4011)
; OTHER INFORMATION: ORF
; FEATURE:
; NAME/KEY: misc_RNA
; LOCATION: (4013)..(4999)
; OTHER INFORMATION: ORF
; FEATURE:
; NAME/KEY: misc_RNA
; LOCATION: (5071)..(6085)
; OTHER INFORMATION: ORF
; US-09-029-603-4

Query Match      17.5%; Score 36.4; DB 4; Length 615;
Best Local Similarity 51.9%; Pred. No. 0.23; Indels 0; Gaps 0;
Matches 82; Conservative 0; Mismatches 76;

QY 6 GAGAGAGCGCTACGACCTGGCCCGGCTGGTGGTATAGGTCAACAGAGAGCTCGGCTG 65
Db 311 GCGAGTTCTACGAGTCTCCCTCGCGGCGAGCTCGGCGGCGAGCCAGCTCGGCGAG 370

QY 66 CATGTGGGAGGCCATACGTGCTGCGAGCTGACCGAGAGAGAGCTGCTGGCCACCATC 125
Db 371 ATCTCGGCGCGCTTCGCTTCGCGGAGGAGAGATGCGGAGCTGATCGACAGATCATCCAG 430

QY 126 GAATATCTGTGGCTGCGCTGCGAGGAGGTGAGACACCAT 163
Db 431 GTCTACGTGAGACGCGCGGAGGAGAGACCCCTTCAT 468

Search completed: September 17, 2003, 12:26:59
Job time : 42.1605 secs
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OM nucleic - nucleic search, using sw model

Run on: September 17, 2003, 11:54:34 ; Search time 108.259 Seconds
(without alignments)
4726.283 Million cell updates/sec

Title: US-09-697-123B-5

Perfect score: 208

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1660708 seqs, 1229959015 residues

Total number of hits satisfying chosen parameters: 3321416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
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9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
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13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	208	100.0	3519	10	US-09-712-363-30
2	89.6	43.1	3495	10	US-09-738-626-547
3	89.6	43.1	5096	10	US-09-984-711-5
4	89.6	43.1	5099	10	US-09-887-052-1
5	89.6	43.1	5099	10	US-09-887-052-3
6	89.6	43.1	5099	10	US-09-887-052-5
7	89.6	43.1	5099	12	US-10-076-406-1
8	89.6	43.1	5099	12	US-10-076-406-3
9	89.6	43.1	5099	12	US-10-076-406-5
10	89.6	43.1	5099	13	US-10-075-460-5
11	89.6	43.1	3309400	10	US-09-738-626-1
12	67.6	32.5	3543	14	US-10-156-761-4898
13	67.6	32.5	9025608	14	US-10-156-761-1
14	40.4	19.4	1215	14	US-10-156-761-2811
15	38.6	18.6	1131	14	US-10-156-761-2479
16	38.6	18.6	9025608	14	US-10-156-761-1

c

17 38.2 18.4 1395 14 US-10-205-032-21 Sequence 21, Appl
18 38.2 18.4 60196 14 US-10-205-032-1 Sequence 1, Appl
19 36.4 17.5 588 14 US-10-156-761-5853 Sequence 5853, Ap
20 35.8 17.2 1509 12 US-09-967-464-64 Sequence 64, Appl
21 35.8 17.2 1509 12 US-09-967-464-68 Sequence 68, Appl
22 35.6 17.1 3756 9 US-09-841-132-425 Sequence 425, App
23 35.4 17.0 1461 14 US-10-156-761-2120 Sequence 2120, Ap
24 35 3774 14 US-10-156-761-2845 Sequence 2845, Ap
25 34.6 16.6 1458 14 US-10-156-761-2845 Sequence 2845, Ap
26 34.6 16.6 2130 14 US-10-156-761-4634 Sequence 4634, Ap
27 34.6 16.6 2140 14 US-10-235-567A-33 Sequence 33, Appl
28 34.6 16.6 2140 14 US-10-185-991-1 Sequence 1, Appl
29 34.6 16.6 2140 14 US-10-238-667-1 Sequence 1, Appl
30 34.4 16.5 1894 8 US-08-841-636A-32 Sequence 32, Appl
31 34.4 16.5 5721 14 US-10-156-761-2880 Sequence 2880, Ap
32 34.4 16.5 125746 14 US-10-156-761-15102 Sequence 15102, A
33 34.2 16.4 1191 14 US-10-156-761-1671 Sequence 1671, Ap
34 34.2 16.4 1398 14 US-10-156-761-2212 Sequence 2212, Ap
35 34.2 16.4 2334 14 US-10-156-761-5079 Sequence 5079, Ap
36 34 16.3 680 9 US-09-841-132-267 Sequence 267, App
37 34 16.3 993 14 US-10-156-761-4673 Sequence 4673, Ap
38 34 16.3 1509 14 US-10-156-761-1592 Sequence 1592, Ap
39 34 16.3 1596 14 US-10-156-761-4136 Sequence 4136, Ap
40 33.8 16.2 723 14 US-10-156-761-6797 Sequence 6797, Ap
41 33.8 16.2 1029 14 US-10-156-761-5440 Sequence 5440, Ap
42 33.8 16.2 1284 14 US-10-156-761-5434 Sequence 5434, Ap
43 33.8 16.2 2715 14 US-10-156-761-2245 Sequence 2245, Ap
44 33.8 16.2 5418 14 US-10-156-761-5959 Sequence 5959, Ap
45 33.6 16.2 825 14 US-10-156-761-2303 Sequence 2303, Ap

ALIGNMENTS

RESULT 1
US-09-712-363-30
; Sequence 30, Application US/09712363
; Patent No. US20020164588A1
; GENERAL INFORMATION:
; APPLICANT: Eisenberg, David
; APPLICANT: Rotstein, Sergio H.
; APPLICANT: Marcotte, Edward M.
; TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND
; TITLE OF INVENTION: INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS
; FILE REFERENCE: 07419-032001
; CURRENT APPLICATION NUMBER: US/09/712,363
; CURRENT FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: PCT/US00/02246
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,531
; PRIOR FILING DATE: 2000-02-01
; PRIOR APPLICATION NUMBER: 60/117,844
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/118,206,
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: 60/126,593
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/134,093
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/134,092
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/165,124
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/165,086
; PRIOR FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 3519
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-09-712-363-30

Query Match 100.0%; Score 208; DB 10; Length 3519;
Best Local Similarity 100.0%; Pred. No. 4e-58;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAGGAGAGCGCTACGACCTGGCCCGCTCGGTGCTATAGGTCAACAAAGCTCG 60
DB 884 TCAGGAGAGCGCTACGACCTGGCCCGCTCGGTGCTATAGGTCAACAAAGCTCG 943
QY 61 GCGTGCATGCGCGAGCGCCATCACGTCGTCGACGCTGACCGAAGAGAGCTGCTGGCCA 120
DB 944 GCGTGCATGCGCGAGCGCCATCACGTCGTCGACGCTGACCGAAGAGAGCTGCTGGCCA 1003
QY 121 CCAATCAATATCTGCTCGCTGTCACAGAGGTCACACCATGACCGCTTCGCGGGGGGG 180
DB 1004 CCAATCAATATCTGCTCGCTGTCACAGAGGTCACACCATGACCGCTTCGCGGGGGGG 1063
QY 181 TCAGGTGCGGCTGGAACCGACGACAT 208
DB 1064 TCAGGTGCGGCTGGAACCGACGACAT 1091

RESULT 2
US-09-738-626-547
; Sequence 547, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIALI, KEIKO
; APPLICANT: YOKOL, HARUHIKO
; APPLICANT: TATEISHI, NAORO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09738, 626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 547
; LENGTH: 3495
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-547

Query Match 43.1%; Score 89.6; DB 10; Length 3495;
Best Local Similarity 69.0%; Pred. No. 1.6e-19;
Matches 138; Conservative 0; Mismatches 59; Indels 3; Gaps 1;

QY 9 AAGCGTAGACCTGGCCCGCTCGGTGCTATAGGTCAACAAAGCTCGGCTGTCAT 68
DB 877 AAGCGTAGACCTGGCTGGGTGCTGCTTACAGATCAACCGAAGCTCGGCCT--T 933
QY 69 GTGGGAGCGCATCAGCTGCTGACGCTGACGAGAGAGCTGCTGGCCACCATCGAA 128
DB 934 GTGGGAGCGCATCAGCTGCTGACGCTGACGAGAGAGCTGCTGGCCACCATCGAG 993
QY 129 TATCTGCTCGCTGTCACGAGGTCACACCATGACCGCTTCGCGGCGGCTCGAGTG 188
DB 994 TACTGTGCTGCTGTCACGAGGTCAGCGGCTCATGACTTCTCCAAATGTTGAAGATC 1053
QY 189 CCGGTGGAACCGAGACAT 208
DB 1054 CCGGTGGAACCGAGATGACAT 1073

RESULT 3
US-09-984-711-5
; Sequence 5, Application US/09984711
; Patent No. US20020119549A1
; GENERAL INFORMATION:
; APPLICANT: MORCKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: STEPHAN, Hans
; APPLICANT: KREUTZER, Caroline
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE rpsL GENE
; FILE REFERENCE: 204209US0
; CURRENT APPLICATION NUMBER: US/09/984,711
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: DE10108230.9
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 5096
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
; OTHER INFORMATION:
US-09-984-711-5

Query Match 43.1%; Score 89.6; DB 10; Length 5096;
Best Local Similarity 69.0%; Pred. No. 1.6e-19;
Matches 138; Conservative 0; Mismatches 59; Indels 3; Gaps 1;

QY 9 AAGCGTAGACCTGGCCCGCTCGGTGCTATAGGTCAACAAAGCTCGGCTGTCAT 68
DB 1578 AAGCGTAGACCTGGCTGGGTGCTGCTTACAGATCAACCGAAGCTCGGCCT--T 1634
QY 69 GTGGGAGCGCATCAGCTGCTGACGCTGACGAGAGAGCTGCTGGCCACCATCGAA 128
DB 1635 GTGGGAGCGCATCAGCTGCTGACGCTGCTTACGAGAGAGATCGCAACCATCGAG 1694
QY 129 TATCTGCTCGCTGTCACGAGGTCACACCATGACCGCTTCGCGGCGGCTCGAGTG 188
DB 1695 TACTGTGCTGCTGTCACGAGGTCAGCGGCTCATGACTTCTCCAAATGTTGAAGATC 1754
QY 189 CCGGTGGAACCGAGACAT 208
DB 1755 CCGGTGGAACCGAGATGACAT 1774

RESULT 4
US-09-887-052-1
; Sequence 1, Application US/09887052
; Patent No. US20020119537A1
; GENERAL INFORMATION:
; APPLICANT: MORCKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE rpoB GENE
; FILE REFERENCE: 204212US0X
; CURRENT APPLICATION NUMBER: US/09/887,052
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: DE10107229.5
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 5099


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; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
; OTHER INFORMATION:
US-10-076-406-1

Query Match          43.1%; Score 89.6; DB 12; Length 5099;
Best Local Similarity 69.0%; Pred. No. 1.6e-19;
Matches 138; Conservative 0; Mismatches 59; Indels 3; Gaps 1;

QY 9 AAGCGTAGACCTGGCCCGGTCGCTATAGGTCACCAAGAGCTCGGCGTCGAT 68
    |||||
Db 1578 AAGCGTAGACCTGGCTCGGTTGCTTACAGATCAACCGAGCTCGGCCT--T 1634

QY 69 GTGGGAGCCCATCAGCTCGTCGACGAGGTCAGACCAAGAGAGCTCGTGGCCACATCGAA 128
    |||||
Db 1635 GTGGGAGCCCATCAGCTCGTCGACGAGGTCAGACCAAGAGAGCTCGTGGCCACATCGAG 1694

QY 129 TATCTGGTCCGCTTGCACGAGGTCAGACCAAGAGAGCTCGTGGCCAGGAGTG 188
    |||||
Db 1695 TACCTGGTCCGCTTGCACGAGGTCAGACCAAGAGAGCTCGTGGCCAGGAGTG 188

QY 189 CCGGTGGAACCGAGCAT 208
    |||||
Db 1755 CCAGTCGAGACCGATGACAT 1774

RESULT 8
US-10-076-406-3
; Sequence 3, Application US/10076406
; Publication No. US20030166884A1
; GENERAL INFORMATION:
; APPLICANT: MORCKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: Nucleotide sequences coding for the rpoB gene
; FILE REFERENCE: 219774USOXIP
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: DE 10107229.5
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 09/887052
; PRIOR FILING DATE: 2001-06-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 3
; LENGTH: 5099
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
; OTHER INFORMATION:
; NAME/KEY: mutation
; LOCATION: (1987)..(1987)
; OTHER INFORMATION: Substitution of adenine by thymine
; NAME/KEY: mutation
; LOCATION: (1288)..(1288)
; OTHER INFORMATION: Substitution of cytosine by thymine
; NAME/KEY: mutation
; LOCATION: (715)..(715)
; OTHER INFORMATION: Substitution of cytosine by thymine
US-10-076-406-3

Query Match          43.1%; Score 89.6; DB 12; Length 5099;
Best Local Similarity 69.0%; Pred. No. 1.6e-19;
Matches 138; Conservative 0; Mismatches 59; Indels 3; Gaps 1;

QY 9 AAGCGTAGACCTGGCCCGGTCGCTATAGGTCACCAAGAGCTCGGCGTCGAT 68
    |||||
Db 1578 AAGCGTAGACCTGGCTCGGTTGCTTACAGATCAACCGAGCTCGGCCT--T 1634

QY 69 GTGGGAGCCCATCAGCTCGTCGACGAGGTCAGACCAAGAGAGCTCGTGGCCACATCGAA 128
    |||||
Db 1635 GTGGGAGCCCATCAGCTCGTCGACGAGGTCAGACCAAGAGAGCTCGTGGCCACATCGAG 1694

QY 129 TATCTGGTCCGCTTGCACGAGGTCAGACCAAGAGAGCTCGTGGCCAGGAGTG 188
    |||||
Db 1695 TACCTGGTCCGCTTGCACGAGGTCAGACCAAGAGAGCTCGTGGCCAGGAGTG 188

QY 189 CCGGTGGAACCGAGCAT 208
    |||||
Db 1755 CCAGTCGAGACCGATGACAT 1774

RESULT 9
US-10-076-406-5
; Sequence 5, Application US/10076406
; Publication No. US20030166884A1
; GENERAL INFORMATION:
; APPLICANT: MORCKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: Nucleotide sequences coding for the rpoB gene
; FILE REFERENCE: 219774USOXIP
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: DE 10107229.5
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 09/887052
; PRIOR FILING DATE: 2001-06-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 5
; LENGTH: 5099
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
; OTHER INFORMATION:
; NAME/KEY: mutation
; LOCATION: (2016)..(2016)
; OTHER INFORMATION: Substitution of cytosine by thymine
US-10-076-406-5

Query Match          43.1%; Score 89.6; DB 12; Length 5099;
Best Local Similarity 69.0%; Pred. No. 1.6e-19;
Matches 138; Conservative 0; Mismatches 59; Indels 3; Gaps 1;

QY 9 AAGCGTAGACCTGGCCCGGTCGCTATAGGTCACCAAGAGCTCGGCGTCGAT 68
    |||||
Db 1578 AAGCGTAGACCTGGCTCGGTTGCTTACAGATCAACCGAGCTCGGCCT--T 1634

QY 69 GTGGGAGCCCATCAGCTCGTCGACGAGGTCAGACCAAGAGAGCTCGTGGCCACATCGAA 128
    |||||
Db 1635 GTGGGAGCCCATCAGCTCGTCGACGAGGTCAGACCAAGAGAGCTCGTGGCCACATCGAG 1694

QY 129 TATCTGGTCCGCTTGCACGAGGTCAGACCAAGAGAGCTCGTGGCCAGGAGTG 188
    |||||
Db 1695 TACCTGGTCCGCTTGCACGAGGTCAGACCAAGAGAGCTCGTGGCCAGGAGTG 188

QY 189 CCGGTGGAACCGAGCAT 208
    |||||
Db 1755 CCAGTCGAGACCGATGACAT 1774

RESULT 10
US-10-075-460-5
; Sequence 5, Application US/10075460
```

; Publication No. US2002015557A1
 ; GENERAL INFORMATION:
 ; APPLICANT: MOCKEL, BETTINA
 ; APPLICANT: BATHE, BRIGITTE
 ; APPLICANT: HANS, STEFAN
 ; APPLICANT: KREUTZER, CAROLINE
 ; APPLICANT: HERMANN, THOMAS
 ; APPLICANT: PFEFFERLE, WALTER
 ; APPLICANT: BINDER, MICHAEL
 ; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE rpsL GENE
 ; FILE REFERENCE: 218472JUSOX
 ; CURRENT APPLICATION NUMBER: US/10/075,460
 ; CURRENT FILING DATE: 2002-02-15
 ; PRIOR APPLICATION NUMBER: DE 10107230.9
 ; PRIOR FILING DATE: 2001-02-16
 ; PRIOR APPLICATION NUMBER: DE 10162386.0
 ; PRIOR FILING DATE: 2001-12-19
 ; NUMBER OF SEQ ID NOS: 14
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 5
 ; TYPE: DNA
 ; LENGTH: 5099
 ; ORGANISM: Corynebacterium glutamicum
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (702)..(4196)
 ; OTHER INFORMATION:
 US-10-075-460-5

 Query Match 43.1%; Score 89.6; DB 13; Length 5099;
 Best Local Similarity 69.0%; Pred. No. 1.6e-19;
 Matches 138; Conservative 0; Mismatches 59; Indels 3; Gaps 1;

 QY 9 AAGCGCTACGACCTGGCCGGCTCGCTATAAGTCAACAAGAGCTCGGCTGCAT 68
 |||||
 DB 1578 AAGCGCTACGACCTGGCTGGCTGGCTTACGAATCAACCGCAAGCTGGGCT---T 1634
 |||||
 QY 69 GTGGCGAGGCCATCACCTCTCGACGCTGACCGAAGAAGAGCTGCTGGCCACCATCGAA 128
 |||||
 DB 1635 GTGGCGAGCCAGATGGTTTGATGACTCTTACTGAAGAGGACATCGCAACACCATCGAG 1694
 |||||
 QY 129 TATCTGTCGGTTCGACGAGGGTCAGACACGATGACCGTTCGGGGGGGGTGGAGGTG 188
 |||||
 DB 1695 TACCTGTGCTGTCGACGAGGTGAGCGGCTCATGACTTCTCCAATGGTGAAGATC 1754
 |||||
 QY 189 CCGGTGGAACCGACGACAT 208
 |||||
 DB 1755 CCAGTCGAGACGATGACAT 1774

 RESULT 11
 US-09-738-626-1
 ; Sequence 1, Application US/09738626
 ; Publication No. US20020197605A1
 ; GENERAL INFORMATION:
 ; APPLICANT: NAKAGAWA, SATOSHI
 ; APPLICANT: MIZOGUCHI, HIROSHI
 ; APPLICANT: ANDO, SEIKO
 ; APPLICANT: HAYASHI, MIKIO
 ; APPLICANT: OCHIALI, KEIKO
 ; APPLICANT: YOKOI, HARUHIKO
 ; APPLICANT: TATEISHI, NAKO
 ; APPLICANT: SENOH, AKIHIRO
 ; APPLICANT: IKEDA, MASATO
 ; APPLICANT: OZAKI, AKIO
 ; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
 ; FILE REFERENCE: 249-125
 ; CURRENT APPLICATION NUMBER: US/09/738,626
 ; CURRENT FILING DATE: 2000-12-18
 ; PRIOR APPLICATION NUMBER: JP 99/377484
 ; PRIOR FILING DATE: 1999-12-16
 ; PRIOR APPLICATION NUMBER: JP 00/159162
 ; PRIOR FILING DATE: 2000-04-07

 Query Match 32.5%; Score 67.6; DB 14; Length 3543;
 Best Local Similarity 61.5%; Pred. No. 2.3e-12;
 Matches 128; Conservative 0; Mismatches 74; Indels 6; Gaps 1;

 QY 1 TCAAGGAGAACGCTACGACCTGGCCGGCTCGCTATAGTCAACGAAGAGCTCG 60
 |||||
 DB 926 TCAACCCGAAGCGCTAGGACCTCGGAGGTCGCGCTACAAGGTCAACGAAGAGCTGG 985
 |||||
 QY 61 GCGTGTATGTGCGGAGGCCATCAGCTGCTGAGCCGAGGACGAGAGACCTCTGCGCCA 120
 |||||
 DB 986 GC-----GGCGAGGCGCGCTGGACGCGCGGATCTCTGACCTCGAGGACATCTCGT 1039
 |||||

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; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 2811
; LENGTH: 1215
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1215)
US-10-156-761-2811

Query Match          19.4%; Score 40.4; DB 14; Length 1215;
Best Local Similarity 58.2%; Pred. No. 0.00157;
Matches 71; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

Qy 55 AGCTCGGCTGCATGTCGGCGAGCGCCATCACGTCGTCGACGCTGACCGAAGAGACGTCG 114
Db 275 ACCGCGTGTGCACGCGCGGCGTCTTCACGAGCGGACCGTCTCATCGACGACGAGTCC 334
Qy 115 TGCGCCACCAACGAATATCTGTCGCGTTCGACGAGGTCACACGACGATCACGCTCCGG 174
Db 335 TCGCCGAGATCGAGCGGCTGATCCCCGTGCGCGCGCTGCACAACCCGGCCACCTCACCG 394
Qy 175 GC 176
Db 395 GC 396

RESULT 15
US-10-156-761-2479
; Sequence 2479, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 2479
; LENGTH: 1131
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1131)
US-10-156-761-2479

Query Match          18.6%; Score 38.6; DB 14; Length 1131;
Best Local Similarity 54.6%; Pred. No. 0.0057;
Matches 77; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

Qy 51 AAGAAGCTCGGGCTGCATGTCGGCGAGCCCATACAGCTGTCGACGTCGACCGAAGAC 110
Db 313 AAGAAGCTCGGGCTGCATGTCGACACACTGATCTCTGTGCGAGCGGACACGCTGAGCAG 372

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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1131)
US-10-156-761-2479

Query Match      18.6%; Score 38.6; DB 14; Length 1131;
Best Local Similarity 54.6%; Pred. No. 0.0057;
Matches 77; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

Qy 51 AAGAAGCTCGGGTGCATGTCGCGGACGCCCATCAGCTGTGCGAGCTGACCCGAAGAAGAC 110
    |||||
Db 313 AAGAAGCTCGGGTGCACATCGACAACCTGATCCTGTGCGACGGCACACGCTGAGCAG 372

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QY
111 GTCGTGCCACCATCGAATATCTGGTCCGTTGCACGAGGGTCAGACCACGATGACCGTT 170

Dδ
373 GCCTCGAGATCGTGACATGCTGGTCCGCTCCGGCCGGCCTCACCTGATGCTCATCGAC 432

Db 373 GCTCTGGAGATCGTGGACATGCTGCTCGCTCCGGGGCGCTCGACCTGATCGTCATCGAC 432

QY 171 CCGGGCGGCTCGAGGTGCCG 191

Db 433 TCCGTCGCCGCCCTGGTGCCG 453

Search completed: September 17, 2003, 13:03:35
Job time : 128.259 secs

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OM nucleic - nucleic search, using sw model

Run on: September 17, 2003, 11:54:34 ; Search time 30.1105 seconds
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3049.028 Million cell updates/sec

Title: US-09-697-123B-6
 Perfect score: 208
 Sequence: 1 tcaaggagaaagcgctac.....ccgtggaaccgacacat 208

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

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Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Database : Issued_Patents_NA:*
1: /cn2.6/ptdata/1/ina/5A_COMB.seq.*
2: /cn2.6/ptdata/1/ina/5B_COMB.seq.*
3: /cn2.6/ptdata/1/ina/6A_COMB.seq.*
4: /cn2.6/ptdata/1/ina/6B_COMB.seq.*
5: /cn2.6/ptdata/1/ina/PCTUS_COMB.seq.*
6: /cn2.6/ptdata/1/ina/backfiles1.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARY

Result	No.	Score	Query Match	Length	DB	ID	Description
C	1	208	100.0	970	1	US-08-250-030-1	Sequence 1, Appli
	2	208	100.0	970	5	PCR-US95-06790-1	Sequence 1, Appli
	3	208	100.0	4403765	3	US-09-103-840A-2	Sequence 1, Appli
	4	208	100.0	4411529	3	US-09-103-840B-1	Sequence 1, Appli
	5	148.8	71.5	3447	2	US-08-313-185-57	Sequence 57, Appl
	6	148.8	71.5	3447	3	US-09-082-614A-57	Sequence 57, Appl
C	7	38.6	18.6	924	4	US-09-252-991A-969	Sequence 969, App
	8	38.6	18.6	939	4	US-09-252-991A-925	Sequence 925, App
	9	38.2	18.4	768	4	US-09-252-991A-1114	Sequence 1114, Ap
	10	37.2	17.9	1412	1	US-08-097-831-1	Sequence 1, Appli
	11	37.2	17.9	1452	4	US-09-252-991A-13650	Sequence 13650, A
	12	37.2	17.9	1980	4	US-09-252-991A-13782	Sequence 13782, A
C	13	37	17.8	6085	3	US-09-039-603-4	Sequence 4, Appli
	14	36.4	17.5	258	4	US-09-252-991A-13457	Sequence 13457, A
	15	36.4	17.5	615	4	US-09-252-991A-13899	Sequence 13899, A
	16	36.4	17.5	1695	4	US-09-252-991A-13695	Sequence 13695, A
	17	36	17.3	870	4	US-09-252-991A-7157	Sequence 7157, Ap
	18	36	17.3	2415	4	US-09-252-991A-7480	Sequence 7480, Ap
C	19	36	17.3	2667	4	US-09-252-991A-7216	Sequence 7216, Ap
	20	35.2	16.9	1326	4	US-09-252-991A-10931	Sequence 10931, A
	21	35.2	16.9	2211	4	US-09-252-991A-11256	Sequence 11256, A
	22	35.2	16.9	2289	4	US-09-252-991A-10995	Sequence 10995, A
	23	34.6	16.6	1621	1	US-08-722-001-13	Sequence 13, Appl
	24	34.6	16.6	1776	1	US-08-722-001-29	Sequence 29, Appl
C	25	34.6	16.6	2002	4	US-09-016-434-1172	Sequence 1172, Ap
	26	34.6	16.6	2140	1	US-08-334-698-1	Sequence 1, Appli
	27	34.6	16.6	2140	1	US-08-228-332-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1

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US-08-250-030-1
; Sequence 1, Application US/08250030
; Patent No. 5643723
; GENERAL INFORMATION:
; APPLICANT: Persing, David H.
; TITLE OF INVENTION: Detection of a Genetic Locus
; TITLE OF INVENTION: Resistance to Rifampin in My
; TITLE OF INVENTION: Clinical Specimens
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSSEE: Schwegman, Lundberg & Woessner
; STREET: 3500 IDS Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402

```

Query Match	100.0%;	Score 208;	DB 1;	Length 970;
Best Local Similarity	100.0%;	Pred. No. 3.6e-48;		

QY 1 TCAAGGAGAGCGCTACGACTGGCCCGCGTGGTGGCTATAAGGTCAACAGAAAGCTCG 60
 |||
 26 TCAAGGAGAGCGCTACGACTGGCCCGCGTGGTGGCTATAAGGTCAACAGAAAGCTCG 85
 |||

QY 61 GCGTCATGTCGGCGAGCCCACTACGTCGTCGACGCTGACCGAAGAGACGTCGTGGCCA 120
 Db 86 GCGTCATGTCGGCGAGCCCACTACGTCGTCGACGCTGACCGAAGAGACGTCGTGGCCA 145
 QY 121 CCATCGAATATCTGGTCGCTTCACGAGGTCAGACGATGACCGTTCGGCGGCG 180
 Db 146 CCATCGAATATCTGGTCGCTTCACGAGGTCAGACGATGACCGTTCGGCGGCG 205
 QY 181 TCGAGTGCCGCTGGAACCGACGACAT 208
 Db 206 TCGAGTGCCGCTGGAACCGACGACAT 233

RESULT 2

PCT-US95-06790-1

; Sequence 1, Application PC/TUS9506790
 ; GENERAL INFORMATION:
 ; APPLICANT: Mayo Foundation for Medical Education and Research
 ; APPLICANT: and Hoffmann-La Roche Inc.
 ; TITLE OF INVENTION: Detection of a Genetic Locus Encoding
 ; TITLE OF INVENTION: Resistance to Rifampin
 ; NUMBER OF SEQUENCES: 15
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Schweman, Lundberg & Woessner
 ; STREET: 3500 IDS Center
 ; CITY: Minneapolis
 ; STATE: MN
 ; COUNTRY: USA
 ; ZIP: 55402

; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US95/06790
 ; FILING DATE: 26-MAY-1995

; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Raasch, Kevin W.
 ; REGISTRATION NUMBER: 35,651
 ; REFERENCE/DOCKET NUMBER: 150.105W01
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 612-339-0331
 ; TELEFAX: 612-339-3061
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 970 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA
 PCT-US95-06790-1

Query Match 100.0%; Score 208; DB 5; Length 970;
 Best Local Similarity 100.0%; Pred. No. 3,6e-48;
 Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAGGAGAAGCGCTACGACTGGCCCGCTGCGTATAGGTCACAAAGAGCTCG 60
 Db 26 TCAAGGAGAAGCGCTACGACTGGCCCGCTGCGTATAGGTCACAAAGAGCTCG 85
 QY 61 GCGTCATGTCGGCGAGCCCACTACGTCGTCGACGCTGACCGAAGAGACGTCGTGGCCA 120
 Db 86 GCGTCATGTCGGCGAGCCCACTACGTCGTCGACGCTGACCGAAGAGACGTCGTGGCCA 145
 QY 121 CCATCGAATATCTGGTCGCTTCACGAGGTCAGACGATGACCGTTCGGCGGCG 180
 Db 146 CCATCGAATATCTGGTCGCTTCACGAGGTCAGACGATGACCGTTCGGCGGCG 205
 QY 181 TCGAGTGCCGCTGGAACCGACGACAT 208
 Db 206 TCGAGTGCCGCTGGAACCGACGACAT 233

RESULT 3

US-09-103-840A-2

; Sequence 2, Application US/09103840A
 ; Patent No. 6294328
 ; GENERAL INFORMATION:
 ; APPLICANT: FLEISCHMAN, Robert D.
 ; APPLICANT: WHITE, Owen R.
 ; APPLICANT: FRASER, Claire M.
 ; APPLICANT: VENTER, John C.

; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
 ; TITLE OF INVENTION: TUBERCULOSIS
 ; FILE REFERENCE: 24366-20007.00

CURRENT APPLICATION NUMBER: US/09/103,840A

CURRENT FILING DATE: 1998-06-24

NUMBER OF SEQ ID NOS: 2

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 2

LENGTH: 4403765

TYPE: DNA

ORGANISM: Mycobacterium tuberculosis

FEATURE:

OTHER INFORMATION: CDC 1551

OTHER INFORMATION: "n" bases at various positions throughout the sequence

OTHER INFORMATION: represent a, t, c or g

US-09-103-840A-2

Query Match 100.0%; Score 208; DB 3; Length 4403765;

Best Local Similarity 100.0%; Pred. No. 1.5e-47;

Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAGGAGAAGCGCTACGACTGGCCCGCTGCGTATAGGTCACAAAGAGCTCG 60
 Db 762648 TCAAGGAGAAGCGCTACGACTGGCCCGCTGCGTATAGGTCACAAAGAGCTCG 762707
 QY 61 GCGTCATGTCGGCGAGCCCACTACGTCGTCGACGCTGACCGAAGAGACGTCGTGGCCA 120
 Db 762708 GCGTCATGTCGGCGAGCCCACTACGTCGTCGACGCTGACCGAAGAGACGTCGTGGCCA 762767
 QY 121 CCATCGAATATCTGGTCGCTTCACGAGGTCAGACGATGACCGTTCGGCGGCG 180
 Db 762768 CCATCGAATATCTGGTCGCTTCACGAGGTCAGACGATGACCGTTCGGCGGCG 762827
 QY 181 TCGAGTGCCGCTGGAACCGACGACAT 208
 Db 762828 TCGAGTGCCGCTGGAACCGACGACAT 762855

RESULT 4

US-09-103-840A-1

; Sequence 1, Application US/09103840A

; Patent No. 6294328

; GENERAL INFORMATION:

; APPLICANT: FLEISCHMAN, Robert D.

; APPLICANT: WHITE, Owen R.

; APPLICANT: FRASER, Claire M.

; APPLICANT: VENTER, John C.

; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM

; TITLE OF INVENTION: TUBERCULOSIS

; FILE REFERENCE: 24366-20007.00

; CURRENT APPLICATION NUMBER: US/09/103,840A

; CURRENT FILING DATE: 1998-06-24

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 1

; LENGTH: 4411529

; TYPE: DNA

; ORGANISM: Mycobacterium tuberculosis

; OTHER INFORMATION: H37Rv

US-09-103-840A-1

Query Match

100.0%; Score 208; DB 3; Length 4411529;

Best Local Similarity 100.0%; Pred. No. 1.5e-47;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAGGAGAGAGCTACAGACCTGCGCGCGCTGCTATAGGTCAACAGAGCTCG 60
DB 760688 TCAGGAGAGAGGCTACGACCTGCGCGCGCTGCTATAGGTCAACAGAGCTCG 760747
QY 61 GCGTCATGTCGCGGAGCCCATCAGCTGCTGACGAGAGAGAGCTGCTGCGCA 120
DB 760748 GCGTCATGTCGCGGAGCCCATCAGCTGCTGACGAGAGAGAGCTGCTGCGCA 760807
QY 121 CCATCGAATATCTGCTGCGCTTGCACGAGGCTCAGACCATGATGACCGTCCGCGGCGG 180
DB 760808 CCATCGAATATCTGCTGCGCTTGCACGAGGCTCAGACCATGATGACCGTCCGCGGCGG 760867
QY 181 TCGAGGTGCGCGGTGGAACCGACGACAT 208
DB 760868 TCGAGGTGCGCGGTGGAACCGACGACAT 760895

RESULT 5

US-08-313-185-57
; Sequence 57, Application US/08313185
; Patent No. 5851763
; GENERAL INFORMATION:
; APPLICANT: Heym, Beate
; APPLICANT: Cole, Stewart
; APPLICANT: Young, Douglas
; APPLICANT: Zhang, Ying
; APPLICANT: Honore, Nadine
; APPLICANT: Telenti, Amalio
; APPLICANT: Bodmer, Thomas
; TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESS: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/313.185
; FILING DATE: 12-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 02356.0068-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3447 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-313-185-57

Query Match 71.5%; Score 148.8; DB 2; Length 3447;
Best Local Similarity 82.2%; Pred. No. 6.4e-32;
Matches 171; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 1 TCAGGAGAGAGCTACAGACCTGCGCGCGCTGCTATAGGTCAACAGAGCTCG 60

DB 809 TCAGGAGAGAGCTACAGACCTGCGCGCGCTGCTATAGGTCAACAGAGCTCG 868
QY 61 GCGTCATGTCGCGGAGCCCATCAGCTGCTGACGCTGACCGAGAGAGCTCGTGGCCA 120
DB 869 GGTTCACGCGCGGTGATGATCAGCTGCTCCACGCTGACCGAGAGAGATGCTGTCGCCA 928
QY 121 CCATCGAATATCTGCTGCGCTTGCACGAGGCTCAGACCATGATGACCGTCCGCGGCGG 180
DB 929 CCATGAGTACCTGCTGCTGCTGATGAGGTGCTGCAATGACTGCTCCAGGTGGGG 988
QY 181 TCGAGGTGCGCGGTGGAACCGACGACAT 208
DB 989 TAGAGTGCCAGTGGAAACTGACGATAT 1016

RESULT 6

US-09-082-614A-57
; Sequence 57, Application US/09082614A
; Patent No. 6124098
; GENERAL INFORMATION:
; APPLICANT: Heym, Beate
; APPLICANT: Cole, Stewart
; APPLICANT: Young, Douglas
; APPLICANT: Zhang, Ying
; APPLICANT: Honore, Nadine
; APPLICANT: Telenti, Amalio
; APPLICANT: Bodmer, Thomas
; TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESS: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/082.614A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/313.185
; FILING DATE: 12-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 02356.0068-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3447 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-082-614A-57

Query Match 71.5%; Score 148.8; DB 3; Length 3447;
Best Local Similarity 82.2%; Pred. No. 6.4e-32;
Matches 171; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 1 TCAGGAGAGAGCTACAGACCTGCGCGCGCTGCTATAGGTCAACAGAGCTCG 60


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Db 809 TCAAGAGAAACGCTACGACCTTGGCCAGGGTGGCTTACAAGGTCAACAAGAGACTCG 868
Qy 61 GGCTCATGTCGGGAGCCCATCAGCTGCTGACGCTGACGAGGAGACGTCFPGGCA 120
Db 869 GTTCCAGCGGTGAGTTCATCAGCTGCTCAGCTGACGAGAGAGATGCTGTCGCCA 928
Qy 121 CCATCGAATATCTGGTCCGCTGTCACAGAGGTTCAGACAGCATGCTCCGGCGCG 180
Db 929 CCATAGATGACTGTTGCTGCTGATGAGGGTTCAGTGCACATGCTCCAGGTGGG 988
Qy 181 TCGAGTCCGGTGGAAACCGAGCAT 208
Db 989 TAGAAGTCCAGTGGAAATGACGATAT 1016

RESULT 7
US-09-252-991A-969
; Sequence 969, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 969
; LENGTH: 924
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-969

Query Match 18.6%; Score 38.6; DB 4; Length 924;
Best Local Similarity 51.4%; Pred. No. 0.061;
Matches 89; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

Qy 17 CGAAGTCCGCGCTGCTGCTATTAAGGTCAACAAGAGCTCGGCTCATGTCGGCA 76
Db 597 CGACCGCTGCGCTGCTGCTGCGGAGCGGTGGCGGCGCACCCTGGTGAG 656
Qy 77 GCCATACGCTGCTGACGCTGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 136
Db 657 CACCGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 716
Qy 137 CGGCTTGACAGAGGTTCAGACCATGACGCTTCCGCGGCGGCTCGAGGTGC 189
Db 717 CCGTCCCTACCATGTAACCGCGCTGCTGATGGGGCGCGGACGATGTAC 769

RESULT 8
US-09-252-991A-925
; Sequence 925, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 925
; LENGTH: 939
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-925

Query Match 18.6%; Score 38.6; DB 4; Length 939;
Best Local Similarity 51.4%; Pred. No. 0.061;
Matches 89; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

Qy 17 CGAAGTCCGCGCTGCTGCTGCTATTAAGGTCAACAAGAGCTCGGCTCATGTCGGCA 76
Db 604 CGACCGCTGCGCTGCTGCTGCGGAGCGGTGGCGGCGGCGGCTGCTGCTGCTGCTG 663
Qy 77 GCCATACGCTGCTGACGCTGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 136
Db 664 CACCGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 723
Qy 137 CGGCTTGACAGAGGTTCAGACCATGACGCTTCCGCGGCGGCTCGAGGTGC 189
Db 724 CCGTCCCTACCATGTAACCGCGCTGCTGATGGGGCGCGGACGATGTAC 776

RESULT 9
US-09-252-991A-1114/c
; Sequence 1114, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 1114
; LENGTH: 768
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1114

Query Match 18.4%; Score 38.2; DB 4; Length 768;
Best Local Similarity 51.5%; Pred. No. 0.076;
Matches 88; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

Qy 17 CGAAGTCCGCGCTGCTGCTGCTATTAAGGTCAACAAGAGCTCGGCTCATGTCGGCA 76
Db 172 CGACCGCTGCGCTGCTGCTGCGGAGCGGTGGCGGCGGCGGCTGCTGCTGCTGCTG 113
Qy 77 GCCATACGCTGCTGACGCTGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 136
Db 112 CACCGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 53
Qy 137 CGGCTTGACAGAGGTTCAGACCATGACGCTTCCGCGGCGGCTCGAGGTGC 187
Db 52 CCGTCCCTACCATGTAACCGCGCTGCTGATGGGGCGCGGACGATGT 2

RESULT 10
US-08-097-831-1
; Sequence 1, Application US/08097831
; Patent No. 5510473
; GENERAL INFORMATION:
; APPLICANT: Camerini-Otero, Rafael D.
; APPLICANT: Angov, Evangelina
; TITLE OF INVENTION: Cloning and Expression of Tag recA
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KNOBBE, MARTENS, OLSON AND BEAR
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
```

```

COUNTRY: USA
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/097,831
FILING DATE: 19930726
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E.
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: NIH066.001A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
TELEFAX: 714-760-9502
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1412 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: Taq recA
FEATURE:
NAME/KEY: CDS
LOCATION: 62..1082
US-08-097-831-1

Query Match 17.9%; Score 37.2; DB 1; Length 1412;
Best Local Similarity 53.4%; Pred. No. 0.16;
Matches 78; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY 50 CAGAGAGCTCGGGCTGCATGTCGGCGAGCCCATCAGCTGTCGACGCTGACCGAAGAAGA 109
Db 370 CAAAGAAGCTCGGGGTGGACGTGCAGGAGCTTCTGGTCTCCACGCGGACACCGGGGAGCA 429
QY 110 CGTCGTGGCCACCATCGAATATCTGCTGCGCTTCACAGAGGTCAGACACGATCACCGT 169
Db 430 GCGTTTGGAGATCGTGGAGCTTCGCGCCCTCGGGGCGGTGGACGTGATCGTGTGGA 489
QY 170 TCCGGGGCGGCGTCGAGGTGCGCGGTG 195
Db 490 TCGGTGGCGCGCTTTGTGTGCCAAG 515

RESULT 11
US-09-252-991A-13650/c
; Sequence 13650, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 13650
; LENGTH: 1452
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13650

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 6085
; TYPE: DNA
; ORGANISM: Streptomyces longisporoflavus
; FEATURE:
; NAME/KEY: misc_RNA
; LOCATION: (378)..(1665)
; OTHER INFORMATION: ORF
; FEATURE:
; NAME/KEY: misc_RNA
; LOCATION: (1747)..(2553)
; OTHER INFORMATION: ORF
; FEATURE:
; NAME/KEY: misc_RNA
; LOCATION: (2593)..(4011)
; OTHER INFORMATION: ORF
; FEATURE:
; NAME/KEY: misc_RNA
; LOCATION: (4013)..(4999)
; OTHER INFORMATION: ORF
; FEATURE:
; NAME/KEY: misc_RNA
; LOCATION: (5071)..(6085)
; OTHER INFORMATION: ORF
US-09-029-603-4

Query Match 17.8%; Score 37; DB 3; Length 6085;
Best Local Similarity 51.5%; Pred. No. 0.23; Indels 0; Gaps 0;
Matches 85; Conservative 0; Mismatches 80; Indels 0; Gaps 0;
QY 18 GACCTGCGCGGTGCGTGTATAGGTCAACAAGAAGCTCGGSGTCATGTCGGCGAG 77
Db 1017 GAGGTGACCGGCGGGCGGAGACGCGGACGATCTGTCACCCCTCCTGTCGGCGGC 1076
QY 78 CCCATCAGTCGTCGACGCTGACCGAAGAGAGCTGTCGGCCACCATGATATCTGTC 137
Db 1077 CGGACACCGGATFCACCGCTCAGCGTGGAGCGCATGTCGGCACTCGCTCCATCTGTC 1136
QY 138 CGCTGTCAGCAGGAGTCAGACCATGATGACGCTTCGCGGGCGGTC 182
Db 1137 ACCGCGGCGACGAGACCAACCACTGCTGCGCAGGCGGTC 1181

RESULT 14
US-09-252-991A-13457/c
; Sequence 13457, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 13457
; LENGTH: 258
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13457

Query Match 17.5%; Score 36.4; DB 4; Length 258;
Best Local Similarity 56.8%; Pred. No. 0.2; Indels 0; Gaps 0;
Matches 67; Conservative 0; Mismatches 51; Indels 0; Gaps 0;
QY 17 CGACTGCGCGGTGCGTGTATAGGTCAACAAGAAGCTCGGSGTCATGTCGGCGGA 76
Db 258 CTACTGTGCTCGAAGGCTTCGAGAGATCGGCCCAATACCTGCCCATGACGAGA 199

QY 77 GCCATCAGCTGTCGACGTGACCGAAGAGACGTCGTGGCCACCATCGAATATCTG 134
Db 198 GCACGCCGAGGAGCAGCGCTGGGGCCCATGTCGACGTGGCGCCCTGGAAAGCAG 141
RESULT 15
US-09-252-991A-13899
; Sequence 13899, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 13899
; LENGTH: 615
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13899

Query Match 17.5%; Score 36.4; DB 4; Length 615;
Best Local Similarity 51.9%; Pred. No. 0.23; Indels 0; Gaps 0;
Matches 82; Conservative 0; Mismatches 76; Indels 0; Gaps 0;
QY 6 GAGAAGCGGTACGACCTGGCCCGCTCGTGTGCTATAGGTCAACAAGAAGCTCGGCTG 65
Db 311 GCGAGTTCTACAGGTCTCCTCGCGGCGAGCTCGGCGCGGAGCCCTCGGCGAG 370
QY 66 CATGTGCGGAGCGCCCATCATGCTGTCGACGCTGACCGAGAGAGAGCTGTCGTGGCCACCATC 125
Db 371 ATCTCGGCGCCCTCTTCTGCGCCAGGAGCAGATGGCGGACGTATCGACAAGATCATCCAG 430
QY 126 GAATATCTGTCGCTGTCGACGAGGTCAGACCAAGAT 163
Db 431 GTCATCTGGAACGCGCGGAGACCCCTTCAT 468

Search completed: September 17, 2003, 12:27:10
Job time : 41.1605 secs

GenCore version 5.1.6
 Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 17, 2003, 11:54:34 ; Search time 108.259 Seconds
 (without alignments)
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Title: US-09-697-123b-6
 Perfect score: 208
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 Gapop 10.0 , Gapext 1.0

Searched: 1660708 seqs, 1229959015 residues

Total number of hits satisfying chosen parameters: 3321416

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
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 16: /cgn2_6/ptodata/1/pubna/US50_NEW_PUB.seq.*
 17: /cgn2_6/ptodata/1/pubna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	208	100.0	3519	10	US-09-712-363-30
2	89.6	43.1	3495	10	US-09-738-626-547
3	89.6	43.1	5096	10	US-09-984-711-5
4	89.6	43.1	5099	10	US-09-887-052-1
5	89.6	43.1	5099	10	US-09-887-052-3
6	89.6	43.1	5099	10	US-09-887-052-5
7	89.6	43.1	5099	12	US-10-076-406-1
8	89.6	43.1	5099	12	US-10-076-406-3
9	89.6	43.1	5099	12	US-10-076-406-5
10	89.6	43.1	5099	13	US-10-075-460-5
11	89.6	43.1	3309400	10	US-09-738-626-1
12	67.6	32.5	3543	14	US-10-156-761-4898
13	67.6	32.5	9025608	14	US-10-156-761-1
14	40.4	19.4	1215	14	US-10-156-761-2811
15	38.6	18.6	1131	14	US-10-156-761-2479
16	38.6	18.6	9025608	14	US-10-156-761-1

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17 38.2 18.4 1395 14 US-10-205-032-21 Sequence 21, Appl

18 38.2 18.4 60196 14 US-10-205-032-1 Sequence 1, Appl

19 36.4 17.5 588 14 US-10-156-761-5853 Sequence 5853, Ap

20 35.8 17.2 1509 12 US-09-967-464-64 Sequence 64, Appl

21 35.8 17.2 1509 12 US-09-967-464-68 Sequence 68, Appl

22 35.6 17.1 3756 9 US-09-841-132-425 Sequence 425, App

23 35.4 17.0 1461 14 US-10-156-761-2120 Sequence 2120, Ap

24 35 16.8 3774 14 US-10-156-761-2845 Sequence 2845, Ap

25 34.6 16.6 2130 14 US-10-156-761-4634 Sequence 4634, Ap

26 34.6 16.6 2130 14 US-10-225-567A-33 Sequence 33, Appl

27 34.6 16.6 2140 14 US-10-185-991-1 Sequence 1, Appl

28 34.6 16.6 2140 14 US-10-238-129-1 Sequence 1, Appl

29 34.6 16.6 2140 14 US-10-238-667-1 Sequence 32, Appl

30 34.4 16.5 1894 8 US-08-841-636A-32 Sequence 2880, Ap

31 34.4 16.5 5721 14 US-10-156-761-2880 Sequence 15102, A

32 34.4 16.5 125746 14 US-10-156-761-15102 Sequence 1671, Ap

33 34.2 16.4 1191 14 US-10-156-761-1671 Sequence 2212, Ap

34 34.2 16.4 1398 14 US-10-156-761-2212 Sequence 5079, Ap

35 34.2 16.4 2334 14 US-10-156-761-5079 Sequence 267, App

36 34 16.3 680 9 US-09-841-132-267 Sequence 4673, Ap

37 34 16.3 993 14 US-10-156-761-4673 Sequence 1592, Ap

38 34 16.3 1509 14 US-10-156-761-1592 Sequence 4136, Ap

39 34 16.3 1596 14 US-10-156-761-4136 Sequence 6797, Ap

40 33.8 16.2 723 14 US-10-156-761-6797 Sequence 5440, Ap

41 33.8 16.2 1029 14 US-10-156-761-5440 Sequence 5434, Ap

42 33.8 16.2 1284 14 US-10-156-761-5434 Sequence 2245, Ap

43 33.8 16.2 2715 14 US-10-156-761-2245 Sequence 5959, Ap

44 33.8 16.2 5418 14 US-10-156-761-5959 Sequence 2309, Ap

45 33.6 16.2 825 14 US-10-156-761-2309

ALIGNMENTS

RESULT 1

US-09-712-363-30

; Sequence 30, Application US/09712363

; Patent No. US20020164588A1

; GENERAL INFORMATION:

; APPLICANT: Eisenberg, David

; APPLICANT: Roelstein, Sergio H.

; APPLICANT: Marcotte, Edward M.

; TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND

; TITLE OF INVENTION: INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS

; FILE REFERENCE: 07419-032001

; CURRENT APPLICATION NUMBER: US/09/712,363

; CURRENT FILING DATE: 2000-11-13

; PRIOR APPLICATION NUMBER: PCT/US00/02246

; PRIOR FILING DATE: 2000-01-28

; PRIOR APPLICATION NUMBER: 60/179,531

; PRIOR FILING DATE: 2000-02-01

; PRIOR APPLICATION NUMBER: 60/117,844

; PRIOR FILING DATE: 1999-01-29

; PRIOR APPLICATION NUMBER: 60/118,206,

; PRIOR FILING DATE: 1999-02-01

; PRIOR APPLICATION NUMBER: 60/126,593

; PRIOR FILING DATE: 1999-03-26

; PRIOR APPLICATION NUMBER: 60/134,093

; PRIOR FILING DATE: 1999-05-14

; PRIOR APPLICATION NUMBER: 60/134,092

; PRIOR FILING DATE: 1999-05-14

; PRIOR APPLICATION NUMBER: 60/165,124

; PRIOR FILING DATE: 1999-11-12

; PRIOR APPLICATION NUMBER: 60/165,086

; PRIOR FILING DATE: 1999-11-12

; NUMBER OF SEQ ID NOS: 292

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 30

; LENGTH: 3519

; TYPE: DNA

; ORGANISM: Mycobacterium tuberculosis

US-09-712-363-30

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Query Match      100.0%; Score 208; DB 10; Length 3519;
Best Local Similarity 100.0%; Pred. No. 4e-56;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAGGAGAGCGCTACGACCTGGCCGCGTCTGCTATAGGTCAACAAGACTCG 60
Db 884 TCAGGAGAGCGCTACGACCTGGCCGCGTCTGCTATAGGTCAACAAGACTCG 943
QY 61 GGCTGATCTCGCGGAGCCCATCAGCTCGTGCAGCTGACCGAAGAAGAGCTGTTGGCCA 120
Db 944 GGCTGATCTCGCGGAGCCCATCAGCTCGTGCAGCTGACCGAAGAAGAGCTGTTGGCCA 1003
QY 121 CATTGATATCTGCTCGCTTCAGAGGGTTCAGACCATGATGACCGTTCGGGGGGGG 180
Db 1004 CATTGATATCTGCTCGCTTCAGAGGGTTCAGACCATGATGACCGTTCGGGGGGGG 1063
QY 181 TCAGGTGCGGTGGAACCGAGACAT 208
Db 1064 TCAGGTGCGGTGGAACCGAGACAT 1091

RESULT 2
US-09-738-626-547
; Sequence 547, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIALI, KEIKO
; APPLICANT: YOKOL, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 547
; LENGTH: 3495
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-547

Query Match      43.1%; Score 89.6; DB 10; Length 3495;
Best Local Similarity 69.0%; Pred. No. 1.6e-19;
Matches 138; Conservative 0; Mismatches 59; Indels 3; Gaps 1;

QY 9 AAGCGCTACGACTGGCCGCGTCTGCTATAGGTCAACAAGACTCGGCTGCAT 68
Db 877 AAGCGCTACGACTGGCTCGGCTGGTTCGTTACAGATCAACCGCAAGCTCGGCT--T 933
QY 59 GTGCGGAGCCCATCAGCTCGTGCAGCTGACCGAAGAAGAGCTGTTGGCCATCGAA 128
Db 934 GTTGGGACACAGATGGTTGATGACTCTTACTGAAGAGGACATCGCAACCATCGAG 993
QY 129 TATCTGCTCGCTTCAGAGGGTTCAGACCATGATGACCGTTCGGGGGGGGTGG 188
Db 994 TATCTGCTCGCTTCAGAGGGTTCAGACCATGATGACCTTCTCCAAATGGTGAAGATC 1053
QY 189 CCGGTGGAACCGAGACAT 208
Db 1054 CCACTGAGACCGATGACAT 1073
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RESULT 3
US-09-984-711-5
; Sequence 5, Application US/09984711
; Patent No. US20020119549A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: STEPHAN, Hans
; APPLICANT: KREUTZER, Caroline
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE rpsL GENE
; FILE REFERENCE: 204209US0
; CURRENT APPLICATION NUMBER: US/09/984,711
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: DE10108230.9
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 5096
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
; OTHER INFORMATION:
US-09-984-711-5

Query Match      43.1%; Score 89.6; DB 10; Length 5096;
Best Local Similarity 69.0%; Pred. No. 1.6e-19;
Matches 138; Conservative 0; Mismatches 59; Indels 3; Gaps 1;

QY 9 AAGCGCTACGACTGGCCGCGTCTGCTATAGGTCAACAAGACTCGGCTGCAT 68
Db 1578 AAGCGCTACGACTGGCTCGGCTGGTTCGTTACAGATCAACCGCAAGCTCGGCT--T 1634
QY 69 GTGCGGAGCCCATCAGCTCGTGCAGCTGACCGAAGAAGAGCTGTTGGCCATCGAA 128
Db 1635 GTTGGGACACAGATGGTTGATGACTCTTACTGAAGAGGACATCGCAACCATCGAG 1694
QY 129 TATCTGCTCGCTTCAGAGGGTTCAGACCATGATGACCGTTCGGGGGGGGTGG 188
Db 1695 TACCTGCTCGCTTCAGAGGGTTCAGAGGGTTCAGAGGGTTCAGAGGGTTCAGAGGGT 1754
QY 189 CCGGTGGAACCGAGACAT 208
Db 1755 CCACTGAGACCGATGACAT 1774

RESULT 4
US-09-887-052-1
; Sequence 1, Application US/09887052
; Patent No. US20020119537A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE rpoB GENE
; FILE REFERENCE: 204212US0X
; CURRENT APPLICATION NUMBER: US/09/887,052
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: DE10107229.5
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 5099
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QY 189 CCGTGGAAACCGAGCAT 208
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; SEQ ID NO 1
; LENGTH: 5099
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; Publication No. US20020155557A1
; GENERAL INFORMATION:
; APPLICANT: MCKEL, BETTINA
; APPLICANT: SATHÉ, BRIGITTE
; APPLICANT: HANS, STEFAN
; APPLICANT: KREUTZER, CAROLINE
; APPLICANT: HERMANN, THOMAS
; APPLICANT: PFEFFERLE, WALTER
; APPLICANT: BINDER, MICHAEL
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE IPSL GENE
; FILE REFERENCE: 218472050X
; CURRENT APPLICATION NUMBER: US/10/075,460
; CURRENT FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: DE 10107230.9
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: DE 10162386.0
; PRIOR FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 5099
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
; OTHER INFORMATION:
; US-10-075-460-5

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Best Local Similarity 69.0%; Pred. No. 1.6e-19;
Matches 138; Conservative 0; Mismatches 59; Indels 3; Gaps 1;

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D 1578 AAGCGCTACGACCTGCGCGCTGCGTCTAAGGTCAACAGAGCTCGGCTGCAT 68
QY 69 GTCGGCGAGCCCATCAGCTGCTGACGCTGACCGAAGAGACGCTGCGCCACCATCGAA 128
D 1635 GTGCGGACCAACAGATGGTTGATGACTCTTACTGAAGAGGACATCGCACCATCATCGAG 1694
QY 129 TATCTGTCGCTGTCGACGAGGGTCAGACCATGATGACCGTTCCGGGGCGGTCGAGGTG 188
D 1695 TACCTGCTGCTGTCGACGAGGTGAGCGCGCTCATGACTTCTCCAAATGGTGAAGAGATC 1754
QY 189 CCGGTGGAACCCAGACAT 208
D 1755 CCACTCGAGACCGATGACAT 1774

RESULT 11
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; Sequence 1, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHITAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENO, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
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; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 1
; LENGTH: 3309400
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; US-09-738-626-1

Query Match 43.1%; Score 89.6; DB 10; Length 3309400;
Best Local Similarity 69.0%; Pred. No. 3.5e-19;
Matches 138; Conservative 0; Mismatches 59; Indels 3; Gaps 1;

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D 513789 AAGCGCTACGACCTGCGCGCTGCGTCTAAGGTCAACAGAGCTCGGCTGCAT 68
QY 69 GTCGGCGAGCCCATCAGCTGCTGACGCTGACCGAAGAGACGCTGCGCCACCATCGAA 128
D 513846 GTGCGGACCAACAGATGGTTGATGACTCTTACTGAAGAGGACATCGCACCATCATCGAG 513905
QY 129 TATCTGTCGCTGTCGACGAGGGTCAGACCATGATGACCGTTCCGGGGCGGTCGAGGTG 188
D 513906 TACCTGCTGCTGTCGACGAGGTGAGCGCGCTCATGACTTCTCCAAATGGTGAAGAGATC 513965
QY 189 CCGGTGGAACCCAGACAT 208
D 513966 CCACTCGAGACCGATGACAT 513985

RESULT 12
US-10-156-761-4898
; Sequence 4898, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 4898
; LENGTH: 3543
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3543)
; US-10-156-761-4898

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Best Local Similarity 61.5%; Pred. No. 2.3e-12;
Matches 128; Conservative 0; Mismatches 74; Indels 6; Gaps 1;
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D 926 TCAACCCGGAAGCGCTACGACCTGGCGAGGTCGGCGCTACAAAGGTCAACAAGAGCTGG 985
QY 61 GCTCATGTCGGGAGCCCATCATGCTGTGAGCTGTACCGTACCGAGAGAGAGCTCGTGCGCA 120
D 986 GC-----GGCGAGCGCGCTGGAGCGCGGAGCTCTGACCGTGGAGGACATCTCTCGT 1039
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3049.028 Million cell updates/sec

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Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
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3: /cgn2_6/prodata/1/ina/6A.COMB.seq: *
4: /cgn2_6/prodata/1/ina/6B.COMB.seq: *
5: /cgn2_6/prodata/1/ina/PCTUS.COMB.seq: *
6: /cgn2_6/prodata/1/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	124.8	58.3	970	1 US-08-250-030-1	Sequence 1, Appli
2	124.8	58.3	970	5 PCT-US95-06790-1	Sequence 1, Appli
3	124.8	58.3	4403765	3 US-09-103-840A-2	Sequence 2, Appli
4	124.8	58.3	4411529	3 US-09-103-840A-1	Sequence 1, Appli
5	104	48.6	3447	2 US-08-313-185-57	Sequence 57, Appli
6	104	48.6	3447	3 US-09-082-614A-57	Sequence 57, Appli
7	43.2	20.2	4403765	3 US-09-103-840A-2	Sequence 2, Appli
8	43.2	20.2	4411529	3 US-09-103-840A-1	Sequence 1, Appli
9	42.2	19.7	1047	4 US-09-252-991A-14678	Sequence 14678, A
10	42.2	19.7	1686	4 US-09-252-991A-14548	Sequence 14548, A
11	42.2	19.7	1815	4 US-09-252-991A-15077	Sequence 15077, A
12	41.6	19.4	999	4 US-09-252-991A-12129	Sequence 12129, A
13	41.6	19.4	1404	4 US-09-252-991A-12291	Sequence 12291, A
14	41.2	19.3	1620	2 US-08-461-775-10	Sequence 10, Appli
15	41.2	19.3	1620	2 US-09-031-606-10	Sequence 10, Appli
16	41.2	19.3	2668	2 US-08-461-775-11	Sequence 11, Appli
17	41.2	19.3	2668	3 US-09-031-606-11	Sequence 11, Appli
18	41	19.2	759	4 US-09-252-991A-982	Sequence 982, App
19	41	19.2	1926	4 US-09-079-955-10	Sequence 10, Appli
20	41	19.2	3000	3 US-09-192-104-1	Sequence 1, Appli
21	41	19.2	3000	4 US-09-543-446-1	Sequence 1, Appli
22	40	18.7	1665	3 US-08-881-784-8	Sequence 8, Appli
23	40	18.7	1665	3 US-09-292-768-3	Sequence 3, Appli
24	40	18.7	1665	3 US-09-292-768-67	Sequence 67, Appli
25	40	18.7	1665	3 US-09-292-768-69	Sequence 69, Appli
26	40	18.7	15872	3 US-09-105-537-1	Sequence 1, Appli
27	39.8	18.6	1548	4 US-09-252-991A-5452	Sequence 5452, Ap

c	28	39.8	18.6	1641	4 US-09-252-991A-5477	Sequence 5477, Ap
c	29	39.2	18.3	579	4 US-09-252-991A-6132	Sequence 6132, Ap
c	30	39.2	18.3	702	4 US-09-252-991A-6046	Sequence 6046, Ap
c	31	39.2	18.3	1203	4 US-09-252-991A-6250	Sequence 6250, Ap
c	32	39.2	18.3	1644	4 US-09-252-991A-6420	Sequence 6420, Ap
c	33	39	18.2	1734	6 5352575-8	Patent No. 5352575
c	34	38.2	17.9	282	4 US-09-252-991A-956	Sequence 956, App
c	35	38.2	17.9	564	4 US-09-252-991A-2572	Sequence 2572, App
c	36	38.2	17.9	870	4 US-09-252-991A-911	Sequence 911, App
c	37	38.2	17.9	1101	4 US-09-252-991A-2487	Sequence 2487, App
c	38	38.2	17.9	1278	4 US-09-252-991A-2643	Sequence 2643, App
c	39	38.2	17.9	1533	4 US-09-252-991A-1124	Sequence 1124, App
c	40	38.2	17.9	1638	4 US-09-252-991A-8733	Sequence 8733, App
c	41	38.2	17.9	2070	4 US-09-252-991A-2189	Sequence 2189, App
c	42	38.2	17.9	77536	4 US-09-410-551B-1	Sequence 1, Appli
c	43	37.6	17.6	735	4 US-09-252-991A-13121	Sequence 13121, A
c	44	37.6	17.6	786	4 US-09-252-991A-12823	Sequence 12823, A
c	45	37	17.3	882	4 US-09-252-991A-2427	Sequence 2427, Ap

ALIGNMENTS

RESULT 1
US-08-250-030-1
; Sequence 1, Application US/08250030
; Patent No. 5643723
; GENERAL INFORMATION:
; APPLICANT: Persing, David H.
; TITLE OF INVENTION: Detection of a Genetic Locus Encoding
; TITLE OF INVENTION: Resistance to Rifampin in Mycobacterial Cultures and in
; TITLE OF INVENTION: Clinical Specimens
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg & Woessner
; STREET: 3500 IDS Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/250,030
; FILING DATE: 26-MAY-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Muetting, Ann M.
; REGISTRATION NUMBER: 33,977
; REFERENCE/DOCKET NUMBER: 150.105U51
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-339-0331
; TELEFAX: 612-339-3061
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 970 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-250-030-1

Query Match 58.3%; Score 124.8; DB 1; Length 970;
Best Local Similarity 77.6%; Pred. No. 2.5e-21;
Matches 166; Conservative 0; Mismatches 42; Indels 6; Gaps 1;
QY 1 TCACGAGAGAGCGCTACGACCTGGCCCGCTGGCCCGTACAGGTGACACAGAGCTGG 60
|||||
Db 26 TCACGAGAGAGCGCTACGACCTGGCCCGCTGGCCCGTATAGGTGACACAGAGCTCG 85
|||||

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QY      61  GTCCTGGCGGTGCGAACC CGGCTTCGTGACTGCGCACACCGCTCACCAGGAGAGACGTGC 120
Db      86  GGCCTCATGTGCGCGAGCC-----CATCACGTGCTGACGCTGACCCGAGAAGACGTGC 139
QY     121  TGCACCACTCGGCTACTCTGGTGCGCTGCAGAGGGCCACACACGATGACCGCCCGC 180
Db     140  TGGCCACCATCATGAATATCTGGTCCGCTGTCAGAGGGTCAAGACACGATGACCGTCCGG 139
QY     181  GGGCGCTCGAGGTCCCGGTCGAGGTGCGACGACAT 214
Db     200  GCGGCGTCGAGTCCCGGTGGAAACCGACGACAT 233

RESULT 2
PCT-US95-06790-1
; Sequence 1, Application PC/TUS9506790
; GENERAL INFORMATION:
; APPLICANT: Mayo Foundation for Medical Education and Research
; APPLICANT: and Hoffmann-La Roche Inc.
; TITLE OF INVENTION: Detection of a Genetic Locus Encoding
; TITLE OF INVENTION: Resistance to Rifampin
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg & Woessner
; STREET: 3500 IDS Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/06790
; FILING DATE: 26-MAY-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Raasch, Kevin W.
; REGISTRATION NUMBER: 35,651
; REFERENCE/DOCKET NUMBER: 150.105W01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-339-0331
; TELEFAX: 612-339-3061
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 970 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; PCT-US95-06790-1

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Query Match	58.3%;	Score 124.8;	DB 5;	Length 970;
Best Local Similarity	77.6%;	Ref. No. 2.5e-21;		
Matches 166;	Conservative	0;	Mismatches 42;	Indels 6; Gaps 1;

QY	1	TCAGAGAGAGCGCTACGACCTGCCCGCGTGGCGCGGTACAGGTCAACAGAAAGCTGG	60
Db	26	TCRAGGAGAGCGCTACGACCTGCCCGCGTGGCGCGGTATAGGTCAACAGAAAGCTCG	85
QY	61	GTCTTTGCGGTTGCCAACCGGCTCTGTGACTGCCACACAGCTCACCGAGGAGAGAGCTCG	120
Db	86	GGCTTGCATGTCGCGGAGCC-----CATCAAGTTCGCTCGACGCTGACCGAAGAGAGCTCG	139
QY	121	TCGCCACCATCGGGTACCTTGGTGGCGCTGCACGAGGGCCAGACACCATGACCGCCCGCG	180
Db	140	TGCCCACCATCGAATATCTGGTGGCTTGCACGAGGTCAGACCACCATGACCGTTCGGG	199
QY	181	CGCGCCTCGAGGTTCCGGTTCGAGTTCGACGACAT	214
Db	200	CGCGCTCGAGGTGCGCGTGGAAACCGACGACAT	233

RESULT 3
 US-09-103-840A-2
 ; Sequence 2, Application US/09103840A
 ; Patent No. 6294328
 ; GENERAL INFORMATION:
 ; APPLICANT: FLEISCHMAN, Robert D.
 ; APPLICANT: WHITE, Owen R.
 ; APPLICANT: FRASER, Claire M.
 ; APPLICANT: VENTER, John C.
 ; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
 ; TITLE OF INVENTION: TUBERCULOSIS
 ; FILE REFERENCE: 24366-20007.00
 ; CURRENT APPLICATION NUMBER: US/09/103,840A
 ; CURRENT FILING DATE: 1998-06-24
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 2
 ; LENGTH: 4403765
 ; TYPE: DNA
 ; ORGANISM: Mycobacterium tuberculosis
 ; FEATURE:
 ; OTHER INFORMATION: CDC 1551
 ; OTHER INFORMATION: "n" bases at various positions throughout the sequence
 ; OTHER INFORMATION: represent a, t, c or g
 US-09-103-840A-2

Query Match	58.3%;	Score 124.8;	DB 3;	Length 4403765;
Best Local Similarity	77.6%;	Prod. No. 5.8e-21;		
Matches 166;	Conservative	0;	Mismatches 42;	Indels 6; Gaps 1;
QY	1	TCAGGAGAACGCTACGACCTGGCCCGCGTGGCGGTACAGGTACACAGAGCTGG	60	
Db	762648	TCAGGAGAGACGCTACGACCTGGCCCGCTGGTTCGCTATAGGTCCACAGAGGCTCG	762707	
QY	61	GTCTTGGCGGTGCCAACCCGGCTCTGTGTACTGCCACCAGCTCACCAGGAGACAGCTCG	120	
Db	762708	GGCTGCATGTGGCGGAGCC-----CATCAGCTCGTCAGGTCACCGAAGAACGCTCG	762761	
QY	121	TGCGCCACCATCTGGGTACTGTGGTGGCCCTGCACGAGGCCAGACACGATGACCCGCCCGG	180	
Db	762762	TGGCCACCATCGAATATCTGGTTCGCTCCGCTTCAGAGGGTCAGACCACGATGACCGTTCGG	762821	
QY	181	GGCGGCTCGAGGTCGGCGGTCTGAGGTCGACGACAT	214	
Db	762822	GGCGGCTCGAGGTCGGCGGTGGAACACGACGACAT	762855	

RESULT 4
 US-09-103-840A-1
 ; Sequence 1, Application US/09103840A
 ; Patent No. 6294328
 ; GENERAL INFORMATION:
 ; APPLICANT: FLEISCHMAN, Robert D.
 ; APPLICANT: WHITE, Owen R.
 ; APPLICANT: FRASER, Claire M.
 ; APPLICANT: VENTER, John C.
 ; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
 ; TITLE OF INVENTION: TUBERCULOSIS
 ; FILE REFERENCE: 24366-20007-00
 ; CURRENT APPLICATION NUMBER: US/09/103,840A
 ; CURRENT FILING DATE: 1998-06-24
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 4411529
 ; TYPE: DNA
 ; ORGANISM: Mycobacterium tuberculosis
 ; OTHER INFORMATION: H37Rv
 US-09-103-840A-1

Query Match
58.3%; Score 124.8; DB 3; Length 4411529;

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Best Local Similarity 77.6%; Pred. No. 5.8e-21;
Matches 166; Conservative 0; Mismatches 42; Indels 6; Gaps 1;

QY 1 TCAAGGAGAAGCGCTACGACTGCGCCCGGTGGCGCGGTGAAACAAGAGCTCG 60
Db 760688 TCAAGGAGAAGCGCTACGACTGCGCCCGGTGGCGCGGTGAAACAAGAGCTCG 760747
QY 61 GTCTTGGCGGTGCCAACCCGGCTCTGGTGACTGCCACACAGCTCACCGAGGAGAGCTCG 120
Db 760748 GGTGTCATGTGGCGAGCC-----CATCACGTCTGACGCTGACCGAGAGAGAGCTCG 760801
QY 121 TCGCCACCAATCGGGTACCTGTGGCTGCGCTGCACGAGGCGGACACACATGACCGCCCGG 180
Db 760802 TGGCCACCAATCGAATATCTGCTCGCTTGCACGAGGCTCAGACACCATGACCGTTCG 760861
QY 181 GCGGCTCGAGGTCCCGCTCGAGTTCGACGACAT 214
Db 760862 GCGGCTCGAGGTCCCGGTGGAACCGACGACAT 760895

RESULT 5
US-08-313-185-57
; Sequence 57, Application US/08313185
; Patent No. 3851763
; GENERAL INFORMATION:
; APPLICANT: Heym, Beate
; APPLICANT: Cole, Stewart
; APPLICANT: Young, Douglas
; APPLICANT: Zhang, Ying
; APPLICANT: Honore, Nadine
; APPLICANT: Telenti, Amalio
; APPLICANT: Bodmer, Thomas
; TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/313,185
; FILING DATE: 12-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 02356.0068-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3447 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-313-185-57

Query Match 48.6%; Score 104; DB 2; Length 3447;
Best Local Similarity 71.5%; Pred. No. 2.4e-16;
Matches 153; Conservative 0; Mismatches 55; Indels 6; Gaps 1;

QY 1 TCAAGGAGAAGCGCTACGACTGCGCCCGGTGAAACAAGAGCTCG 60
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Db 809 TCAAGGAGAAGCGCTACGACTGCGCCCGGTGGCTGTACAGGTCAACAAGAGCTCG 868
QY 61 GTCTTGGCGGTGCCAACCCGGCTCTGGTGACTGCCACACAGCTCACCGAGGAGAGCTCG 120
Db 869 GGTTCACGCGCGGTGAGT-----TGATCACGTCTGCTCCACGCTGACCGAAGAGGATCG 922
QY 121 TCGCCACCAATCGGGTACCTGTGGCTGCGCTGCACGAGGCGGACACACATGACCGCCCGG 180
Db 923 TCGCCACCAATGAGTACTGCTGCTGCTGATGAGGTGAGTGAACACTGACGATAT 982
QY 181 GCGGCTCGAGGTCCCGCTCGAGTTCGACGACAT 214
Db 983 GTGGGTAGAGTGGCAGTGGAAACTGACGATAT 1016

RESULT 6
US-09-082-614A-57
; Sequence 57, Application US/09082614A
; Patent No. 6124098
; GENERAL INFORMATION:
; APPLICANT: Heym, Beate
; APPLICANT: Cole, Stewart
; APPLICANT: Young, Douglas
; APPLICANT: Zhang, Ying
; APPLICANT: Honore, Nadine
; APPLICANT: Telenti, Amalio
; APPLICANT: Bodmer, Thomas
; TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/082,614A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/313,185
; FILING DATE: 12-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 02356.0068-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3447 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-082-614A-57

Query Match 48.6%; Score 104; DB 3; Length 3447;
Best Local Similarity 71.5%; Pred. No. 2.4e-16;
Matches 153; Conservative 0; Mismatches 55; Indels 6; Gaps 1;

QY 1 TCAAGGAGAAGCGCTACGACTGCGCCCGGTGAAACAAGAGCTCG 60
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Db 809 TCAGGAGAACGCTAGACCTGGCCAGGGTTGGTCTGTACAGGTCAACAGAGCTCG 868
QY 61 GCTCTGGGGTGGCAACCCGGCTGTGACTGCCACAGCTTCACCGAGGAGACGCTCG 120
Db 869 GTTTCACGCGCGGTGAGT-----TGATCAGCTGCTCCAGCTGACCGAGAGATGTC 922
QY 121 TCGCCACCATCGGCTACCTGTGGTGGCCCTGTCACGAGGCGCCAGACCAACCGCCCGC 180
Db 923 TCGCCACCATAGATACCTGTGGTGGTCTGTCATGAGGCTCAGTCGACAACTGCTGCCAG 982
QY 181 GCGGCTCAGGTCGCGGTGCGAGTGCAGCAT 214
Db 983 GTGGGGTAGAAGTGCACGTGGAACACTGCAGTAT 1016
US-09-103-840A-2/c

RESULT 7

US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match 20.2%; Score 43.2; DB 3; Length 4403765;
Best Local Similarity 52.2%; Pred. No. 0.12; 88; Indels 0; Gaps 0;
Matches 96; Conservative 0; Mismatches 88; Indels 0; Gaps 0;
QY 24 GCGCGCTGGGCGCGTACAGGTGAACAGAGCTGGGTCTTGGGGTGGCCCAACCCGGCT 83
Db 2839155 GCGATCGCGAGCGCGGTGAAGAGACCTGGGAGCTCGTGGAGGCTGGGCGCAAGCATGTC 2839096
QY 84 CTGTGTACTGCCACCGCTCACCGAGGAGACCTGCTGCCACCATCGGTACTGGTGTG 143
Db 2839095 ACCGTGCGAGGTGCGCTGGCGACCCGCGAGGGCGACGAGCTTCGCGGCGCGCATGGC 2839036
QY 144 CGCTGTGACGAGGCCAGACCAACGATGATCGCCCGCGGCGCTCGAGGTCCCGGTGAG 203
Db 2839035 CACCTGTGACGAGGCGCGGTGGCGGCTGCCCGCTCCGTCACAGGTATCATGACGCGCG 2838976
QY 204 GTCG 207
Db 2838975 GTCG 2838972

RESULT 8

US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; OTHER INFORMATION: TUBERCULOSIS

FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match 20.2%; Score 43.2; DB 3; Length 4411529;
Best Local Similarity 52.2%; Pred. No. 0.12;
Matches 96; Conservative 0; Mismatches 88; Indels 0; Gaps 0;
QY 24 GCGCGCTGGGCGGTACAGGTGAACAGAGCTGGGTCTTGGCGGTGCCCAACCCGGCT 83
Db 2843702 GCGATCGCGAGCGCGGTGAAGAGACCTGGGAGCTCGGTGAGGGCTGGGCGCAAGCATGTC 2843643
QY 84 CTGTGTACTGCCACCGCTCACCGAGGAGACCTGCTGCCACCATCGGTACTGGTGTG 143
Db 2843642 ACCGTGCGAGGTGCGGTGGGCGACCCGCGAGGGCGAGCATGGC 2843583
QY 144 CGCTGTGACGAGGCGCGAGACCAACGATGATCGCCCGCGGCGCTCGAGGTCCCGGTGAG 203
Db 2843582 CACCTGTGACGAGGCGCGCTGGCGCATGCCCGCTCCGTCGACAGGTATCATGACGCGCG 2843523
QY 204 GTCG 207
Db 2843522 GTCG 2843519

RESULT 9

US-09-252-991A-14678
; Sequence 14678, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 14678
; LENGTH: 1047
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-14678

Query Match 19.7%; Score 42.2; DB 4; Length 1047;
Best Local Similarity 50.2%; Pred. No. 0.09; 103; Indels 0; Gaps 0;
Matches 104; Conservative 0; Mismatches 103; Indels 0; Gaps 0;
QY 5 GGAGAGCGGTACGACCTGGCCCGCGCTGGCGGTGACAGGTGAACAGAGCTGGGTCT 64
Db 609 GCGATGAGCGCGCGCTGGCGAGTTTCTACTCGCGAGATTCACCGCCACTGCTGAT 668
QY 65 TGGCGGTGCCAACCCCGCTCTGTGTACTGCGCACACAGCTCACCGAGAGAGACGTCTGCG 124
Db 669 GCTGGCGCGCGCGCACCGCGCTGGCGCGTTTCACCGCGATGCTCGAACGATCGCGCAACA 728
QY 125 CACCATCGGGTACTGTGTGGCTTCACAGAGGCGCACACGATGACCGCCCGCGCG 184
Db 729 GGGCAGCGCGCACCGCTGCTACGCGGTGACCGAGCTCGAGCTGCGGTGCG 788
QY 185 CCGTCAAGTCCCGGTGAGGTGACGA 211

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Db      789  TCTCGAGCGCTGGAGGCGTTGCGCGA  815

RESULT 10
US-09-252-991A-14548
; Sequence 14548, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 14548
; LENGTH: 1686
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-14548

Query Match      19.7%; Score 42.2; DB 4; Length 1686;
Best Local Similarity 50.2%; Pred. No. 0.095;
Matches 104; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

QY      5  GGAGAAGCGCTACGACTCGGCCCGCGTGGCGCGGTACAAAGGTGAACAAGAGCTGGGTCT  64
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Db      1219  GCGATGAGCGGCCCGCTGGCAGTTTCTACCTGCGGAGATTCACCGGCCACTCGTGTAT  1278

QY      65  TGGCGGTGTCACCAACCGCGCTGCTGACTGCGACACGACGACGAGGAGAGCTGCTGCG  124
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      1279  GCTGGCGGGCGGCGACCGCTGGCGCTTACCGGGGTGACGACGAGATCGCGCGAACA  1338

QY      125  CACCATCGGTACTGTCGCGCTGACGAGGCGGACGACGATGACCGCCCGCGCGG  184
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      1339  GGGCAGCGCGCACCCCGCTGCACTGTCTACGGGGTGACCCAGGAGCTGACCTGTGTCG  1398

QY      185  CTGAGAGTCCCGGTGCGAGGTGCGACGA  211
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      1399  TCTCGAGCGCTGGAGGCGTTGCGCGA  1425

RESULT 11
US-09-252-991A-15077/c
; Sequence 15077, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 15077
; LENGTH: 1815
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-15077

Query Match      19.7%; Score 42.2; DB 4; Length 1815;
Best Local Similarity 50.2%; Pred. No. 0.096;
Matches 104; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

QY      5  GGAGAAGCGCTACGACTGGCCCGCGTGGCGCGGTACAAAGGTGAACAAGAGCTGGGTCT  64
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Db      643  GCGATGGACGGCCCGCTGGGCAGTTTCTACCTGCGGAGATTCACCGCCACTGCTGAT  584
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY      65  TGGGTTGCCAACCCCGGCTCTGGTACTGCCACACGCTACCGAGGAAGACGTCGTGCG  124
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      583  GCTGGCGGGGCGACCGGCTGGCGCGTTTCACCGGATGCTCGAAGGATCGCCGAACA  524
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY      125  CACCATCGGTACTGTCGCGCTGACAGGCGGCGGACGACGATGACCGCCCGCGCGG  184
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      523  GGGCAGCGCCACCCCGCTGACCTGGTCTACGGGGTGACCCAGACGTCGACCTGGTTCGG  464
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY      185  CTTGAGGTCCTCGGTGCGAGTTCGACGA  211
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      463  TCTCGAGCGCTGGAGGCGTTGCGCGA  437

RESULT 12
US-09-252-991A-12129
; Sequence 12129, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 12129
; LENGTH: 999
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-12129

Query Match      19.4%; Score 41.6; DB 4; Length 999;
Best Local Similarity 55.6%; Pred. No. 0.12;
Matches 80; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY      66  GCGGTGCCAACCCCGCTGTCGTGCTGCCACCGCTACCGAGGAAGACGTCGTGCGC  125
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      106  GCGATGCCAACTGGCTGCTGGCGAATATCGGACGATCTCCGTGGCGTGTGTCGAG  165

QY      126  ACCATCGGTACTGTCGCGCTGACAGGCGGCGGACGACGATGACCGCCCGCGCGG  185
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      166  CGGTGCGGTAGCGCACCGCTCGCGCGCTGCGGCGGCGGATCATCTCGGCTTT  225
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY      186  CTCGAGGTCCCGGTGCGAGGTGCGAC  209
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      226  CTCGCGCTGCTGTCGCGCTCGCC  249

RESULT 13
US-09-252-991A-12291/c
; Sequence 12291, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 12291
; LENGTH: 1404

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; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-12291

Query Match 19.4%; Score 41.6; DB 4; Length 1404;
Best Local Similarity 55.6%; Pred. No. 0.13;
Matches 80; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 66 GCGGCTGCAACCGCGCTGCTGACTGCCACCGCTCAACGAGGAGACGTCGTCGCC 125
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 198 GCGGATGCCACTGGCTGCTGGGGAATATCGGAGCATCTCCGTGGGGTCTGCTGAG 139
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 126 ACCATCGGTACTGGTGGCGCTGCACAGAGGCCACAGACGACGACGACGACGACG 185
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 138 CCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 79
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 186 CTCGAGGTCCCGTGGAGTCGAC 209
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 78 CTCGCGCTGCTGCTGGCGCTCGCC 55
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 14
US-08-461-775-10
; Sequence 10, Application US/08461775
; Patent No. 5858773
; GENERAL INFORMATION:
; APPLICANT: MAZODIER, Philippe
; APPLICANT: GUZLIERI, Gerard
; TITLE OF INVENTION: REGULATORY NUCLEOTIDE SEQUENCE OF THE
; TITLE OF INVENTION: INITIATION OF TRANSCRIPTION
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: George Mason Bldg., Washington & Prince Sts.
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,775
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/050,313
; FILING DATE: 10-MAY-1993
; APPLICATION NUMBER: FR 901186
; FILING DATE: 10-SEP-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Crane-Feury, Sharon E
; REGISTRATION NUMBER: 36,113
; REFERENCE/DOCKET NUMBER: 010830-035
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1620 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1620

Query Match 19.3%; Score 41.2; DB 2; Length 1620;
Best Local Similarity 49.5%; Pred. No. 0.16;
Matches 106; Conservative 0; Mismatches 108; Indels 0; Gaps 0;

Matches 106; Conservative 0; Mismatches 108; Indels 0; Gaps 0;
QY 1 TCAGGAGAGCGCTACGACCTGGCCCGCGTGGCGGTACAGGTGACACAGACTGG 60
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Db 1268 TCAGGTCTCTGGACGACACCTCGCGCCACCGCGGAGAGGCCACCGGTGTCGGGTCG 1327
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 GTCTTGGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 120
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1328 TCAGGAGAGCGCTACGACCTGGCCCGCGTGGCGGTACAGGTGACACAGACTGG 1387
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 121 TCAGGAGAGCGCTACGACCTGGCCCGCGTGGCGGTACAGGTGACACAGACTGG 180
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1388 ACCTCATCACCACCAAGGTGGCGGAGCTCGACAGGGGCCAGGGGCTTCAACGGGCGCCG 1447
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 181 GCGGCTGAGGTCCCGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGG 214
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1448 GCGAGTACGCGACCTGCTCAAGCGCGCGCTCAT 1481
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 15
US-09-031-606-10
; Sequence 10, Application US/09031606
; Patent No. 6153404
; GENERAL INFORMATION:
; APPLICANT: MAZODIER, Philippe
; APPLICANT: GUZLIERI, Gerard
; TITLE OF INVENTION: REGULATORY NUCLEOTIDE SEQUENCE OF THE
; TITLE OF INVENTION: INITIATION OF TRANSCRIPTION
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: George Mason Bldg., Washington & Prince Sts.
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/031,606
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/050,313
; FILING DATE: 10-MAY-1993
; APPLICATION NUMBER: FR 901186
; FILING DATE: 10-SEP-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Crane-Feury, Sharon E
; REGISTRATION NUMBER: 36,113
; REFERENCE/DOCKET NUMBER: 010830-035
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1620 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1620

Query Match 19.3%; Score 41.2; DB 3; Length 1620;
Best Local Similarity 49.5%; Pred. No. 0.16;
Matches 106; Conservative 0; Mismatches 108; Indels 0; Gaps 0;

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OM nucleic - nucleic search, using sw model

Run on: September 17, 2003, 11:54:34 ; Search time 111.382 Seconds
(without alignments)
4726.283 Million cell updates/sec

Title: US-09-697-123b-7
Perfect score: 214
Sequence: 1 tcaaggagagcgctacgac.....ccggtcgagtcgacgacat 214

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1660708 seqs, 1229959015 residues

Total number of hits satisfying chosen parameters: 3321416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Result No.	Score	Query Match	Length	ID	Description
1	124.8	58.3	3519	10 US-09-712-363-30	Sequence 30, Appl
2	88.4	41.3	3495	10 US-09-738-626-547	Sequence 547, App
3	88.4	41.3	5096	10 US-09-984-711-5	Sequence 5, Appli
4	88.4	41.3	5099	10 US-09-887-052-1	Sequence 1, Appli
5	88.4	41.3	5099	10 US-09-887-052-3	Sequence 3, Appli
6	88.4	41.3	5099	10 US-09-887-052-5	Sequence 5, Appli
7	88.4	41.3	5099	12 US-10-076-406-1	Sequence 1, Appli
8	88.4	41.3	5099	12 US-10-076-406-3	Sequence 3, Appli
9	88.4	41.3	5099	12 US-10-076-406-5	Sequence 5, Appli
10	88.4	41.3	5099	13 US-10-075-460-5	Sequence 5, Appli
11	88.4	41.3	3309400	10 US-09-738-626-1	Sequence 1, Appli
12	72.8	34.0	3543	14 US-10-156-761-4898	Sequence 4898, Ap
13	72.8	34.0	9025608	14 US-10-156-761-1	Sequence 1, Appli
14	45	21.0	933	14 US-10-156-761-4618	Sequence 4618, Ap
15	43.2	20.2	9220	14 US-09-712-363-100	Sequence 100, App
16	42.6	19.9	9227	14 US-10-156-761-7471	Sequence 7471, Ap

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	124.8	58.3	3519	10 US-09-712-363-30	Sequence 30, Appl
2	88.4	41.3	3495	10 US-09-738-626-547	Sequence 547, App
3	88.4	41.3	5096	10 US-09-984-711-5	Sequence 5, Appli
4	88.4	41.3	5099	10 US-09-887-052-1	Sequence 1, Appli
5	88.4	41.3	5099	10 US-09-887-052-3	Sequence 3, Appli
6	88.4	41.3	5099	10 US-09-887-052-5	Sequence 5, Appli
7	88.4	41.3	5099	12 US-10-076-406-1	Sequence 1, Appli
8	88.4	41.3	5099	12 US-10-076-406-3	Sequence 3, Appli
9	88.4	41.3	5099	12 US-10-076-406-5	Sequence 5, Appli
10	88.4	41.3	5099	13 US-10-075-460-5	Sequence 5, Appli
11	88.4	41.3	3309400	10 US-09-738-626-1	Sequence 1, Appli
12	72.8	34.0	3543	14 US-10-156-761-4898	Sequence 4898, Ap
13	72.8	34.0	9025608	14 US-10-156-761-1	Sequence 1, Appli
14	45	21.0	933	14 US-10-156-761-4618	Sequence 4618, Ap
15	43.2	20.2	9220	14 US-09-712-363-100	Sequence 100, App
16	42.6	19.9	9227	14 US-10-156-761-7471	Sequence 7471, Ap

ALIGNMENTS

RESULT 1

US-09-712-363-30
; Sequence 30, Application US/09712363
; Patent No. US20020164588A1
; GENERAL INFORMATION:
; APPLICANT: Eisenberg, David
; APPLICANT: Rotstein, Sergio H.
; APPLICANT: Marcotte, Edward M.
; TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND
; TITLE OF INVENTION: INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS
; FILE REFERENCE: 07419-032001
; CURRENT APPLICATION NUMBER: US/09/712,363
; CURRENT FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: PCT/US00/02246
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,531
; PRIOR FILING DATE: 2000-02-01
; PRIOR APPLICATION NUMBER: 60/117,844
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/118,206,
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: 60/126,593
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/134,093
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/134,092
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/165,124
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/165,086
; PRIOR FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 3519
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-09-712-363-30

Sequence 1, Appli
Sequence 6208, Ap
Sequence 1184, Ap
Sequence 5097, Ap
Sequence 1, Appli
Sequence 2638, Ap
Sequence 11405, A
Sequence 5604, Ap
Sequence 1283, Ap
Sequence 3840, Ap
Sequence 1305, Ap
Sequence 1915, Ap
Sequence 3590, Ap
Sequence 2885, Ap
Sequence 15102, A
Sequence 6478, Ap
Sequence 7, Appli
Sequence 5, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 488, App
Sequence 1135, Ap
Sequence 1296, Ap
Sequence 4994, Ap
Sequence 1093, Ap
Sequence 4911, Ap
Sequence 4574, Ap

c 17 42.6 19.9 9025608 14 US-10-156-761-1
c 18 2631 14 US-10-156-761-6208
c 19 1188 14 US-10-156-761-1184
20 41.8 19.5 963 14 US-10-156-761-5097
21 41.6 19.4 963 14 US-09-957-189-1
22 41 19.2 3000 10 US-10-156-761-2638
23 40.8 19.1 1338 14 US-10-156-761-11405
24 40.8 19.1 3408 14 US-10-156-761-5604
25 40.6 19.0 1584 14 US-10-156-761-1283
26 40.4 18.9 1116 14 US-10-156-761-3840
27 40.2 18.8 984 14 US-10-156-761-1305
28 40.2 18.8 1365 14 US-10-156-761-1915
29 40.2 18.8 1629 14 US-10-156-761-3590
30 40.2 18.8 14520 14 US-10-156-761-2885
31 40.2 18.8 125746 14 US-10-156-761-15102
32 40 18.7 1170 14 US-10-156-761-6478
33 40 18.7 3343 10 US-09-950-772-7
34 40 18.7 3343 14 US-10-289-360-5
35 40 18.7 15872 10 US-09-861-289-1
36 40 18.7 15872 10 US-09-860-846-1
37 40 18.7 15872 11 US-09-988-384B-1
38 40 18.7 15872 11 US-09-836-821-1
39 39.8 18.6 813 14 US-10-156-761-488
40 39.6 18.5 1014 14 US-10-156-761-7135
41 39.6 18.5 1587 14 US-10-156-761-1296
42 39.6 18.5 1734 14 US-10-156-761-4994
43 39.6 18.5 1923 14 US-10-156-761-1093
44 39.4 18.4 663 14 US-10-156-761-4911
45 39.2 18.3 828 14 US-10-156-761-4574

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Query Match      58.3%; Score 124.8; DB 10; Length 3519;
Best Local Similarity 77.6%; Pred. No. 2.4e-24;
Matches 166; Conservative 0; Mismatches 42; Indels 6; Gaps 1;

QY 1 TCAGGAGAGCGCTACGACCTGCGCGGTGGCGGTGACAGGTGAACAAGACTGG 60
DB 384 TCAGGAGAGCGCTACGACCTGCGCGGTGGCGGTGACAGGTGAACAAGACTGG 943
QY 61 GTCTTGGCGGTGCCAACCGGCTCTGGTGACTGCCACCGCTCACCGAGGAGAGCTGG 120
DB 944 GGCTGATGTCGGCGAGCC-----CATCAGCTGCTGCAAGCTGACCGAGAGAGCTGG 997
QY 121 TCGCCACATCGGGTACCTGCTGCTGCGCTGCACGAGGCGCCAGACAGCTGACCGCCCGG 180
DB 998 TGGCCACCATCGGAATATCTGCTGCTGCGCTGCACGAGGCTCAGACCAAGCTGACCGTTCCGG 1057
QY 181 CGGCTCTGAGTCCCGTTCGAGTTCGAGTTCGAGCAT 214
DB 1058 CGCGCTGAGTTCGCGGTGGAACCGAGCAT 1091

RESULT 2
US-09-738-626-547
; Sequence 547, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIALI, KEIKO
; APPLICANT: YOKOL, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENO, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/097738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 547
; LENGTH: 3495
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-547

Query Match      41.3%; Score 88.4; DB 10; Length 3495;
Best Local Similarity 68.4%; Pred. No. 1.1e-14;
Matches 141; Conservative 0; Mismatches 56; Indels 9; Gaps 1;

QY 9 AAGCGTACGACTGGCCCGGTGACAGGTGAACAAGACTGGCTTTGGC 68
DB 877 AAGCGTACGACTGGCTGGCTGTTGCTGTTACAGATCAACCGCAAGCTCGCTTGGT 936
QY 69 GGTGCCAACCGGCTCTGGTGAATGCCACCGCTCAGGAGGAGCTGTCGCCACC 128
DB 937 GGGACACGATGGTTGATGACT-----CTTACTGAAGAGGACATCGCAACACC 987
QY 129 ATCGGTACTGCTGGCTGCGCTGACGAGGCGCCAGACAGTACCGCCCGCGGCTTC 188
DB 988 ATCGGTACTGCTGGCTGCTGCACCGAGGTGACCGGCTCATGCTTCTCCAAATGGTGA 1047
QY 189 GAGTCCCGTCTGAGTTCGAGCAT 214
DB 1048 GAGATCCCGTCTGAGACCGATGACAT 1073
```

```
RESULT 3
US-09-984-711-5
; Sequence 5, Application US/09984711
; Patent No. US20020119549A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: STEPHAN, Hans
; APPLICANT: KREUTZER, Caroline
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE rpsL GENE
; FILE REFERENCE: 204209US0
; CURRENT APPLICATION NUMBER: US/09/984,711
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: DE10108230.9
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 5096
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
; OTHER INFORMATION:
US-09-984-711-5

Query Match      41.3%; Score 88.4; DB 10; Length 5096;
Best Local Similarity 68.4%; Pred. No. 1.1e-14;
Matches 141; Conservative 0; Mismatches 56; Indels 9; Gaps 1;

QY 9 AAGCGTACGACTGGCCCGGTGACAGGTGAACAAGACTGGCTTTGGC 68
DB 1578 AAGCGTACGACTGGCTGGCTGTTGCTTACAGATCAACCGCAAGCTCGGCTTGGT 1637
QY 69 GGTGCCAACCGGCTCTGGTGAATGCCACCGCTCAGGAGGAGAGCTGTCGCCACC 128
DB 1638 GCGACACAGATGTTGATGACT-----CTTACTGAAGAGGACATCGCAACACC 1688
QY 129 ATCGGTACTGCTGGCTGCGCTGACGAGGCGCCAGACAGTACCGCCCGCGGCTTC 188
DB 1689 ATCGGTACTGCTGGCTGCTGCACGAGGTGAGCGGCTCATGCTTCTCCAAATGGTGA 1748
QY 189 GAGTCCCGTCTGAGTTCGAGCAT 214
DB 1749 GAGATCCCGTCTGAGACCGATGACAT 1774

RESULT 4
US-09-887-052-1
; Sequence 1, Application US/09887052
; Patent No. US20020119537A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE rpoB GENE
; FILE REFERENCE: 204212US0X
; CURRENT APPLICATION NUMBER: US/09/887,052
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: DE10107229.5
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 5099
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; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
; US-09-887-052-1

Query Match      41.3%; Score 88.4; DB 10; Length 5099;
Best Local Similarity 68.4%; Pred. No. 1.1e-14;
Matches 141; Conservative 0; Mismatches 56; Indels 9; Gaps 1;

QY 9 AAGCGCTACGACCTGGCGCCGCGGTACAGGTGAACAAGAGTGGGCTTTGGC 68
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1578 AAGCGCTACGACCTGGCGCGGTGCTGTTACAGATCAACCGCAAGCTGGCTTGGT 1637

QY 69 GTGCGCAACCGCGCTCTGGTGACTGCCACCGCTCACCGAGGAAGACGTCTGCCACC 128
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1638 GCGGACCAACGATGGTTGATGACT-----CTTACTGAAGGACATCGCAACCACC 1688

QY 129 ATCGGGTACCTGGTGGCCCTGACGAGGCCAGACGATGACCGCCCGCGGCGCTC 188
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1689 ATCGAGTACCTGGTGGCTGCTGACGAGGTGAGCGCGTCATGACTTCTCCAAATGGTGAA 1748

QY 189 GAGGTCCGGTCGAGGTCGACGACAT 214
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1749 GAGATCCCGAGTCGACCGATGACAT 1774

RESULT 5
US-09-887-052-3
; Sequence 3, Application US/09887052
; Patent No. US20020119537A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE IPOB GENE
; FILE REFERENCE: 2042120SX
; CURRENT APPLICATION NUMBER: US/09/887,052
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: DE10107229.5
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 5099
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
; US-09-887-052-3

Query Match      41.3%; Score 88.4; DB 10; Length 5099;
Best Local Similarity 68.4%; Pred. No. 1.1e-14;
Matches 141; Conservative 0; Mismatches 56; Indels 9; Gaps 1;

QY 9 AAGCGCTACGACCTGGCGCCGCGGTACAGGTGAACAAGAGTGGGCTTTGGC 68
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1578 AAGCGCTACGACCTGGCGCGGTGCTGTTACAGATCAACCGCAAGCTGGCTTGGT 1637

QY 69 GTGCGCAACCGCGCTCTGGTGACTGCCACCGCTCACCGAGGAAGACGTCTGCCACC 128
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1638 GCGGACCAACGATGGTTGATGACT-----CTTACTGAAGGACATCGCAACCACC 1688

QY 129 ATCGGGTACCTGGTGGCCCTGACGAGGCCAGACGATGACCGCCCGCGGCGCTC 188
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1689 ATCGAGTACCTGGTGGCTGCTGACGAGGTGAGCGCGTCATGACTTCTCCAAATGGTGAA 1748

QY 189 GAGGTCCGGTCGAGGTCGACGACAT 214
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1749 GAGATCCCGAGTCGACCGATGACAT 1774

RESULT 6
US-09-887-052-5
; Sequence 5, Application US/09887052
; Patent No. US20020119537A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE IPOB GENE
; FILE REFERENCE: 2042120SX
; CURRENT APPLICATION NUMBER: US/09/887,052
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: DE10107229.5
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 5099
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
; US-09-887-052-5

Query Match      41.3%; Score 88.4; DB 10; Length 5099;
Best Local Similarity 68.4%; Pred. No. 1.1e-14;
Matches 141; Conservative 0; Mismatches 56; Indels 9; Gaps 1;

QY 9 AAGCGCTACGACCTGGCGCCGCGGTACAGGTGAACAAGAGTGGGCTTTGGC 68
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1578 AAGCGCTACGACCTGGCGCGGTGCTGTTACAGATCAACCGCAAGCTGGCTTGGT 1637

QY 69 GTGCGCAACCGCGCTCTGGTGACTGCCACCGCTCACCGAGGAAGACGTCTGCCACC 128
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1638 GCGGACCAACGATGGTTGATGACT-----CTTACTGAAGGACATCGCAACCACC 1688

QY 129 ATCGGGTACCTGGTGGCCCTGACGAGGCCAGACGATGACCGCCCGCGGCGCTC 188
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1689 ATCGAGTACCTGGTGGCTGCTGACGAGGTGAGCGCGTCATGACTTCTCCAAATGGTGAA 1748

QY 189 GAGGTCCGGTCGAGGTCGACGACAT 214
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1749 GAGATCCCGAGTCGACCGATGACAT 1774

RESULT 7
US-10-076-406-1
; Sequence 1, Application US/10076406
; Publication No. US20030166884A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: Nucleotide sequences coding for the rpoB gene
; FILE REFERENCE: 219774USOXCP
; CURRENT APPLICATION NUMBER: US/10/076,406
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: DE 10107229.5
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 09/887052
; PRIOR FILING DATE: 2001-06-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 5099
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; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
; OTHER INFORMATION:
US-10-076-406-1

Query Match 41.3%; Score 88.4; DB 12; Length 5099;
Best Local Similarity 68.4%; Pred. No. 1.1e-14;
Matches 141; Conservative 0; Mismatches 56; Indels 9; Gaps 1;

QY 9 AAGCGTACGACCTGGCCCGCTGGTGCCTGACAGTGCACACGAGGAGAGCGTCTGCGCAC 128
Db 1578 AAGCGTACGACCTGGCTCGGTTGCTGTTACAAAGATCAACCGCAAGCTCGGCCCTTGGT 1637
QY 69 GGTGCCAACCCGCTCTGGTGCCTGACAGTGCACACGAGGAGAGCGTCTGCGCAC 128
Db 1638 GCGACCCAGTGGTTGATGACT-----CTTACTGAAGAGGACATCGCAACCAACC 1688
QY 129 ATCGGTACCTGGTGCCTGACAGGCGCCAGTGCACAGTGCACGCGGCTCATGACTTCTCCAATGGTGAA 1748
Db 1689 ATCGAGTACCTGGTGCCTGACAGGCGGCTCATGACTTCTCCAATGGTGAA 1748
QY 189 GAGTCCCGGTGAGTGCAGCAT 214
Db 1749 GAGATCCAGTCGAGACCGATGACAT 1774

RESULT 8

US-10-076-406-3
; Sequence 3, Application US/10076406
; Publication No. US20030166884A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; FILE OF INVENTION: Nucleotide sequences coding for the rpoB gene
; CURRENT APPLICATION NUMBER: US/10/076,406
; PRIOR FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: DE 10107229.5
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 09/887052
; PRIOR FILING DATE: 2001-06-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 3

; LENGTH: 5099
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
; OTHER INFORMATION:
; NAME/KEY: mutation
; LOCATION: (1987)..(1987)
; OTHER INFORMATION: Substitution of adenine by thymine
; NAME/KEY: mutation
; LOCATION: (1288)..(1288)
; OTHER INFORMATION: Substitution of cytosine by thymine
; NAME/KEY: mutation
; LOCATION: (715)..(715)
; OTHER INFORMATION: Substitution of cytosine by thymine
US-10-076-406-3

Query Match 41.3%; Score 88.4; DB 12; Length 5099;
Best Local Similarity 68.4%; Pred. No. 1.1e-14;
Matches 141; Conservative 0; Mismatches 56; Indels 9; Gaps 1;

QY 9 AAGCGTACGACCTGGCCCGCTGGTGCCTGACAGTGCACAAAGAGCTGGGTCTTGGC 68

Db 1578 AAGCGTACGACCTGGCTCGGTTGCTGTTACAAAGATCAACCGCAAGCTCGGCCCTTGGT 1637
QY 69 GGTGCCAACCCGCTCTGGTGCCTGACAGTGCACACGAGGAGAGCGTCTGCGCAC 128
Db 1638 GCGACCCAGTGGTTGATGACT-----CTTACTGAAGAGGACATCGCAACCAACC 1688
QY 129 ATCGGTACCTGGTGCCTGACAGGCGCCAGTGCACAGTGCACGCGGCTCATGACTTCTCCAATGGTGAA 1748
Db 1689 ATCGAGTACCTGGTGCCTGACAGGCGGCTCATGACTTCTCCAATGGTGAA 1748
QY 189 GAGTCCCGGTGAGTGCAGCAT 214
Db 1749 GAGATCCAGTCGAGACCGATGACAT 1774

RESULT 9

US-10-076-406-5
; Sequence 5, Application US/10076406
; Publication No. US20030166884A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; FILE OF INVENTION: Nucleotide sequences coding for the rpoB gene
; CURRENT APPLICATION NUMBER: US/10/076,406
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: DE 10107229.5
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 09/887052
; PRIOR FILING DATE: 2001-06-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 5
; LENGTH: 5099
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
; OTHER INFORMATION:
; NAME/KEY: mutation
; LOCATION: (2016)..(2016)
; OTHER INFORMATION: Substitution of cytosine by thymine
US-10-076-406-5

Query Match 41.3%; Score 88.4; DB 12; Length 5099;
Best Local Similarity 68.4%; Pred. No. 1.1e-14;
Matches 141; Conservative 0; Mismatches 56; Indels 9; Gaps 1;
QY 9 AAGCGTACGACCTGGCCCGCTGGTGCCTGACAGTGCACAAAGAGCTGGGTCTTGGC 68
Db 1578 AAGCGTACGACCTGGCTCGGTTGCTGTTACAAAGATCAACCGCAAGCTCGGCCCTTGGT 1637
QY 69 GGTGCCAACCCGCTCTGGTGCCTGACAGTGCACACGAGGAGAGCGTCTGCGCAC 128
Db 1638 GCGACCCAGTGGTTGATGACT-----CTTACTGAAGAGGACATCGCAACCAACC 1688
QY 129 ATCGGTACCTGGTGCCTGACAGGCGCCAGTGCACAGTGCACGCGGCTCATGACTTCTCCAATGGTGAA 1748
Db 1689 ATCGAGTACCTGGTGCCTGACAGGCGGCTCATGACTTCTCCAATGGTGAA 1748
QY 189 GAGTCCCGGTGAGTGCAGCAT 214
Db 1749 GAGATCCAGTCGAGACCGATGACAT 1774

RESULT 10

US-10-075-460-5
; Sequence 5, Application US/10075460

```
; Publication No. US2002015557A1
; GENERAL INFORMATION:
; APPLICANT: MOCKEL, BETTINA
; APPLICANT: BATHE, BRIGITTE
; APPLICANT: HANS, STEFAN
; APPLICANT: KREUTZER, CAROLINE
; APPLICANT: HERMANN, THOMAS
; APPLICANT: PFEFFERLE, WALTER
; APPLICANT: BINDER, MICHAEL
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE rpsL GENE
; FILE REFERENCE: 218472US0X
; CURRENT APPLICATION NUMBER: US/10/075,460
; CURRENT FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: DE 10107230.9
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: DE 10162386.0
; PRIOR FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 5099
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
; OTHER INFORMATION:
US-10-075-460-5

Query Match      41.3%; Score 88.4; DB 13; Length 5099;
Best Local Similarity 68.4%; Pred. No. 1.le-14;
Matches 141; Conservative 0; Mismatches 56; Indels 9; Gaps 1;

QY 9 AAGCGTAGACCTGGCCGCGTGGTACAGGTGACCAAGGTCGAGGTCGCTGGTGGT 68
Db 1578 AAGCGTAGACCTGGCTGGTGGTGGTACAGATCAACCGAAGCTGGCGCTGGT 1637
QY 69 GGTGCCAACCCGCGTCTGGTGAATGCCACCACTCACCAGGAGAGAGCTGTCGCCACC 128
Db 1638 GCGACCAACGATGTTGATGACT-----CCTACTGAGAGAGACATCGCAACACC 1688
QY 129 ATCGGTACTCTGGTGGCTCGACAGGGCCAGACACATGACGCGCCCGCGGCGCTC 188
Db 1689 ATCGAGTAGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1748
QY 189 GAGTCCCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 214
Db 1749 GAGATCCAGTCGAGACCGATGACAT 1774

RESULT 11
US-09-738-626-1
; Sequence 1, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIALI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OKAZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
```

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; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 1
; LENGTH: 3309400
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-1

Query Match      41.3%; Score 88.4; DB 10; Length 3309400;
Best Local Similarity 68.4%; Pred. No. 6.le-15;
Matches 141; Conservative 0; Mismatches 56; Indels 9; Gaps 1;

QY 9 AAGCGTAGACCTGGCCGCGTGGTACAGGTGACCAAGGTCGAGGTCGCTGGTGGT 68
Db 513789 AAGCGTAGACCTGGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 513848
QY 69 GGTGCCAACCCGCGTCTGGTGAATGCCACCACTCACCAGGAGAGAGCTGTCGCCACC 128
Db 513849 GCGACCAACGATGTTGATGACT-----CCTACTGAGAGAGACATCGCAACACC 513899
QY 129 ATCGGTACTCTGGTGGCTCGACAGGGCCAGACACATGACGCGCCCGCGGCGCTC 188
Db 513900 ATCGAGTAGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 513959
QY 189 GAGTCCCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 214
Db 513960 GAGATCCAGTCGAGACCGATGACAT 513985

RESULT 12
US-10-156-761-4898
; Sequence 4898, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 4898
; LENGTH: 3543
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3543)
US-10-156-761-4898

Query Match      34.0%; Score 72.8; DB 14; Length 3543;
Best Local Similarity 63.1%; Pred. No. 1.5e-10;
Matches 135; Conservative 0; Mismatches 67; Indels 12; Gaps 1;
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QY 1 TCAAGGAGAGCGCTACGACCTGGCGCGTGGCGGTGACAGGTGACCAAGAGCTGG 60
Db 926 TCAACCGAAGCGCTACGACCTGGCGCGTGGCGGTGACAGGTGACCAAGAGCTGG 985
QY 61 GTCTTGGCGGTGCCAACCCCGGCTCTGGTGAATGCCACAGCTACCGGAGAGAGCTCG 120
Db 986 G-----CGCGGAGGCGCGGTGGACCGCGGATCTGTGACCGTCGAGGACATCA 1033
```

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QY 121 TCGCACCATCGGTACCTGGTGGCTGCACGAGGCGCAGACACCATGATACCGCCCGCCG 180
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1034 TCTCGTCATCACTACCTGGTGAAGCTGCACGCGGTGAGACCGGATGCGCGACA 1093
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 181 GCGGCTCGAGTCCCGGTGCGAGTGCAGGACAT 214
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1094 ACGGCACCTCGATCGTCTGCGAGACCGAGGACAT 1127
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 13
US-10-156-761-1
; Sequence 1, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
; LENGTH: 9025608
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; NAME/KEY: misc_feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1

Query Match 34.0%; Score 72.8; DB 14; Length 9025608;
Best Local Similarity 63.1%; Pred. No. 7.8e-11;
Matches 135; Conservative 0; Mismatches 67; Indels 12; Gaps 1;

QY 1 TCAAGAGAAGCGGTACGACCTGGCCGCGGTGGCGGTACAAGGTGAACAAGAGCTGG 60
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5970494 TCAACCCGAAGCGGTACGACCTGGCGAAGTGGCGCGCTACAAGGTCAACAAGAGCTGG 5970553
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 61 GTCTTGGCGGTGCCAACCCGCGTCTGGTGACTGCACACGCTCACCGGAGGAGAGCTGC 120
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5970554 G-----CGGCGAGGCGCCCTGGAGCGCGGGGATCCTGACCGTCGAGGACATCA 5970601
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 121 TCGCCACCATCGGTACCTGGTGGCGCTGCACGAGGCGCAGACCATGATGACCGCCCGC 180
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5970602 TCTCGTCGATCACTACCTGGTGAAGCTGCACGCGGTGAGACCGGACCGTGGCGACA 5970661
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 181 GCGGCTCGAGTCCCGGTGCGAGTGCAGGACAT 214
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5970662 ACGGCACCTCGATCGTCTGCGAGACCGAGGACAT 5970695
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 14
US-10-156-761-4618
; Sequence 4618, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
```

```
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 4618
; LENGTH: 933
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(933)
US-10-156-761-4618

Query Match 21.0%; Score 45; DB 14; Length 933;
Best Local Similarity 51.8%; Pred. No. 0.004;
Matches 102; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

QY 16 ACGACCTGGCCCGGTGGCGGTACAAGGTGAACAAGAGCTGGGTCTTGGCGGTGCA 75
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 131 AGGACCTCCCGCGCGCGGATCGTCATCGHGGCAACGATGCCCGCTGCCGATTCG 190
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 76 ACCCGGTCTGGTGAATGCCACACCTCACCGAGGAAGACGTCGTCGCCACCATCGGGT 135
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 191 CCGGCGCTGGACCTGCCCGCGGAGGTACCGGATCGAGGTGGACGAGAACCTCGGCT 250
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 136 ACCTGGTGGCTGTCAGGAGGCGCAGACGATGACCGCCCGCGCGCTTCGAGGTCC 195
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 251 GCCCGCGCGGCGAAGTGGCCCTGGCGAAGCTGCGGGAGTTTCGGGGACGTCGACGTG 310
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 196 CGGTGAGGTGCGACGAC 212
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 311 TCGTCGAACGCGACGAC 327
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RESULT 15
US-09-712-363-100
; Sequence 100, Application US/09712363
; Patent No. US20020164588A1
; GENERAL INFORMATION:
; APPLICANT: Eisenberg, David
; APPLICANT: Rotstein, Sergio H.
; APPLICANT: Marcotte, Edward M.
; TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND
; TITLE OF INVENTION: INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS
; FILE REFERENCE: 07419-032001
; CURRENT APPLICATION NUMBER: US/09/712,363
; CURRENT FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: PCT/US00/02246
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,531
; PRIOR FILING DATE: 2000-02-01
; PRIOR APPLICATION NUMBER: 60/117,844
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/118,206,
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: 60/126,593
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/134,093
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/134,092
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/165,124
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/165,086
; PRIOR FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 100
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; LENGTH: 9210
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-09-712-363-100

Query Match      20.2%; Score 43.2; DB 10; Length 9210;
Best Local Similarity 52.2%; Pred. No. 0.01;
Matches 96; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

Qy  24  GCGCCGCGGCGCGGTACAGGTGAACAAGAGCTGGGTCTTGGCGGTGCCAAOCCGGCT 83
      ||| || | ||| ||| || | ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  5629 GCATCGCGCGAGCGCGGTGAAGAAGACCTGGGAGCTCGGTGAGGGCTGGGCCCAAGCATGTC 5688

Qy  84  CTGGTGACTGCCACCAAGCTCACCGAGGAGAGCGTCTCGCCACCACATCGGGTACCTGGTG 143
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  5689 ACCGTCGAGGTGCGGCTGGGCAACCCCGAGGGGACAGCGGTTCCGCGCGGCGCCCATGGGC 5748

Qy  144  CGCCTGCAAGAGGGCCAGACCGATGACCGCGCGCGCGCGCTCGAGGTCCCGGTCGAG 203
      | ||||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  5749 CACCTGCACGAGGGCGCGCTGGCGGATGCCGCTCCGTCGACAAAGGTCAATCGACGCGGCG 5808

Qy  204  GTCG 207
      ||||
Db  5809 GTCG 5812
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Search completed: September 17, 2003, 13:04:16
Job time : 132.382 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 17, 2003, 11:54:34 : Search time 30.1105 Seconds
(without alignments)
3049.028 Million cell updates/sec

Title: US-09-697-123B-8
Perfect score: 208
Sequence: 1 tcagagagagcgctacgac.....ccggtgggaaccgacgacat 208

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents.NA.*

- 1: /cgn2.6/prodata/1/ina/5A.COMB.seq.*
- 2: /cgn2.6/prodata/1/ina/5B.COMB.seq.*
- 3: /cgn2.6/prodata/1/ina/6A.COMB.seq.*
- 4: /cgn2.6/prodata/1/ina/6B.COMB.seq.*
- 5: /cgn2.6/prodata/1/ina/PCTUS.COMB.seq.*
- 6: /cgn2.6/prodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	166.4	80.0	970	1 US-08-250-030-1	Sequence 1, Appli
2	166.4	80.0	970	5 PCT-US95-06790-1	Sequence 1, Appli
3	166.4	80.0	4403765	3 US-09-103-840A-2	Sequence 2, Appli
4	166.4	80.0	4411529	3 US-09-103-840A-1	Sequence 1, Appli
5	142.4	68.5	3447	2 US-08-313-185-57	Sequence 57, Appli
6	142.4	68.5	3447	3 US-09-082-614A-57	Sequence 57, Appli
7	39.4	18.9	1894	3 US-09-329-350-32	Sequence 32, Appli
8	39	18.8	1100	3 US-09-248-335-53	Sequence 53, Appli
9	38.2	18.4	468	4 US-09-252-991A-9731	Sequence 9731, Ap
10	38.2	18.4	468	4 US-09-252-991A-16394	Sequence 16394, A
11	38.2	18.4	1482	4 US-09-252-991A-9689	Sequence 9689, Ap
12	38.2	18.4	1587	4 US-09-252-991A-16504	Sequence 16504, A
c 13	38.2	18.4	1614	4 US-09-252-991A-9607	Sequence 9607, Ap
c 14	38.2	18.4	1623	4 US-09-252-991A-9650	Sequence 9650, Ap
c 15	38.2	18.4	2070	4 US-09-252-991A-16098	Sequence 16098, A
c 16	38	18.3	2742	3 US-09-232-468A-1	Sequence 1, Appli
c 17	38	18.3	2742	4 US-09-784-984B-1	Sequence 1, Appli
c 18	38	18.3	4897	6 5196516-7	Patent No. 5196516
c 19	37	17.8	540	4 US-09-252-991A-7249	Sequence 7249, Ap
c 20	37	17.8	1722	4 US-09-252-991A-7450	Sequence 7450, Ap
c 21	36.8	17.7	77536	4 US-09-410-551B-1	Sequence 1, Appli
c 22	36.8	17.7	4403765	3 US-09-103-840A-2	Sequence 2, Appli
c 23	36.8	17.7	4411529	3 US-09-103-840A-1	Sequence 1, Appli
c 24	36.2	17.4	1014	4 US-09-252-991A-2663	Sequence 2663, Ap
c 25	36.2	17.4	1155	4 US-09-252-991A-2762	Sequence 2762, Ap
c 26	36.2	17.4	1233	4 US-09-252-991A-3203	Sequence 3203, Ap
c 27	36.2	17.4	2634	1 US-08-196-218-31	Sequence 31, Appli

28 36.2 17.4 2634 1 US-08-681-953-31 Sequence 31, Appli

29 36 17.3 987 4 US-09-252-991A-12047 Sequence 12047, A

30 36 17.3 1155 4 US-09-252-991A-12078 Sequence 12078, A

c 31 36 17.3 1251 4 US-09-252-991A-11928 Sequence 11928, A

32 35.8 17.2 734 4 US-09-221-017B-1070 Sequence 1070, Ap

33 35.6 17.1 750 4 US-09-252-991A-9464 Sequence 9464, Ap

c 34 35.6 17.1 918 4 US-09-252-991A-9337 Sequence 9337, Ap

35 35.6 17.1 1440 4 US-09-252-991A-9411 Sequence 9411, Ap

36 35.6 17.1 55216 4 US-09-716-865-23 Sequence 23, Appli

c 37 35.4 17.0 579 4 US-09-252-991A-2876 Sequence 2876, Ap

38 35.4 17.0 1536 4 US-09-252-991A-3182 Sequence 3182, Ap

c 39 35.4 17.0 2070 4 US-09-252-991A-2687 Sequence 2687, Ap

40 35 16.8 402 4 US-09-252-991A-8726 Sequence 8726, Ap

41 35 16.8 780 4 US-09-252-991A-2544 Sequence 2544, Ap

42 35 16.8 981 4 US-09-252-991A-5092 Sequence 5092, Ap

43 35 16.8 1149 4 US-09-252-991A-5033 Sequence 5033, Ap

c 44 35 16.8 1251 4 US-09-252-991A-2376 Sequence 2376, Ap

45 35 16.8 1299 4 US-09-252-991A-8945 Sequence 8945, Ap

ALIGNMENTS

RESULT 1

US-08-250-030-1

: Sequence 1, Application US/08250030

: Patent No. 5643723

: GENERAL INFORMATION:

: APPLICANT: Persing, David H.

: TITLE OF INVENTION: Detection of a Genetic Locus Encoding

: TITLE OF INVENTION: Resistance to Rifampin in Mycobacterial Cultures and in

: TITLE OF INVENTION: Clinical Specimens

: NUMBER OF SEQUENCES: 15

: CORRESPONDENCE ADDRESS:

: ADDRESSEE: Schwegman, Lundberg & Woessner

: STREET: 3500 IDS Center

: CITY: Minneapolis

: STATE: MN

: COUNTRY: USA

: ZIP: 55402

: COMPUTER READABLE FORM:

: MEDIUM TYPE: Floppy disk

: COMPUTER: IBM PC compatible

: OPERATING SYSTEM: PC-DOS/MS-DOS

: SOFTWARE: PatentIn Release #1.0, Version #1.25

: CURRENT APPLICATION DATA:

: APPLICATION NUMBER: US/08/250,030

: FILING DATE: 26-MAY-1994

: CLASSIFICATION: 435

: ATTORNEY/AGENT INFORMATION:

: NAME: Mueting, Ann M.

: REGISTRATION NUMBER: 33,977

: REFERENCE/DOCKET NUMBER: 150.105051

: TELECOMMUNICATION INFORMATION:

: TELEPHONE: 612-339-0331

: TELEFAX: 612-339-3061

: INFORMATION FOR SEQ ID NO: 1:

: SEQUENCE CHARACTERISTICS:

: LENGTH: 970 base pairs

: TYPE: nucleic acid

: STRANDEDNESS: single

: TOPOLOGY: linear

: MOLECULE TYPE: DNA

US-08-250-030-1

Query Match 80.0%; Score 166.4; DB 1; Length 970;

Best Local Similarity 87.5%; Pred. No. 4.6e-33;

Matches 182; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

Qy 1 TCAAGGAGAGCGCTACGACCTGGCCCGCTGTCGCCGATACAGGTCTACAGAGAGCTGG 60

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Db 26 TCAAGGAGAGCGCTACGACCTGGCCCGCTGTCGCCGATACAGGTCTACAGAGAGCTGG 85

Query Match 80.0%; Score 166.4; DB 3; Length 4411529;

[illegible]

Best Local Similarity 87.5%; Pred. No. 1.4e-32;
Matches 182; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 1 TCAAGGAGAGCGCTACGACCTGGCCCGGTGTCGCGCCGATACAGGTTCACACAGAGCTGG 60
Db 760688 TCAAGGAGAGCGCTACGACCTGGCCCGGTGTCGCGCCGATACAGGTTCACACAGAGCTGG 760747
QY 61 GCGTGAACACCAATCATCCGATCCACGACGAGCGCTGACCGAAGAGACGTCGTCGCCA 120
Db 760748 GCGTGAATGTCGCGGAGCCCATCAGTGTGAGCGCTGACCGAGAGAGCTGTCGCCA 760807
QY 121 CCANGAGATATCTGGTTCGCGCTGCACGAGGGCCACGACGATGACCGCTGCGGGCGGG 180
Db 760808 CCATCGAATATCTGGTTCGCGCTGCACGAGGGTCAGACCGATGACCGCTTCGGGGCGGG 760867
QY 181 TCGAGGTCCGGTGGAAACCGACGACAT 208
Db 760868 TCGAGGTCCGGTGGAAACCGACGACAT 760895

RESULT 5

US-08-313-185-57
; Sequence 57, Application US/08313185
; Patent No. 5851763
; GENERAL INFORMATION:
; APPLICANT: Heym, Beate
; APPLICANT: Cole, Stewart
; APPLICANT: Young, Douglas
; APPLICANT: Zhang, Ying
; APPLICANT: Honore, Nadine
; APPLICANT: Telenti, Anallo
; APPLICANT: Bodmer, Thomas
; TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
; TITLE OF INVENTION: in Mycobacterium Tuberculosis
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/313,185
; FILING DATE: 12-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 02356.0068-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3447 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)

Query Match 68.5%; Score 142.4; DB 2; Length 3447;
Best Local Similarity 80.3%; Pred. No. 5.1e-27;
Matches 167; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 1 TCAAGGAGAGCGCTACGACCTGGCCCGGTGTCGCGCGATACAAGGTCAACAAGAGCTGG 60

Db 809 TCAAGGAGAGCGCTACGACCTGGCCCGGTGTCGTTACAGGTCAACAAGAGCTGG 868
QY 61 GCGTGAACACCAATCATCCGATCCACGACGAGCGCTGACCGAAGAGAGCTGTCGCCA 120
Db 869 GGTTCACGCGGTGAGTTGATCAGCTGCTCCACGCTGACCGAAGAGAGTATGTCGCCA 928
QY 121 CCATCGAGTATCTGGTTCGCGCTGCACGAGGGCCACGACGATGACCGTGCAGCGGGG 180
Db 929 CCATGAGTACTCTGGTTCGCTGCTCATGAGGTTCAGTCCACATGACTGTCCACAGGTGGG 986
QY 181 TCGAGGTCCGGTGGAAACCGACGACAT 208
Db 989 TAGAAGTCCAGTGGAAACTGACGATAT 1016

RESULT 6

US-09-082-614A-57
; Sequence 57, Application US/09082614A
; Patent No. 6124098
; GENERAL INFORMATION:
; APPLICANT: Heym, Beate
; APPLICANT: Cole, Stewart
; APPLICANT: Young, Douglas
; APPLICANT: Zhang, Ying
; APPLICANT: Honore, Nadine
; APPLICANT: Telenti, Anallo
; APPLICANT: Bodmer, Thomas
; TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
; TITLE OF INVENTION: in Mycobacterium Tuberculosis
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/082,614A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/313,185
; FILING DATE: 12-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 02356.0068-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3447 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)

Query Match 68.5%; Score 142.4; DB 3; Length 3447;
Best Local Similarity 80.3%; Pred. No. 5.1e-27;
Matches 167; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 1 TCAAGGAGAGCGCTACGACCTGGCCCGGTGTCGCGCGATACAAGGTCAACAAGAGCTGG 60
|||||

Db 809 TCAAGGAGAAAGCTACAGCTGGCCAGGGTGGTTCGTTACAAAGTCAACAGAAAGCTCG 868
QY 61 GCGTGAACCAATATCCGATCACCACGACGACGCTGACCGAAGAGAGCTGTCGCCCA 120
Db 869 GGTTCACGCGGTTGATGATCACTGCTCCACCTGACCGAGAGGATGTCGTCGCCA 928
QY 121 CATTCGAGTATCTGTCGCTGCTGACGAGAGGCCACGATGACGCTGCGCGGGGGG 180
Db 929 CCATAGAGTACCTGGTTCGCTCATGATGAGGTCTGCTGACATGCTGCCAGGTGGG 988
QY 181 TCGAGGTGCGGTGGAAACCGACGACAT 208
Db 989 TAGAGTGCAGTGGAAACTGACGATAT 1016

RESULT 7
US-09-329-350-32
; Sequence 32, Application US/09329350
; Patent No. 6184019
; GENERAL INFORMATION:
; APPLICANT: Miettinen-Oinonen, Arja
; APPLICANT: Londresborough, John
; APPLICANT: Vehmaanper, Jari
; APPLICANT: Haakana, Heli
; APPLICANT: M ntyl, Arja
; APPLICANT: Lantto, Raija
; APPLICANT: Elvoinio, Minna
; APPLICANT: Joutsjoki, Vesa
; APPLICANT: Paloheimo, Marja
; APPLICANT: Suominen, Pirkko
; TITLE OF INVENTION: NOVEL CELLULASES, THE GENES ENCODING THEM AND
; TITLE OF INVENTION: USES THEREOF
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/329,350
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/841,636
; FILING DATE: 30-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/005,335
; FILING DATE: 17-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/007,926
; FILING DATE: 04-DEC-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/020,840
; FILING DATE: 28-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/732,181
; FILING DATE: 16-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FI96/00550
; FILING DATE: 17-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Shea Jr., Timothy
; REGISTRATION NUMBER: 41,306
; REFERENCE/DOCKET NUMBER: 1716.0510006/NAC/TJS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)371-2600

TELEFAX: (202)371-2540
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1894 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Melanocarpus albobryces
; STRAIN: ALKO4237
; FEATURE:
; NAME/KEY: exon
; LOCATION: 233..838
; OTHER INFORMATION: /product= "50K-cellulase"
; FEATURE:
; NAME/KEY: exon
; LOCATION: 916..1596
; OTHER INFORMATION: /product= "50K-cellulase"
US-09-329-350-32

Query Match 18.9%; Score 39.4; DB 3; Length 1894;
Best Local Similarity 55.5%; Pred. No. 0.21;
Matches 76; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 56 GCTGGCCTGAACCAATATCCGATCACCACGACGACGCTGACCGAAGAGAGCTGCT 115
Db 1131 GTTCGCGTTCGACACGCGCGGCCCTTCACCGTGTGACGAGTTCGCCGCGCGCGGA 1190
QY 116 CGCCACCATTCGAGTATCTGTCGCTGACGAGAGGCCACGATGACGCTGCGCGGG 175
Db 1191 GGGCGGCTCGAGAGCATCCACCGGCTGTACGTGACGAGCGCGCAAGGTGATCGAGTCTGA 1250
QY 176 CGGGGTGCGAGTGGCGG 192
Db 1251 CGTCTCGACGCGCGG 1267

RESULT 8
US-09-248-335-53
; Sequence 53, Application US/09248335
; Patent No. 6096504
; GENERAL INFORMATION:
; APPLICANT: MCGONIGLE, BRIAN
; APPLICANT: O'KEEF, DANIEL
; TITLE OF INVENTION: PLANT GLUTATHIONE-S-TRANSFERASE ENZYMES
; FILE REFERENCE: CL-1128-A
; CURRENT APPLICATION NUMBER: US/09/248,335
; CURRENT FILING DATE: 1999-02-10
; EARLIER APPLICATION NUMBER: 08/924,759
; EARLIER FILING DATE: 1997-September-05
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Microsoft Word Version 7.0A
; SEQ ID NO 53
; LENGTH: 1100
; TYPE: DNA
; ORGANISM: maize
US-09-248-335-53

Query Match 18.8%; Score 39; DB 3; Length 1100;
Best Local Similarity 52.8%; Pred. No. 0.24;
Matches 84; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

QY 47 CAACAGAGAGTGGGCGCTGAACCAATATCCGATCACCACGACGACGCTGACCGAAGA 106
Db 193 CAGAGCGGCTCTCTCTGGGATCCACCGGTGCACAGAGCGTCCGGTGTCTCTCCA 252
QY 107 AGACGTGCTGCCACCATTCGATGATCTGTCGCTGACGAGGCCAGGCCACGATGAC 166
Db 253 CGCGCGCGCGCCATAACGAGTCCCGAGTCTCTGAGTACATCGACGAGGTGGGC 312
QY 167 GTGCGCGCGGGGTTCGAGGTGCGGTGGAAACCGACGA 205

Db 313 GGGAGCGGGCGCGCGTCTTCGGCGGACCCCTACGA 351

RESULT 9
US-09-252-991A-9731
; Sequence 9731, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 9731
; LENGTH: 426
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-9731

Query Match 18.4%; Score 38.2; DB 4; Length 426;
Best Local Similarity 49.7%; Pred. No. 0.34; Mismatches 98; Indels 0; Gaps 0;
Matches 97; Conservative 0;

QY 1 TCAAGAGAGCGCTACGACCTGGCCCGTGTGCGCGGATACACAGAGTCAACAGAGCTGG 60
Db 43 TCGAGCAATACCTCAACAGCGCTTCGCGTCCGGCGGAGACCTCAACCTCAAGCTCATAC 102
QY 61 GCCTGACACCATCATCCGATCACACGACGACGCTGACCCGAGAGACGCTGCTGCGCA 120
Db 103 CCAGCGCCAGGACCAAGTGTGTCGCGCCCTGCGAGCGTGGCGAGGCGACCTGCTGCGCC 162
QY 121 CCATCGAGTATCTGGTCTGCGCTGCACGAGGCGCCAGCATGACCGCTGCGGCGCGGG 180
Db 163 CGGCGAAGTCTGCGCGGCGACGAGCGCTGCGAGGTCACCCGAGCGCGCGGTGCGG 222
QY 181 TCGAGGTGCGCGTGG 195
Db 223 CCGATGTGCGCGTGG 237

RESULT 10
US-09-252-991A-16394
; Sequence 16394, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 16394
; LENGTH: 468
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-16394

Query Match 18.4%; Score 38.2; DB 4; Length 468;
Best Local Similarity 54.7%; Pred. No. 0.34; Mismatches 63; Indels 0; Gaps 0;
Matches 76; Conservative 0;

QY 56 GCTGGCGCTGAACACCAATCATCCGATCACACGACGACGCTGACCGAAGAGAGCTGCT 115

Db 277 SCAGGCGCTGAGCATCAACACGAGCGAGCTGGAGCGGATCTCTGACCAAGTGGCCGACT 336
QY 116 GGCACCATCGAGTATCTGTCTCGCTGCACAGAGGCGCCAGCCACGATGACCGTCCCGGG 175
Db 337 GCGGATCACCGGCGAGGAGCTTACTGTGATGGTGGACGATGCCGACACGCTCCAGGACAG 396
QY 176 CGGGGTGAGGTGCCGGTG 194
Db 397 CGCGCTGGAAGTGTGTTG 415

RESULT 11
US-09-252-991A-9689
; Sequence 9689, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 9689
; LENGTH: 1482
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-9689

Query Match 18.4%; Score 38.2; DB 4; Length 1482;
Best Local Similarity 49.7%; Pred. No. 0.4; Mismatches 97; Conservative 0; Gaps 0;
Matches 97; Indels 0;

QY 1 TCAAGAGAGCGCTACGACCTGGCCCGTGTGCGCGGATACACAGGTCACACAGAGCTGG 60
Db 284 TCGAGCAATACCTCAACAGCGCTTCGCGTCCGGCGGAGACCTCAACCTCAAGCTCATAC 343
QY 61 GCCTGACACCAATCATCCGATCACACGAGCGCTGACCCGAGAGAGAGCTGCTGCGCA 120
Db 344 CCAGCGCCAGGACCAAGTGTGTCGCGCCCTGCGAGCGTGGCGAGGCGACCTGCTGCGCC 403
QY 121 CCATCGAGTATCTGGTCTGCGCTGCACGAGGCGCCAGCATGACCGTGGCGGCGGG 180
Db 404 CGGCGAAGTCTGCTGCGGCGGACGAGCGCTGCGAGTCAAGCGCGCGCGGTGCGCG 463
QY 181 TCGAGGTGCGCGTGG 195
Db 464 CCGATGTGCGCGTGG 478

RESULT 12
US-09-252-991A-16504
; Sequence 16504, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 16504
; LENGTH: 1587

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; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-16504

Query Match      18.4%; Score 38.2; DB 4; Length 1587;
Best Local Similarity 54.7%; Pred. No. 0.4;
Matches 76; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 56 GCTGGGCTGACACCAATATCCGATCACACGACGCTGACCGAAGAGAGCTGCT 115
DB 306 GAGGGCTGAGCATCAACAGCGAGCTGGAGGCGATCTGACCAAGGTGGCGACGT 365
QY 116 GCCCACCATCGAGTATCTGGTCGCTGCACGAGGGCCAGCCACGATGACCGTCCGGG 175
DB 366 GGCGATCACCAGGCGAGGAGCTTACCTGATGTGGAGCATGCCAACACGCTCCAGGACAG 425
QY 176 CGGGGTGAGTGCCTGGT 194
DB 426 CGCGCTGGAAGTGTGTTG 444

RESULT 13
US-09-252-991A-9607/c
; Sequence 9607, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 9607
; LENGTH: 1614
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-9607

Query Match      18.4%; Score 38.2; DB 4; Length 1614;
Best Local Similarity 49.7%; Pred. No. 0.4;
Matches 97; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 1 TCAGGAGAGCGCTACGACCTGGCCCGTGTGCGCGCATACAGGTCAACAGAGAGCTGG 60
DB 1229 TCGAGCAATACCTCAACAGCGCTTTCGCGTCCGCGCGGAACTCACCCCTCAAGCTCATAC 1170
QY 61 GCCTGAACACCAATCATCCGATCACCACGACGCTGACCGAAGAGAGCTGCTCGCCA 120
DB 1169 CCAAGCCCAAGACCACTGCTTGGCCGCTTCGACGCTGGGAGGAGGACCTGTCGCC 1110
QY 121 CCATCGAGTATCTGTCGCTGCACGAGGCGCCAGGCGACGATGACCGTCCGCGGGG 180
DB 1109 CGGGGAACTGCTCGCGCGCAAGCGCTGACGCTCAGCCGCGGCGCGCTGCGCG 1050
QY 181 TCGAGTGCCTGGTGG 195
DB 1049 CCGATGTGCGCGTGG 1035

RESULT 14
US-09-252-991A-9650
; Sequence 9650, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
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; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 9650
; LENGTH: 1623
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-9650

Query Match      18.4%; Score 38.2; DB 4; Length 1623;
Best Local Similarity 49.7%; Pred. No. 0.4;
Matches 97; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 1 TCAGGAGAGCGCTACGACCTGGCCCGTGTGCGCGCATACAGGTCAACAGAGAGCTGG 60
DB 486 TCGAGCAATACCTCAACAGCGCTTTCGCGTCCGCGGAACTCACCCCTCAAGCTCATAC 545
QY 61 GCCTGAACACCAATCATCCGATCACCACGACGCTGACCGAAGAGAGCTGCTCGCCA 120
DB 546 CCAAGCCCAAGACCACTGCTTTCGCGCGCTTCGAGCGTGGGAGGACCTGTCGCC 605
QY 121 CCATCGAGTATCTGTCGCGCTGCACGAGGCGCCAGGCGACGATGACCGTCCGCGGGG 180
DB 606 CCGGCGAACTGCTGCGCGCGCAGCAGCGCTGCGAGTCCAGCCGCGCGCGTGGCGG 665
QY 181 TCGAGTGCCTGGTGG 195
DB 666 CCGATGTGCGCGTGG 680

RESULT 15
US-09-252-991A-16098/c
; Sequence 16098, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 16098
; LENGTH: 2070
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-16098

Query Match      18.4%; Score 38.2; DB 4; Length 2070;
Best Local Similarity 54.7%; Pred. No. 0.4;
Matches 76; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 56 GCTGGGCTGACACCAATATCCGATCACCACGACGCTGACCGAAGAGAGAGCTGCT 115
DB 679 GCAGGGCTGAGCATCAACAGCGAGCGCTTGGAGCGATCTGACCAAGGTGGCGACGT 620
QY 116 CGCCACCATCGAGTATCTGTCGCGCTGCACGAGGCGCCAGGCGACGATGACCGTCCGGG 175
DB 619 GCGGATCACCAGGCGAGGAGCTTACCTGATGTGGAGCATGCCAACACGCTCCAGGACAG 560
QY 176 CGGGGTGAGTGCCTGGT 194
DB 559 CGCGCTGGAAGTGTGTTG 541
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Search completed: September 17, 2003, 12:27:48
Job time : 46.1605 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 17, 2003, 11:54:34 ; Search time 108.259 Seconds
(without alignments)
4726.283 Million cell updates/sec

Title: US-09-697-123b-8
Perfect score: 208
Sequence: 1 tcaggagagcgctacgac.....ccggtggaaccgacgacat 208

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1660708 seqs, 1229959015 residues

Total number of hits satisfying chosen parameters: 3321416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_NA.*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
- 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
- 15: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
- 16: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
- 17: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	166.4	80.0	3519	10 US-09-712-363-30	Sequence 30, Appl
2	80	38.5	3495	10 US-09-738-626-547	Sequence 547, Appl
3	80	38.5	5096	10 US-09-984-711-5	Sequence 5, Appl
4	80	38.5	5099	10 US-09-887-052-1	Sequence 1, Appl
5	80	38.5	5099	10 US-09-887-052-3	Sequence 3, Appl
6	80	38.5	5099	10 US-09-887-052-5	Sequence 5, Appl
7	80	38.5	5099	12 US-10-076-406-1	Sequence 1, Appl
8	80	38.5	5099	12 US-10-076-406-3	Sequence 3, Appl
9	80	38.5	5099	12 US-10-076-406-5	Sequence 5, Appl
10	80	38.5	5099	13 US-10-075-460-5	Sequence 5, Appl
11	80	38.5	3309400	10 US-09-738-626-1	Sequence 1, Appl
12	70.8	34.0	3543	14 US-10-156-761-4898	Sequence 4898, Appl
13	70.8	34.0	9025608	14 US-10-156-761-1	Sequence 1, Appl
14	39.4	18.9	1416	14 US-10-156-761-4207	Sequence 4207, Appl
15	39.4	18.9	1894	8 US-08-841-636A-32	Sequence 32, Appl
16	39.4	18.9	9025608	14 US-10-156-761-1	Sequence 1, Appl

c

17 39.2 18.8 1317 14 US-10-028-245-4
18 39.2 18.8 1826 14 US-10-028-245-1
19 38.4 18.5 8825 10 US-10-156-761-2303
20 38.4 18.5 8825 10 US-09-976-059-1
21 37.6 18.1 704 13 US-10-062-254-109
22 37.6 18.1 752 13 US-10-062-254-111
23 37.6 18.1 897 9 US-09-815-242-4001
24 37.6 18.1 1629 14 US-10-156-761-3330
25 37.4 18.0 1509 12 US-09-967-464-64
26 37.2 17.9 14520 14 US-10-156-761-2885
27 37.2 17.9 125746 14 US-10-156-761-15102
28 37 17.8 492 9 US-09-815-242-7946
29 37 17.8 1509 12 US-09-967-464-68
30 36.8 17.7 933 14 US-10-156-761-4618
31 36.8 17.7 86114 15 US-10-080-170-648
32 36.6 17.6 1914 14 US-10-156-761-2351
33 36.4 17.5 387 14 US-10-156-761-6187
34 36.4 17.5 1170 14 US-10-156-761-7006
35 36.4 17.5 1176 14 US-10-156-761-1625
36 36.2 17.4 278 9 US-09-294-093B-1392
37 36.2 17.4 1874 14 US-10-180-375-127
38 36.2 17.4 2693 10 US-09-880-107-3678
39 36.2 17.4 11058 14 US-10-156-761-3629
40 36.2 17.4 82993 15 US-10-080-170-645
41 36 17.3 1548 14 US-10-156-761-1248
42 36 17.3 1692 14 US-10-156-761-1808
43 36 17.3 1809 14 US-10-156-761-4041
44 36 17.3 3759 14 US-10-156-761-2268
45 35.8 17.2 672 14 US-10-156-761-2604

ALIGNMENTS

RESULT 1
US-09-712-363-30
; Sequence 30, Application US/09712363
; Patent No. US20020164588A1
; GENERAL INFORMATION:
; APPLICANT: Eisenberg, David
; APPLICANT: Roystein, Sergio H.
; APPLICANT: Marcotte, Edward M.
; TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND
; TITLE OF INVENTION: INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS
; FILE REFERENCE: 07419-032001
; CURRENT APPLICATION NUMBER: US/09/712,363
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: PCT/US00/02246
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,531
; PRIOR FILING DATE: 2000-02-01
; PRIOR APPLICATION NUMBER: 60/117,844
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/118,206,
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: 60/126,593
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/134,093
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/134,092
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/165,124
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/165,086
; PRIOR FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-09-712-363-30


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Query Match      80.0%; Score 166.4; DB 10; Length 3519;
Best Local Similarity 87.5%; Pred. No. 4.4e-41;
Matches 182; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 1 TCAAGAGAGAGCGGTACGACTGGCCCGTGTGCGGCCGATACAGGTCAACAGAGAGCTGG 60
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Db 884 TCAAGAGAGAGCGGTACGACTGGCCCGTGTGCGGCCGATACAGGTCAACAGAGAGCTGG 943
   |||||

QY 61 GCGTGAACCAATCATCCGATCACCACGACGACGCTGACCGAGAGAGAGCGTCTGCACA 120
   |||||
Db 944 GCGTGAATCGCGGAGGCCATCAGCTGTCGACGCTGACCGAGAGAGAGCGTCTGCACA 1003
   |||||

QY 121 CCATCGATATCTGTCGCTCGCTGACGAGGCGCCAGGCCACGATGACCGTCCGCGGCGGG 180
   |||||
Db 1004 CCATCGAATATCTGTCGCTCGCTGACGAGGCGTCAAGCCAGATGACCGTTCGCGGCGGG 1063
   |||||

QY 181 TCGAGTCCCGTGGAAACGACGACAT 208
   |||||
Db 1064 TCGAGTCCCGTGGAAACGACGACAT 1091
   |||||

RESULT 2
US-09-738-626-547
; Sequence 547, Application US/09738626
; Publication No. US20020197609A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OKIHAL, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738, 626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1995-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 547
; LENGTH: 3495
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-547

Query Match      38.5%; Score 80; DB 10; Length 3495;
Best Local Similarity 66.0%; Pred. No. 8.3e-15;
Matches 132; Conservative 0; Mismatches 65; Indels 3; Gaps 1;

QY 9 AAGCGTAGACCTGGCCCGTGTGCGGCCGATACAGGTCAACAGAGAGCTGGCCCTGAAC 68
   |||||
Db 877 AAGCGTAGACCTGGCTGGCTGGTGTGCTTACAGATCACCGAAGCTCGCCCTGTGT 936
   |||||

QY 69 ACCATCATCCGATCACCAAGACGCTGACCGAGAGAGAGCGTCTGCCACCATCGAG 128
   |||||
Db 937 GCGGACCATGATGGTTT---GATGACTCTTACTGAAGAGAGATCGCAACCATCGAG 993
   |||||

QY 129 TATCTGGTCCGCTCAGAGGCGCAGGCCACGATCACCGTCCGCGGCGGGTTCGAGGTG 188
   |||||
Db 994 TACTGGTGGCTCTCAGCGAGGTGAGCGGTCATGACTTCTCCAAATGTTGAAGAGATC 1053
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QY 189 CCGGTGGAACCGACGACAT 208
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Db 1054 CCAGTCGAGCCGATGACAT 1073
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RESULT 3
US-09-984-711-5
; Sequence 5, Application US/09984711
; Patent No. US20020119549A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: STEPHAN, Hans
; APPLICANT: KREUTZER, Caroline
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE rpsL GENE
; FILE REFERENCE: 204209U0
; CURRENT APPLICATION NUMBER: US/09/984,711
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: DE10108230.9
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 5096
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
; OTHER INFORMATION:
US-09-984-711-5

Query Match      38.5%; Score 80; DB 10; Length 5096;
Best Local Similarity 66.0%; Pred. No. 8.8e-15;
Matches 132; Conservative 0; Mismatches 65; Indels 3; Gaps 1;

QY 9 AAGCGTAGACCTGGCCCGTGTGCGGCCGATACAGGTCAACAGAGAGCTGGCCCTGAAC 68
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Db 1578 AAGCGTAGACCTGGCTGGCTGGTGTGCTTACAGATCACCGAAGCTCGCCCTGTGT 1637
   |||||

QY 69 ACCATCATCCGATCACCAAGACGCTGACCGAGAGAGAGCGTCTGCCACCATCGAG 128
   |||||
Db 1638 GCGGACCATGATGGTTT---GATGACTCTTACTGAAGAGAGATCGCAACCATCGAG 1694
   |||||

QY 129 TATCTGGTCCGCTCAGAGGCGCAGGCCACGATCACCGTCCGCGGCGGGTTCGAGGTG 188
   |||||
Db 1695 TACTGTGGTGGCTCTGCGAGGAGTGAAGCGGTCATGACTTCTCCAAATGTTGAAGATC 1754
   |||||

QY 189 CCGGTGGAACCGACGACAT 208
   |||||
Db 1755 CCAGTCGAGCCGATGACAT 1774
   |||||

RESULT 4
US-09-887-052-1
; Sequence 1, Application US/09887052
; Patent No. US20020119537A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE rpoB GENE
; FILE REFERENCE: 204212U0X
; CURRENT APPLICATION NUMBER: US/09/887,052
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: DE10107229.5
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 5099
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Db 1755 CCAGTCGAGCCGATGACAT 1774

RESULT 6

US-09-887-052-5

Sequence 5, Application US/09887052

Patent No. US20020119537A1

GENERAL INFORMATION:

APPLICANT: MOECKEL, Bettina

APPLICANT: BATHE, Brigitte

APPLICANT: HERMANN, Thomas

APPLICANT: PFEFFERLE, Walter

APPLICANT: BINDER, Michael

TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE *ipoB* GENE

FILE REFERENCE: 2042120S0X

CURRENT APPLICATION NUMBER: US/09/887,052

CURRENT FILING DATE: 2001-06-25

PRIOR APPLICATION NUMBER: DE10107229.5

PRIOR FILING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 8

SOFTWARE: PatentIn version 3.0

SEQ ID NO 5

LENGTH: 5099

TYPE: DNA

ORGANISM: *Corynebacterium glutamicum*

FEATURE:

NAME/KEY: CDS

LOCATION: (702)..(4196)

US-09-887-052-5

Query Match 38.5%; Score 80; DB 10; Length 5099;

Best Local Similarity 66.0%; Pred. No. 8.8e-15;

Matches 132; Conservative 0; Mismatches 65; Indels 3; Gaps 1;

QY 9 AAGCGCTACGACCTGGCCGCTGTGGCCGATACAAGSTCAACAAGAGCTGGGCGCTGAAC 68

1578 AAGCGCTACGACCTGGCTCGCGTTGGTTCGTTACAGATCACCCAGACTCGGCCCTTGGT 1637

QY 69 ACCAATCATCCGATCACACGACGACGCTGACCCGAAGAAGAGCTGCTGCCACCATCGAG 128

1638 GGCAGCCAGATGGTTT---GATGACTCTTACTGAAGAGGAGACATCGCACCATCGAG 1694

QY 129 TATCTGGTCGGCTCGACGAGGGCCAGGCCGATGACCGTGGTTCGTCGCCACCATCGAG 188

1695 TACCTGGTCGGCTCGACGAGGTGAGCGCGTCATGACTTCTTCCAAATGGTGAAGAGATC 1754

QY 189 CCGGTGGAACCGAGACAT 208

1755 CCAGTCGAGCCGATGACAT 1774

RESULT 7

US-10-076-406-1

Sequence 1, Application US/10076406

Publication No. US20030166884A1

GENERAL INFORMATION:

APPLICANT: MOECKEL, Bettina

APPLICANT: BATHE, Brigitte

APPLICANT: HERMANN, Thomas

APPLICANT: PFEFFERLE, Walter

APPLICANT: BINDER, Michael

TITLE OF INVENTION: Nucleotide sequences coding for the *ipoB* gene

FILE REFERENCE: 219774US0XIP

CURRENT APPLICATION NUMBER: US/10/076,406

CURRENT FILING DATE: 2002-02-19

PRIOR APPLICATION NUMBER: DE 10107229.5

PRIOR FILING DATE: 2001-02-16

PRIOR APPLICATION NUMBER: US 09/887052

PRIOR FILING DATE: 2001-06-25

NUMBER OF SEQ ID NOS: 12

SOFTWARE: PatentIn version 3.1

SEQ ID NO 1

LENGTH: 5099

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; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
; OTHER INFORMATION:
US-10-076-406-1

Query Match          38.5%; Score 80; DB 12; Length 5099;
Best Local Similarity 66.0%; Pred. No. 8.8e-15;
Matches 132; Conservative 0; Mismatches 65; Indels 3; Gaps 1;

QY 9 AAGCGCTAGACCTGGCCCTGTCGCGGATACAAAGGTCAACAAAGCTGGGCTTGAC 68
    |||||
Db 1578 AAGCGCTAGACCTGGCTGGCTGCTTACAAAGATCAACCCAGCTCGGCTTGGT 1637

QY 69 ACCAATCATCCGATCACCACGACGACGCTGACCGGAGAGACGTCGCGCCACCATCGAG 128
    |||||
Db 1638 GCGACCCAGATGGTTT---GATGACTCTTACTGAAGAGGACATCGCAACCATCGAG 1694

QY 129 TATCTGGTCCGCTGCGACGAGGCCACGATGACCGTGC CGGGGTCGAGGTG 188
    |||||
Db 1595 TACCTGGTGGCTGTCGACGAGGTGAGCGGCTCACTTCTCCAAATGTTGAGAGATC 1754

QY 189 CCGGTGGAACCGAGGACAT 208
    |||||
Db 1755 CCAGTCGAGACCGATGACAT 1774

RESULT 9
US-10-076-406-5
; Sequence 5, Application US/10076406
; Publication No. US20030166884A1
; GENERAL INFORMATION:
; APPLICANT: MORCKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: Nucleotide sequences coding for the rpoB gene
; FILE REFERENCE: 219774USOXCIP
; CURRENT APPLICATION NUMBER: US/10/076,406
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: DE 10107229.5
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 09/887052
; PRIOR FILING DATE: 2001-06-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 5099
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
; OTHER INFORMATION:
; NAME/KEY: mutation
; LOCATION: (2016)..(2016)
; OTHER INFORMATION: Substitution of cytosine by thymine
US-10-076-406-5

Query Match          38.5%; Score 80; DB 12; Length 5099;
Best Local Similarity 66.0%; Pred. No. 8.8e-15;
Matches 132; Conservative 0; Mismatches 65; Indels 3; Gaps 1;

QY 9 AAGCGCTAGACCTGGCCCTGTCGCGGATACAAAGGTCAACAAAGCTGGGCTTGAC 68
    |||||
Db 1578 AAGCGCTAGACCTGGCTGGCTGCTTACAAAGATCAACCCAGCTCGGCTTGGT 1637

QY 69 ACCAATCATCCGATCACCACGACGACGCTGACCGGAGAGACGTCGCGCCACCATCGAG 128
    |||||
Db 1638 GCGACCCAGATGGTTT---GATGACTCTTACTGAAGAGGACATCGCAACCATCGAG 1694

QY 129 TATCTGGTCCGCTGCGACGAGGCCACGATGACCGTGC CGGGGTCGAGGTG 188
    |||||
Db 1695 TACCTGGTGGCTGTCGACGAGGTGAGCGGCTCACTTCTCCAAATGTTGAGAGATC 1754

QY 189 CCGGTGGAACCGAGGACAT 208
    |||||
Db 1755 CCAGTCGAGACCGATGACAT 1774

RESULT 10
US-10-075-460-5
; Sequence 5, Application US/10075460
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; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
; OTHER INFORMATION:
US-10-076-406-1

Query Match          38.5%; Score 80; DB 12; Length 5099;
Best Local Similarity 66.0%; Pred. No. 8.8e-15;
Matches 132; Conservative 0; Mismatches 65; Indels 3; Gaps 1;

QY 9 AAGCGCTAGACCTGGCCCTGTCGCGGATACAAAGGTCAACAAAGCTGGGCTTGAC 68
    |||||
Db 1578 AAGCGCTAGACCTGGCTGGCTGCTTACAAAGATCAACCCAGCTCGGCTTGGT 1637

QY 69 ACCAATCATCCGATCACCACGACGACGCTGACCGGAGAGACGTCGCGCCACCATCGAG 128
    |||||
Db 1638 GCGACCCAGATGGTTT---GATGACTCTTACTGAAGAGGACATCGCAACCATCGAG 1694

QY 129 TATCTGGTCCGCTGCGACGAGGCCACGATGACCGTGC CGGGGTCGAGGTG 188
    |||||
Db 1595 TACCTGGTGGCTGTCGACGAGGTGAGCGGCTCACTTCTCCAAATGTTGAGAGATC 1754

QY 189 CCGGTGGAACCGAGGACAT 208
    |||||
Db 1755 CCAGTCGAGACCGATGACAT 1774

RESULT 8
US-10-076-406-3
; Sequence 3, Application US/10076406
; Publication No. US20030166884A1
; GENERAL INFORMATION:
; APPLICANT: MORCKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: Nucleotide sequences coding for the rpoB gene
; FILE REFERENCE: 219774USOXCIP
; CURRENT APPLICATION NUMBER: US/10/076,406
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: DE 10107229.5
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 09/887052
; PRIOR FILING DATE: 2001-06-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 5099
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
; OTHER INFORMATION:
; NAME/KEY: mutation
; LOCATION: (1987)..(1987)
; OTHER INFORMATION: Substitution of adenine by thymine
; NAME/KEY: mutation
; LOCATION: (1288)..(1288)
; OTHER INFORMATION: Substitution of cytosine by thymine
; NAME/KEY: mutation
; LOCATION: (715)..(715)
; OTHER INFORMATION: Substitution of cytosine by thymine
US-10-076-406-3

Query Match          38.5%; Score 80; DB 12; Length 5099;
Best Local Similarity 66.0%; Pred. No. 8.8e-15;
Matches 132; Conservative 0; Mismatches 65; Indels 3; Gaps 1;

QY 9 AAGCGCTAGACCTGGCCCTGTCGCGGATACAAAGGTCAACAAAGCTGGGCTTGAC 68
```

```
; Publication No. US20020155557A1
; GENERAL INFORMATION:
; APPLICANT: MOCKEL, BETTINA
; APPLICANT: BATHE, BRIGITTE
; APPLICANT: HANS, STEFAN
; APPLICANT: KREUTZER, CAROLINE
; APPLICANT: HERMANN, THOMAS
; APPLICANT: PFEFFERLE, WALTER
; APPLICANT: BINDER, MICHAEL
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE TP5L GENE
; FILE REFERENCE: 218472USOX
; CURRENT APPLICATION NUMBER: US/10/075,460
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: DE 10107230.9
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: DE 10162386.0
; PRIOR FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 5099
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
; OTHER INFORMATION:
US-10-075-460-5

Query Match      38.5%; Score 80; DB 13; Length 5099;
Best Local Similarity 66.0%; Pred. No. 8.8e-15;
Matches 132; Conservative 0; Mismatches 65; Indels 3; Gaps 1;

QY 9 AAGCGCTACGACCTGGCCGCTGTCGGCGGATACAAAGGTCAACAAGAGCTGGGCGCTGAAC 68
D 1578 AAGCGCTACGACCTGGCTGGTGGTTCGTTACAAAGATCAACCGCAAGCTCGGCTTGGT 1637
QY 69 ACCAATCATCCGATCACCACGACGAGCTGACCGGAAGAGAGCTGTCGCCACCATCGAG 128
D 1638 GCGCACCACGATGGTT---GATGACTCTTACTGAAGAGGACATCGCAACCATCGAG 1694
QY 129 TATCTGTGCGCTGCACGAGGCGCAGGCCACGATGACCGTCCGGGGGGGTGAGGTG 188
D 1695 TACCTGTGGTGTGCTGCACGAGCTGAGCGGCTCATGACTTCTCCAAATGGTGAAGAGATC 1754
QY 189 CCGGTGGAACCGACGACAT 208
D 1755 CCAGTCGAGACCGATGACAT 1774

RESULT 11
US-10-738-626-1
; Sequence 1, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07

; Publication No. US20020155557A1
; GENERAL INFORMATION:
; APPLICANT: MOCKEL, BETTINA
; APPLICANT: BATHE, BRIGITTE
; APPLICANT: HANS, STEFAN
; APPLICANT: KREUTZER, CAROLINE
; APPLICANT: HERMANN, THOMAS
; APPLICANT: PFEFFERLE, WALTER
; APPLICANT: BINDER, MICHAEL
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE TP5L GENE
; FILE REFERENCE: 218472USOX
; CURRENT APPLICATION NUMBER: US/10/075,460
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: DE 10107230.9
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: DE 10162386.0
; PRIOR FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 1
; LENGTH: 3309400
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; US-09-738-626-1

Query Match      38.5%; Score 80; DB 10; Length 3309400;
Best Local Similarity 66.0%; Pred. No. 2e-14;
Matches 132; Conservative 0; Mismatches 65; Indels 3; Gaps 1;

QY 9 AAGCGCTACGACCTGGCCGCTGTCGGCGGATACAAAGGTCAACAAGAGCTGGGCGCTGAAC 68
D 513789 AAGCGCTACGACCTGGCTGGTGGTTCGTTACAAGATCAACCCGAAGCTCGGCTTGGT 513848
QY 69 ACCAATCATCCGATCACCACGACGAGCTGACCGGAAGAGAGCTGTCGCCACCATCGAG 128
D 513849 GCGCACCACGATGGTT---GATGACTCTTACTGAAGAGGACATCGCAACCATCGAG 513905
QY 129 TATCTGTGCGCTGCACGAGGCGCAGGCCACGATGACCGTCCGGGGGGGTGAGGTG 188
D 513906 TACCTGTGGTGTGCTGCACGAGGAGTGAGCGGCTCATGACTTCTCCAAATGGTGAAGAGATC 513965
QY 189 CCGGTGGAACCGACGACAT 208
D 513966 CCAGTCGAGACCGATGACAT 513985

RESULT 12
US-10-156-761-4898
; Sequence 4898, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 4898
; LENGTH: 3543
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3543)
US-10-156-761-4898

Query Match      34.0%; Score 70.8; DB 14; Length 3543;
Best Local Similarity 62.5%; Pred. No. 5.2e-12;
Matches 130; Conservative 0; Mismatches 72; Indels 6; Gaps 1;

QY 1 TCAAGGAGAAGCGCTACGACCTGGCCGCTGTCGGCGGATACAAAGGTCAACAAGAGCTGG 60
D 926 TCAACCCGGAAGCGCTACGACCTCGCGAAGGTTCGCGGCTTACAAAGGTCAACAAGAGCTGG 985
QY 61 GCCTGAACACCAATCATCCGATCACCACGAGGAGCTGTCGCCGAGGAGAGAGCTGCTGCCCA 120
D 986 GCGGCGAGGCGG-----CGCTGGAGCGCGGGATCTCGACCTCGAGGACATCATCTCGT 1039
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QY 121 CCATCGAGTATCTGTCGCGCTGCACGAGGCGCCAGGACGATGACCGTCCGCGGCGGG 180
Db 1040 CGATCAAGTACTGCTGGAAGCTGCACGCGGTGAGACCGGAGACCGCTGGCGGCAACGGCA 1099
QY 181 TCAGGTGCGCGGTGGAACCGAGACAT 208
Db 1100 CCTCGATGCTGCTGAGACCGAGACAT 1127

RESULT 13
US-10-156-761-1
; Sequence 1, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
; LENGTH: 9025608
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1

Query Match 34.0%; Score 70.8; DB 14; Length 9025608;
Best Local Similarity 62.5%; Pred. No. 1.4e-11;
Matches 130; Conservative 0; Mismatches 72; Indels 6; Gaps 1;

QY 1 TCAAGGAGAGCGCTACGACCTGCGCGGTGTCGGCGGATACAGGTCAACAAGAGAGCTGG 60
Db 5970494 TCAACCCGAAGCGCTACGACCTCGCGAAGTCTGCGCGGTACAGGTCAACAAGAGCTGG 5970553
QY 61 GCCTGACACCAATCATCCGATCACACGACGCTGACCGAAGAGAGAGCTGTCGCCA 120
Db 5970554 GCGGCGAGGCG-----CCGCTGACCGCGGGATCTTACCTCGAGGACATCATCTCGT 5970607
QY 121 CCATCGAGTATCTGTCGCGCTGCACGAGGCGCCAGGACGATGACCGTCCGCGGCGGG 180
Db 5970608 CGATCAAGTACTCTGTAAGCTGCACGCGGTGAGACCGGATCTTGGCGCAACGGCA 5970667
QY 181 TCAGGTGCGCGGTGGAACCGAGACAT 208
Db 5970668 CCTCGATGCTGCTGAGACCGAGACAT 5970695

RESULT 14
US-10-156-761-4207
; Sequence 4207, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
```

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; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 4207
; LENGTH: 1416
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1416)
US-10-156-761-4207

Query Match 18.9%; Score 39.4; DB 14; Length 1416;
Best Local Similarity 55.5%; Pred. No. 0.017;
Matches 76; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 46 TCAACAAGAGCTGGCGCTGAACACCAATCATCCGATCACACGAGCGGTGACCGAAG 105
Db 368 TCGGTACACGCTGGCCAGGACACGAGGATCGCGGCTCGACGCGTCTCCGCT 427
QY 106 AAGAGCTGTCGCCACCATCATCTGTCGCCCTGCACGAGGCGCCAGGCGGACGATGA 165
Db 428 CCGACAGCGCGGCTCGTCAAGCGGACGCGGCGGCGGCGGCGGCGGCGGCGGCGG 487
QY 166 CCGTCCGCGGCGGGGTC 182
Db 488 CGCTCGCGAGCAGGTC 504

RESULT 15
US-08-841-636A-32
; Sequence 32, Application US/08841636A
; Publication No. US20020168751A1
; GENERAL INFORMATION:
; APPLICANT: Miettinen-Oinonen, Arja
; APPLICANT: Lonsborough, John
; APPLICANT: Vehmaanper, Jari
; APPLICANT: Haakana, Heli
; APPLICANT: M ntyl, Arja
; APPLICANT: Lantto, Raija
; APPLICANT: Elvainen, Minna
; APPLICANT: Joutsio, Vesa
; APPLICANT: Paloheimo, Marja
; APPLICANT: Suominen, Pirkko
; TITLE OF INVENTION: NOVEL CELLULASES, THE GENES ENCODING THEM AND
; TITLE OF INVENTION: USES THEREOF
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/841,636A
; FILING DATE: 30-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/005,335
; FILING DATE: 17-OCT-1995
; PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 60/007,926
FILING DATE: 04-DEC-1995
PRIOR APPLICATION DATA: US 60/020,840
FILING DATE: 28-JUN-1996
PRIOR APPLICATION DATA: US 08/732,181
FILING DATE: 16-OCT-1996
PRIOR APPLICATION DATA: PCT/US96/00550
FILING DATE: 17-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Timothy J. Shea, Jr.
REGISTRATION NUMBER: 41,306
REFERENCE/DOCKET NUMBER: 1716.0510005/MAC/TJS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 1894 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Melanocarpus albomyces
STRAIN: ALKO4237
FEATURE:
NAME/KEY: exon
LOCATION: 233..838
OTHER INFORMATION: /product= "50K-cellulase"
FEATURE:
NAME/KEY: exon
LOCATION: 916..1596
OTHER INFORMATION: /product= "50K-cellulase"
US-08-841-636A-32

Query Match 18.9%; Score 39,4; DB 8; Length 1894;
Best Local Similarity 55.5%; Pred. No. 0.017;
Matches 76; Conservative 0; Mismatches 61; Indels 0; Gaps 0;
QY 56 GGTGGGCTGAACACCAATATCCGATCACCACGACGCTGACCGAAGAGACGTCGT 115
DB 1131 GTTCGGCTGCACACGCGGCCCTTCACCGTGTGTGACGCACTTCCGCGCCGACGCCGA 1190
QY 116 CCCCACCATCGATCTGTGTCGCTGCACAGGGCCAGCCACGATGACCGTGCCTGG 175
DB 1191 GGGCCGGCTCGAGAGCATCCACCGCTGTACGTGCAGGACGCGCAAGGTGATCGAGTCGTA 1250
QY 176 CGGGGTGAGGTGCCG 192
DB 1251 CGTGTGACGCGCGG 1267

Search completed: September 17, 2003, 13:04:36
Job time : 128.259 secs

Best Local Similarity 80.7%; Pred. No. 2.9e-23;
Matches 180; Conservative 0; Mismatches 28; Indels 15; Gaps 1;

QY 1 TCAAGGAGAGCGCTACGACCTGGCCCGCTCGCGCGCTACAGGTCAACAGAGAGCTGG 60
|||||
Db 760688 TCAAGGAGAGCGCTACGACCTGGCCCGCTCGCGCGCTACAGGTCAACAGAGAGCTGG 760747
|||||
QY 61 GTCTGCACGCGCGGAGCGATCAGCTGCTCCAGCTGACCGAGGAGAGCTGCTGCGGA 120
|||||
Db 760748 GCTGCTATGTCGGGAGGCCATCAGCTGCTGCGAGCTGACCGAGAGAGCTGCTGCGGA 760807
|||||
QY 121 CCATCGAATACCTGTCGCGGTGACACGCGCGCTACGAGTGCACGCGCGCTCATGA 180
|||||
Db 760808 CCATCGAATACCTGTCGCGGTGACACGCGCGCTACGAGTGCACGCGCGCTCATGA 180
|||||
QY 181 CTGTCCCGCGGCGCATCGAGGTGCGGCTGGAGACCGACGACAT 223
|||||
Db 760853 CCGTTCGCGGCGCGCTCGAGGTGCGGCTGGAGACCGACGACAT 760895
|||||

RESULT 5
US-08-313-185-57
; Sequence 57, Application US/08313185
; Patent No. 5851763
; GENERAL INFORMATION:
; APPLICANT: Heym, Beate
; APPLICANT: Cole, Stewart
; APPLICANT: Young, Douglas
; APPLICANT: Zhang, Ying
; APPLICANT: Honore, Nadine
; APPLICANT: Telenti, Amalio
; APPLICANT: Bodmer, Thomas
; TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/313,185
; FILING DATE: 12-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 02356.0068-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3447 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-313-185-57

Query Match 52.6%; Score 117.4; DB 2; Length 3447;
Best Local Similarity 74.9%; Pred. No. 1.6e-18;
Matches 167; Conservative 0; Mismatches 41; Indels 15; Gaps 1;

QY 1 TCAAGGAGAGCGCTACGACCTGGCCCGCTCGCGCGCTACAGGTCAACAGAGAGCTGG 60
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Db 809 TCAAGGAGAGCGCTACGACCTGGCCCGCTCGCGCTACAGGTCAACAGAGAGCTGG 868
|||||
QY 61 GTCTGCACGCGCGGAGCGCATCAGCTGCTCCAGCTGACCGAGGAGAGCTGCTGCGGA 120
|||||
Db 869 GGTTCACGCGCGGTGAGTTGATCAGCTGCTCCAGCTGACCGAGGAGAGCTGCTGCGGA 928
|||||
QY 121 CCATCGAATACCTGTCGCGGTGACACGCGCGCTACGAGTGCACGCGCGCTCATGA 180
|||||
Db 929 CCATAGAGTACCTGCTGCTGCTGATGAGGTGATCG-----ACAATGA 973
|||||
QY 181 CTGTCCCGCGGCGCATCGAGGTGCGGCTGGAGACCGACGACAT 223
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Db 974 CTGTCCCGAGGTGAGTAGAGTGCACGCTGGAACTGACGATAT 1016
|||||

RESULT 6
US-09-082-614A-57
; Sequence 57, Application US/09082614A
; Patent No. 6124098
; GENERAL INFORMATION:
; APPLICANT: Heym, Beate
; APPLICANT: Cole, Stewart
; APPLICANT: Young, Douglas
; APPLICANT: Zhang, Ying
; APPLICANT: Honore, Nadine
; APPLICANT: Telenti, Amalio
; APPLICANT: Bodmer, Thomas
; TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/082,614A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/313,185
; FILING DATE: 12-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 02356.0068-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3447 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-082-614A-57

Query Match 52.6%; Score 117.4; DB 3; Length 3447;
Best Local Similarity 74.9%; Pred. No. 1.6e-18;
Matches 167; Conservative 0; Mismatches 41; Indels 15; Gaps 1;

QY 1 TCAAGGAGAGCGCTACGACCTGGCCCGCTCGCGCGCTACAGGTCAACAGAGAGCTGG 60
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Db 809 TCAGGAGAAAGCTACAGCTGGCCAGGGTTGCTGTTACAGGTCAACAGAAAGCTCG 868
QY 61 GTCTGACCCGCGGAGCGATCAGCTCGTCCACGCTGACCGAGGAGAGCTGTCGGGA 120
Db 869 GGTTCGACCGGTTGATGATCAGCTGCTCCAGCTGACCGAGAGGATGTCGTGCCA 928
QY 121 CCATCGAATACCTGTCGGCTGCACACGCGGCTGACGAGGATGGCCAGCGCGGTCATGA 180
Db 929 CCATAGAGTACCTGTTGCTGCTGCATGAGGTCAGTGC-----ACAATGA 973
QY 181 CTGTCCCGGGGATGAGGTCGCGGTGGAGACGACGACAT 223
Db 974 CTGTCCAGGTGGGTGAGAGTCCAGTGGAACTGACGATAT 1016

RESULT 7
US-09-252-991A-14743/c
; Sequence 14743, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 14743
; LENGTH: 1491
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-14743

Query Match 18.9%; Score 42.2; DB 4; Length 1491;
Best Local Similarity 50.2%; Pred. No. 0.15;
Matches 104; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

QY 17 CGACCTGCGCCGCTGACAGGTCAAGGTCAACAGAGCTGGTCTGCACCGCGGA 76
Db 1408 CGAGAGCGCCGCGCTGCTGCTGAGGATACAGAGAGAGGCTATCCCGCGC 1349
QY 77 GCGCATCAGCTGCTCCAGCTGACGAGGAGAGCTGCTGCGACCATCAATACCTGT 136
Db 1348 GCGCAAGGCGCTGACCCAGATGGCCAGGAGCAGATGTCAGACCGCTCAAGGACTCCGG 1289
QY 137 CCGGCTGCACACGCGCTGAGTGGCCAGGATGGCCGCGGCTGACTGTCGCCGGCGCAT 196
Db 1288 CCTCAAGGGCGCGCGCGGCTGTCCTCCACCGCGGTGAAGTGGGGCTGATGCCGAA 1229
QY 197 CGAGGTGCGCGTGGAGACCGACGACAT 223
Db 1228 GGACGAGTGCCTGACATCCGCTACCT 1202

RESULT 8
US-09-252-991A-14886
; Sequence 14886, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
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; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 14886
; LENGTH: 1539
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-14886

Query Match 18.9%; Score 42.2; DB 4; Length 1539;
Best Local Similarity 50.2%; Pred. No. 0.15;
Matches 104; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

QY 17 CGACCTGCGCCGCTGCGCGCTACAGGTCAACAGAGCTGGTCTGCACCGCGGA 76
Db 142 CGAAGACGCCAGCCGCTGCTGAGGATACAGAGCAAGGACGGCTATGCCGCGC 201
QY 77 GCGCATCAGCTGCTCCAGCTGACCGAGGAGAGCTGCTGCGGACCATCAATACCTGT 136
Db 202 GCGCAGGGGCTGACCCAGATGGCCAGGAGCAGATCTCCAGACCTCAAGACTCCGG 261
QY 137 CCGGCTGCACACGCGCTGAGGATGGCCGCGGCTTCCCACCGCGTGAAGTGGGGCTGATGCCGAA 321
Db 262 CCTCAAGGGCGCGCGCGGCTTCCCACCGCGTGAAGTGGGGCTGATGCCGAA 321
QY 197 CGAGGTGCGCGTGGAGACCGACGACAT 223
Db 322 GGACGAGTGCCTGACATCCGCTACCT 348

RESULT 9
US-09-252-991A-15010
; Sequence 15010, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 15010
; LENGTH: 1614
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-15010

Query Match 18.9%; Score 42.2; DB 4; Length 1614;
Best Local Similarity 50.2%; Pred. No. 0.15;
Matches 104; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

QY 17 CGACCTGCGCCGCTGCGCGCTACAGGTCAACAGAGCTGGTCTGCACCGCGGA 76
Db 345 CGAAGACGCCAGCCGCTGCTGAGGATACAGAGCAAGGACGGCTATGCCGCGC 404
QY 77 GCGCATCAGCTGCTCCAGCTGACCGAGGAGAGCTGCTGCGGACCATCAATACCTGT 136
Db 405 GCGCAGGGGCTGACCCAGATGGCCAGGAGCAGATCTCCAGACCTCAAGACTCCGG 464
QY 137 CCGGCTGCACACGCGCTGAGGATGGCCAGGCGCGCTGACTGATGCTGCCGCGGAT 196
Db 465 CCTCAAGGGCGCGCGCGGCTTCCCACCGCGTGAAGTGGGGCTGATGCCGAA 524
QY 197 CGAGGTGCGCGTGGAGACCGACGACAT 223
Db 525 GGACGAGTGCCTGACATCCGCTACCT 551

RESULT 10
US-09-410-551B-1/c
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APPLICANT: MARC J. RUBENSTEIN ET AL.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONA

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 10931

; LENGTH: 1326

; TYPE: DNA

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-10931

Query Match 18.2%; Score 40.6; DB 4; Length 1326;

Best Local Similarity 49.8%; Pred. No. 0.35;

Matches 103; Conservative 0; Mismatches 104; Indels 0; Gaps 0;

QY 4 AGGAGAAGCGTACGACTGGCCCGGTGGCGCGCTACAAAGGTCAACAAGAGCTGGGTC 63

DB 747 AGTGGCTGCATCCGGTGTGGCCACAGCAGCGGCCACCTGACCCACTACGTCCGGG 806

QY 64 TGCAGCGCGAGCCGATCACTGCTCCACGCTGACGAGGAGAGCTGTCGCGACA 123

DB 807 TGTTCCTCCGACTGAGCAGCATCAAGCGCTCGAGAGAGCTGGACTTCCTCGCCACC 866

QY 124 TCGAATACCTGTGCTCCGCTGCACACGCCGCTGACGATGGCCAGCCCGCGCTCATGACTG 183

DB 867 AGGACTCGCTGACCGGCTGCCCAACCGGTGCTGTCGCGAGCAGCATCGAGCAGGCGC 926

QY 184 TCCCGCGGCGATCGAGGTCCCGGTGG 210

DB 927 TGGAGACGGCAAGGACCGGAGCGGTGG 953

RESULT 14

US-09-252-991A-369

; Sequence 369, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 369

; LENGTH: 1470

; TYPE: DNA

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-369

Query Match

18.2%; Score 40.6; DB 4; Length 1470;

Best Local Similarity 48.9%; Pred. No. 0.35;

Matches 109; Conservative 0; Mismatches 114; Indels 0; Gaps 0;

QY 1 TCAGAGAGAGCGCTACGACTGGCCCGGTGCGCGCTACAGGTCAACAGAGCTGG 60

DB 66 TCAGCAGGCGCGCAGCGGCTGAACACGAGCGCGCGCGCGGCTGGTGAAGAACCTGC 125

QY 61 GTCTGACGCGGAGCGGATCACTGCTCCACGCTGACGAGGAGAGCTGTCGCGGA 120

DB 126 TGTTCATGTGCGCAAGGCGCTTCGAGTCGCGCGGATCCGCGCTCTCTGAAGAACAT 185

QY 121 CCATCGAATACCTGGTCCGCTGCGCAGCGCCGCTACGGATGGCCAGCGCGCTCATGA 180

DB 186 ACGGCTCGAGAGGCGCTGCCCGACACAGAGAGCGGTGGACGCGCGCGCGCTCG 245

QY 181 CTGTCGCCGCGGCGATCGAGGTGCGCGTGGAGACCGACGACAT 223

DB 246 CCGACCGGACCGGAGCGGATGCTGCGTGGTGGTGCCTT 288

RESULT 15

US-09-252-991A-11256/c

; Sequence 11256, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 11256

; LENGTH: 2211

; TYPE: DNA

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-11256

Query Match 18.2%; Score 40.6; DB 4; Length 2211;

Best Local Similarity 49.8%; Pred. No. 0.35;

Matches 103; Conservative 0; Mismatches 104; Indels 0; Gaps 0;

QY 4 AGGAGAAGCGTACGACTGGCCCGGTGGCGCGCTACAAAGGTCAACAAGAGCTGGGTC 63

DB 1478 AGTGGCTGCATCCGGTGTGGCCACAGCAGCGGCCACCTGACCCACTACGTCCGGG 1419

QY 64 TGCAGCGCGGCGAGCCGATCACTGCTCCACGCTGACGAGGAGAGCTGTCGCGACA 123

DB 1418 TGTTCCTCCGACTGAGCAGCATCAAGCGCTGGAGAACGAGCTGGACTTCCTCGCCACC 1359

QY 124 TCGAATACCTGTGCTCCGCTGCACACGCCGCTGACGATGGCCAGCCCGCGCTCATGACTG 183

DB 1358 AGGACTCGCTGACCGGCTGCCCAACCGGCTGCTCTCCGAGCGCATCGAGCAGGCGC 1299

QY 184 TCCCGCGGCGATCGAGGTCCCGGTGG 210

DB 1298 TGGAGACGGCAAGGACCGGAGCGGTGG 1272

Search completed: September 17, 2003, 12:28:05

Job time : 49.3319 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 17, 2003, 11:54:34 ; Search time 116.066 Seconds
(without alignments)
4726.283 Million cell updates/sec

Title: US-09-697-123B-9
Perfect score: 223
Sequence: 1 taaaggagaagcgtacgac.....ccggtggagaccagacat 223

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1660708 seqs, 1229959015 residues

Total number of hits satisfying chosen parameters: 3321416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications, NA:*

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3: /cgn2.6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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5: /cgn2.6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2.6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2.6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
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10: /cgn2.6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2.6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2.6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13: /cgn2.6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2.6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2.6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
16: /cgn2.6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
17: /cgn2.6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	138.2	62.0	3519	10	US-09-712-363-30
2	66	29.6	3543	14	US-10-156-761-4898
3	66	29.6	9025608	14	US-10-156-761-1
4	59.6	26.7	3495	10	US-09-738-626-547
5	59.6	26.7	5096	10	US-09-984-711-5
6	59.6	26.7	5099	10	US-09-887-052-1
7	59.6	26.7	5099	10	US-09-887-052-3
8	59.6	26.7	5099	10	US-09-887-052-5
9	59.6	26.7	5099	12	US-10-076-406-1
10	59.6	26.7	5099	12	US-10-076-406-3
11	59.6	26.7	5099	12	US-10-076-406-5
12	59.6	26.7	5099	13	US-10-075-460-5
13	59.6	26.7	3309400	10	US-09-738-626-1
14	48.6	21.8	1287	14	US-10-156-761-5314
15	46.6	20.9	2298	14	US-10-156-761-270
16	46.6	20.9	9025608	14	US-10-156-761-1

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17 46.4 20.8 1560 14 US-10-156-761-5120
18 43.8 19.6 5778 14 US-10-205-032-13
19 43.8 19.6 60196 14 US-10-205-032-1
20 43.4 19.5 1185 14 US-10-166-037-2
21 43 19.3 1836 14 US-10-156-761-2659
22 42.8 19.2 7407 12 US-10-246-330-3
23 41.8 18.7 861 14 US-10-156-761-5852
24 41.6 18.7 2341 14 US-10-156-761-7482
25 41.2 18.5 1413 14 US-10-156-761-6095
26 41 18.4 2133 13 US-10-124-800-17
27 41 18.4 4446 14 US-10-331-061-69
28 41 18.4 8730 13 US-10-124-800-1
29 41 18.4 536165 11 US-09-939-964-1
30 40.6 18.2 7419 9 US-09-815-242-4009
31 40.4 18.1 1452 14 US-10-156-761-5123
32 40.2 18.0 594 14 US-10-156-761-367
33 39.8 17.8 1242 14 US-10-156-761-5818
34 39.6 17.8 4443 14 US-10-156-761-3260
35 39.4 17.7 243 14 US-10-156-761-3106
36 39.4 17.7 3969 14 US-10-156-761-2515
37 39.2 17.6 2091 14 US-10-245-538-1
38 39.2 17.6 2091 14 US-10-245-538-3
39 39.2 17.6 2231 12 US-10-180-719-24
40 39 17.5 1347 9 US-09-815-242-4060
41 39 17.5 3972 14 US-10-156-761-5427
42 38.8 17.4 2046 14 US-10-156-761-1901
43 38.8 17.4 3066 14 US-10-156-761-1742
44 38.8 17.4 88421 10 US-09-976-059-1
45 38.6 17.3 915 14 US-10-156-761-4050

ALIGNMENTS

RESULT 1

US-09-712-363-30
; Sequence 30, Application US/09712363
; Patent No. US20020164588A1
; GENERAL INFORMATION:
; APPLICANT: Eisenberg, David
; APPLICANT: Rotstein, Sergio H.
; APPLICANT: Marcotte, Edward M.
; TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND
; FILE REFERENCE: 07419-032001
; CURRENT APPLICATION NUMBER: US/09/712,363
; CURRENT FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: PCT/US00/02246
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,531
; PRIOR FILING DATE: 2000-02-01
; PRIOR APPLICATION NUMBER: 60/117,844
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/118,206,
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: 60/126,593
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/134,093
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/134,092
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/165,124
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/165,086
; PRIOR FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 3519
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-09-712-363-30


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; ORGANISM: Corynebacterium glutamicum
US-09-738-626-547

Query Match          26.7%; Score 59.6; DB 10; Length 3495;
Best Local Similarity 69.6%; Pred. No. 7.2e-08;
Matches 96; Conservative 0; Mismatches 39; Indels 3; Gaps 1;

QY 9 AAGCGCTACGACCTGGCCGCGCTACGAAGTCAACAAGAAGCTGGTCTGCAC 68
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Db 877 AAGCGCTACGACCTGGCCGCGCTGGTGGTTACAGATCAACGCAAGCTGGCCTT--- 933

QY 69 GCCGGCAGCGGATACGTCGTCACGCTGACCGAGGAAGAGCTGCGGACCATCGAA 128
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 934 GGTGGCGACCAACGATGGTTGATGACTCTTACTGAAGAGGACATCGCAACCAACCATCGAG 993

QY 129 TACCTGGTCGGCTGCAC 146
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Db 994 TACCTGGTCGTGCAC 1011

RESULT 5
US-09-984-711-5
; Sequence 5, Application US/09984711
; Patent No. US20020119549A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: STEPHAN, Hans
; APPLICANT: KREUTZER, Caroline
; APPLICANT: HERMANN, Thomas
; APPLICANT: BINDER, Michael
; APPLICANT: FFEFERLE, Walter
; FILE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE ipdL GENE
; CURRENT APPLICATION NUMBER: US/09/984,711
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: DE10108230.9
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 5096
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
; OTHER INFORMATION:
US-09-984-711-5

Query Match          26.7%; Score 59.6; DB 10; Length 5096;
Best Local Similarity 69.6%; Pred. No. 7.2e-08;
Matches 96; Conservative 0; Mismatches 39; Indels 3; Gaps 1;

QY 9 AAGCGCTACGACCTGGCCGCGCTACGAAGTCAACAAGAAGCTGGTCTGCAC 68
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1578 AAGCGCTACGACCTGGCCGCGCTGGTGGTTACAGATCAACGCAAGCTGGCCTT--- 1634

QY 69 GCCGGCAGCGGATACGTCGTCACGCTGACCGAGGAAGAGCTGCGGACCATCGAA 128
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1635 GGTGGCGACCAACGATGGTTGATGACTCTTACTGAAGAGGACATCGCAACCAACCATCGAG 1694

QY 129 TACCTGGTCGGCTGCAC 146
    ||||| ||||| ||||| |||||
Db 1695 TACCTGGTCGTGCAC 1712

RESULT 6
US-09-887-052-1
; Sequence 1, Application US/09887052
; Patent No. US20020119537A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
```

```
; APPLICANT: BATHE, Brigitte
; APPLICANT: HERMANN, Thomas
; APPLICANT: FFEFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE ipdL GENE
; FILE REFERENCE: 204212US0X
; CURRENT APPLICATION NUMBER: US/09/887,052
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: DE10107229.5
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 5099
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
US-09-887-052-1

Query Match          26.7%; Score 59.6; DB 10; Length 5099;
Best Local Similarity 69.6%; Pred. No. 7.2e-08;
Matches 96; Conservative 0; Mismatches 39; Indels 3; Gaps 1;

QY 9 AAGCGCTACGACCTGGCCGCGCTACGAAGTCAACAAGAAGCTGGTCTGCAC 68
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1578 AAGCGCTACGACCTGGCCGCGCTGGTGGTTACAGATCAACGCAAGCTGGCCTT--- 1634

QY 69 GCCGGCAGCGGATACGTCGTCACGCTGACCGAGGAAGAGCTGCGGACCATCGAA 128
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1635 GGTGGCGACCAACGATGGTTGATGACTCTTACTGAAGAGGACATCGCAACCAACCATCGAG 1694

QY 129 TACCTGGTCGGCTGCAC 146
    ||||| ||||| ||||| |||||
Db 1695 TACCTGGTCGTGCAC 1712

RESULT 7
US-09-887-052-3
; Sequence 3, Application US/09887052
; Patent No. US20020119537A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: HERMANN, Thomas
; APPLICANT: FFEFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE ipdL GENE
; FILE REFERENCE: 204212US0X
; CURRENT APPLICATION NUMBER: US/09/887,052
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: DE10107229.5
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 5099
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
US-09-887-052-3

Query Match          26.7%; Score 59.6; DB 10; Length 5099;
Best Local Similarity 69.6%; Pred. No. 7.2e-08;
Matches 96; Conservative 0; Mismatches 39; Indels 3; Gaps 1;

QY 9 AAGCGCTACGACCTGGCCGCGCTACGAAGTCAACAAGAAGCTGGTCTGCAC 68
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1578 AAGCGCTACGACCTGGCCGCGCTGGTGGTTACAGATCAACGCAAGCTGGCCTT--- 1634
```

QY	69	CGCGCGAGCCGATCAGCTCTCCAGCAGGAGGAGAGCTGTCGGACCATCGAA	128
Db	1635	GGTGGACACAGATGGTTTGATGACTCTTACTGAGAGGACATCGAACCATTCGAG	1694
QY	129	TACCTGGTCGGCTGCAC	146
Db	1695	TACCTGGTCGGCTGCAC	1712

RESULT 8

```

US-09-887-052-5
; Sequence 5, Application US/09887052
; Patent No. US20020119537A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE rpoB GENE
; FILE REFERENCE: 204212USOX
; CURRENT APPLICATION NUMBER: US/09/887,052
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: DE10107229.5
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 5099
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
US-09-887-052-5

```

Query Match	26.7%;	Score 59.6;	DB 10;
Best Local Similarity	69.6%;	Mism.No. 7.2e-08;	
Matches	96;	Conservative	0; Indels 3; Gaps 1;
QY	9	AAGCGCTACGACTGGCCGGTCGGCGGTACAGAGTCAACAAGAGCTGGGCTTGCGAC	68
Db	1578	AAGCGCTACGACTGGCTCGGGTTGGTCGTACAAAGATCAACCGCAAGCTCGGCCT---	1634
QY	69	GCCGCGAGCGCATCAGCTGCTGCCACGCTCAOCGAGGAGAGCGTCTCGCGACCACATCGAA	128
Db	1635	GGTGGCACACAGATGGTTTGAATGACTCTTACTGAGAGGACATCGCACCCACCATCGAG	1694
QY	129	TACCTGTGCGGCTGCGAC	146
Db	1695	TACCTGGTGGCTCTGCGAC	1712

RESULTS

```

> US-10-076-406-1
> Sequence 1, Application US/10076406
> Publication No. US2003016684A1
> GENERAL INFORMATION:
> APPLICANT: MOECKEL, Bettina
> APPLICANT: BATHE, Brigitte
> APPLICANT: HERMANN, Thomas
> APPLICANT: PFEFFERLE, Walter
> APPLICANT: BINDER, Michael
> TITLE OF INVENTION: Nucleotide sequences coding for the rpoB gene
> FILE REFERENCE: 219774USOXCIP
> CURRENT APPLICATION NUMBER: US/10/076.406
> CURRENT FILING DATE: 2003-02-19
> PRIOR APPLICATION NUMBER: DE 10107229.5
> PRIOR FILING DATE: 2001-02-16
> PRIOR APPLICATION NUMBER: US 09/887052
> PRIOR FILING DATE: 2001-06-25
> NUMBER OF SEQ ID NOS: 12
> SOFTWARE: PatentIn version 3.1

```

```

; SEQ ID NO 1
; LENGTH: 5099
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
; OTHER INFORMATION:
US-10-076-406-1

Query Match      26.7%; Score 59.6; DB 12; Length 5099;
Best Local Similarity 69.6%; Prid. No. 7.2e-08;
Matches 96; Conservative 0; Mismatches 39; Indels 3; Gaps 1;

Qy      9  AAGCGCTACGACGTGGCGCGGTGCGCGGCTACAGGCTACACAGAGAGCTGGGCTGCGAC 68
          |||||
Db      1578  AAGCGCTACGACGTGGCTGGCGGTGGTTCACAGATCAACCGCAAGCTCGGCGCT--- 1634
          |||||

Qy      69  GCGCGGCGAGCGGATCATCGTTCGCTCCACCTGACCGAGGAGAGCTGCTCGGAGCATTGAA 128
          |||||
Db      1635  GGTGGGACACGACGAGTTTATGACTCTTACTGAGAGGACATCGCAACCAACCATCGAG 1694
          |||||

Qy      129  TACTGTGTCGGCTGCAC 146
          |||||
Db      1695  TACCTGGTGGCTGTCGAC 1712
          |||||

```

RESULTS

```

US-10-076-406-3
; Sequence 3, Application US/10076406
; Publication NO. US2003016684A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, Bettina
; APPLICANT: BATHE, Brigitte
; APPLICANT: HERMANN, Thomas
; APPLICANT: PFEFFERLE, Walter
; APPLICANT: BINDER, Michael
; TITLE OF INVENTION: Nucleotide sequences coding for the rpoB gene
; FILE REFERENCE: 21974U50XCIP
; CURRENT APPLICATION NUMBER: US/10/076,406
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: DE 10107229.5
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 09/887052
; PRIOR FILING DATE: 2001-06-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 5099
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (702)..(4196)
; OTHER INFORMATION:
; NAME/KEY: mutation
; LOCATION: (1987)..(1987)
; OTHER INFORMATION: Substitution of adenine by thymine
; NAME/KEY: mutation
; LOCATION: (1288)..(1288)
; OTHER INFORMATION: Substitution of cytosine by thymine
; NAME/KEY: mutation
; LOCATION: (715)..(715)
; OTHER INFORMATION: Substitution of cytosine by thymine
; US-10-076-406-3

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Query Match: 26.7%; Score 59.6; DB 12; Length 5099;
 Best Local Similarity 69.6%;
 Matches 96; Conservative 0; Mismatches 35; Indels 3; Gaps 1;
 QY 9 AAGCGCTAGACCTGGCCGCGTCCGGCGGTCAAGGCTCAACGAAGCTGGTCTGCAC 68
 1578 AAGCGCTAGACCTGGCTCGCGTGGTGGCTTCAAGATCAACCGCAAGCTGGCGCTT --- 1634
 Db

Query Match	26.7%	Score 59.6;	DB 10;	Length 3309400;
Best Local Similarity	69.6%;	Pred. NO. 5.3e-08;		
Matches 96;	Conservative	0;	Mismatches 39;	Indels 3; Gaps 1;

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QY 9 AAGCGTACGACCTGGCGCGCTGCTACAGGTCAACAGAGCTGGTCTGCAC 68
Db 513789 AAGCGTACGACCTGGCGCTGCTGCTTACAGATCAACGCGAAGCTGGGCTT--- 513845
QY 69 GCGCGGAGCGGATCAGCTGCTCCAGCTGACCGAGGAGAGCTGCTCGCGACCATGGAA 128
Db 513846 GGTGGCGGACGACGATGGTTTGATGACTCTTACTGAAGAGACATCGCAACCATCGAG 513905
QY 129 TACCTGGTCCGGCTGCGAC 146
Db 513906 TACCTGGTCCGGCTGCGAC 513923
```

RESULT 14

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US-10-156-761-5314
; Sequence 5314, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 5314
; LENGTH: 1287
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1287)
US-10-156-761-5314
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Query Match 21.8%; Score 48.6; DB 14; Length 1287;
Best Local Similarity 51.1%; Pred. No. 9.9e-05;
Matches 114; Conservative 0; Mismatches 109; Indels 0; Gaps 0;
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QY 1 TCAGAGGAGAGCGGTACGACCTGGCGCGCTGCTACAGGTCAACAGAGCTGG 60
Db 614 TCCGCGGAGAGACTACGACCTGGACCGCTGCTGCTCGCGCTCGACAGCTGCTGA 673
QY 61 GTCTGCAGCGCGGAGCGGATCACGCTGCTCCACGCTGACCGAGGAGAGCTGCTCGGA 120
Db 674 TTCTGCAGCGGAGGACGAGCAGAGTGTGACCTCCACGCTGCTGCTGCTGCTGCT 733
QY 121 CATTGGAATACCTGCTGGCTGCACACGCGCGCTGACGATGGCGAGCGCGCGCTGATGA 180
Db 734 CGCAGGCGGAACATCTTGGCTGCTGATCTCCGCGCGGATCTCCGCTCTGGGCGCGCTGC 793
QY 181 CTGTCGCCGGGGATCGAGTGGCTGGAGACCGAGCAT 223
Db 794 ACGGTGGCGCCNACAGTCGCTCTGAGATGCTCGAGGGCAT 836
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RESULT 15

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US-10-156-761-270
; Sequence 270, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
```

```
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 270
; LENGTH: 2298
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2298)
US-10-156-761-270
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Query Match 20.9%; Score 46.6; DB 14; Length 2298;
Best Local Similarity 52.3%; Pred. No. 0.00035;
Matches 103; Conservative 0; Mismatches 94; Indels 0; Gaps 0;
```

```
QY 2 CAAGGAGAAGCGGTACGACCTGGCGCGCTGCTACAGGTCAACAGAGCTGGG 61
Db 498 CACGATGAGCTGTACAAGCAGTCCAGCCGCGACAGCGCGGACGATCAGAGGT 557
QY 62 TCTGCAGCGCGGAGCGGATCACGCTGCTCCACGCTGACCGAGGAGAGCTGCTCGGAC 121
Db 558 CATGGAGCGGCAAGTCTGCTCGTCCAGTGTGCTGCGCGAGCGCGCGCTGGAT 617
QY 122 CATGGAATACCTGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 181
Db 618 GATCAATTCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 677
QY 182 TGTCCCGCGCGCATCG 198
Db 678 GCTGCCCGCGCGCG 694
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Search completed: September 17, 2003, 13:04:57
Job time : 137.066 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 16, 2003, 16:37:01 : Search time 43.8462 Seconds
(without alignments)
191.266 Million cell updates/sec.

Title: US-09-697-123B-25

Perfect score: 19
Sequence: 1 tcaaggagagcgctacga 19

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents.NA.*

- 1: /cgn2.6/prodata/2/ina/5A.COMB.seq.*
- 2: /cgn2.6/prodata/2/ina/5B.COMB.seq.*
- 3: /cgn2.6/prodata/2/ina/6A.COMB.seq.*
- 4: /cgn2.6/prodata/2/ina/6B.COMB.seq.*
- 5: /cgn2.6/prodata/2/ina/PCRUS.COMB.seq.*
- 6: /cgn2.6/prodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	19	100.0	970	1	US-08-250-030-1
2	19	100.0	970	5	PCT-US93-08790-1
3	19	100.0	4403765	3	US-09-103-840A-2
4	19	100.0	4411529	3	US-09-103-840A-1
5	17.4	91.6	3447	2	US-08-313-185-57
6	17.4	91.6	3447	3	US-09-082-614A-57
7	16.4	86.3	915	4	US-09-282-991A-15932
8	16.4	86.3	2814	4	US-09-282-991A-15765
9	16.4	86.3	3357	4	US-09-252-991A-15868
10	15.8	83.2	1958	4	US-08-961-527-360
11	15.8	83.2	3752	4	US-08-961-527-208
12	15.8	83.2	4854	4	US-08-961-527-178
13	15.8	83.2	6516	4	US-08-961-527-105
14	15.8	83.2	11309	4	US-08-961-527-108
15	15	78.9	1238	4	US-09-996-243-356
16	15	78.9	1470	4	US-09-996-243-356
17	15	78.9	3027	4	US-09-252-991A-2857
18	15	78.9	4403765	3	US-09-252-991A-2758
19	15	78.9	4411529	3	US-09-103-840A-1
20	14.8	77.9	459	4	US-09-252-991A-1738
21	14.8	77.9	1008	4	US-09-252-991A-6338
22	14.8	77.9	1638	4	US-09-252-991A-11500
23	14.8	77.9	1668	4	US-09-252-991A-11742
24	14.8	77.9	1764	4	US-09-252-991A-6133
25	14.8	77.9	2395	4	US-09-724-864-24
26	14.8	77.9	3228	4	US-09-252-991A-1816
27	14.8	77.9	3546	4	US-09-252-991A-2143

28	14.8	77.9	6559	4	US-09-234-186-1	Sequence 1, Appli
29	14.8	77.9	6559	4	US-09-233-527-1	Sequence 1, Appli
30	14.8	77.9	6560	5	PCT-US93-05651-1	Sequence 1, Appli
c 31	14.4	75.8	515	3	US-08-998-416-125	Sequence 125, App
c 32	14.4	75.8	711	4	US-09-221-017B-476	Sequence 476, App
c 33	14.4	75.8	789	4	US-09-627-536-11	Sequence 11, Appl
c 34	14.4	75.8	2419	4	US-09-627-536-10	Sequence 10, Appl
35	14.4	75.8	3460	4	US-09-620-312D-666	Sequence 666, App
36	14.2	74.7	22	2	US-08-494-151-6	Sequence 6, Appli
37	14.2	74.7	534	4	US-09-252-991A-12119	Sequence 12119, A
38	14.2	74.7	678	4	US-09-252-991A-5030	Sequence 5030, Ap
39	14.2	74.7	756	3	US-08-413-974-3	Sequence 3, Appli
40	14.2	74.7	756	3	US-08-434-418-3	Sequence 3, Appli
41	14.2	74.7	756	3	US-08-433-288-3	Sequence 3, Appli
42	14.2	74.7	756	3	US-08-174-739A-3	Sequence 3, Appli
43	14.2	74.7	756	4	US-08-434-256-3	Sequence 3, Appli
44	14.2	74.7	805	4	US-08-858-207A-1	Sequence 1, Appli
45	14.2	74.7	810	3	US-08-413-974-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1

US-08-250-030-1

; Sequence 1, Application US/08250030

; Patent No. 5643723

; GENERAL INFORMATION:

; APPLICANT: Persing, David H.

; TITLE OF INVENTION: Detection of a Genetic Locus Encoding

; TITLE OF INVENTION: Resistance to Rifampin in Mycobacterial Cultures and in

; NUMBER OF SEQUENCES: 15

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Schwegman, Lundberg & Woessner

; STREET: 3500 IDS Center

; CITY: Minneapolis

; STATE: MN

; COUNTRY: USA

; ZIP: 55402

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/250,030

; FILING DATE: 26-MAY-1994

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Muetting, Ann M.

; REGISTRATION NUMBER: 33,977

; REFERENCE/DOCKET NUMBER: 150.105US1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 612-339-0331

; TELEFAX: 612-339-3061

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 970 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA

US-08-250-030-1

Query Match 100.0%; Score 19; DB 1; Length 970;

Best Local Similarity 100.0%; Pred. No. 1.7;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAGGAGAGCGCTACGA 19

|||||

26 TCAAGGAGAGCGCTACGA 44

```

; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match      100.0%; Score 19; DB 3; Length 4403765;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TCAAGGAGAGCGCTACGA 19
      |||
Db      762648 TCAAGGAGAGCGCTACGA 762666

RESULT 4
US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match      100.0%; Score 19; DB 3; Length 4411529;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TCAAGGAGAGCGCTACGA 19
      |||
Db      760688 TCAAGGAGAGCGCTACGA 760706

RESULT 5
US-08-313-185-57
; Sequence 57, Application US/08313185
; Patent No. 5851763
; GENERAL INFORMATION:
; APPLICANT: Heym, Beate
; APPLICANT: Cole, Stewart
; APPLICANT: Young, Douglas
; APPLICANT: Zhang, Ying
; APPLICANT: Honore, Nadine
; APPLICANT: Telenti, Amalio
; APPLICANT: Bodmer, Thomas
; TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
; TITLE OF INVENTION: in Mycobacterium Tuberculosis
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; OTHER INFORMATION: CDC 1551
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/313.185
; FILING DATE: 12-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 02356.0068-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3447 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-313-185-57

Query Match          91.6%; Score 17.4; DB 2; Length 3447;
Best Local Similarity 94.7%; Pred. No. 12;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 TCAAGGAGGAGCGCTACGA 19
        ||||| ||||| ||||| |||||
Db      809 TCAAGGAGGAGCGCTACGA 827

RESULT 6
US-09-082-614A-57
; Sequence 57, Application US/09082614A
; Patent No. 6124098
; GENERAL INFORMATION:
; APPLICANT: Heym, Beate
; APPLICANT: Cole, Stewart
; APPLICANT: Young, Douglas
; APPLICANT: Zhang, Ying
; APPLICANT: Honore, Nadine
; APPLICANT: Telenti, Amalio
; APPLICANT: Bodmer, Thomas
; TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
; TITLE OF INVENTION: in Mycobacterium Tuberculosis
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/082.614A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/313.185
; FILING DATE: 12-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 02356.0068-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 3447 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-082-614A-57

Query Match          91.6%; Score 17.4; DB 3; Length 3447;
Best Local Similarity 94.7%; Pred. No. 12;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 TCAAGGAGGAGCGCTACGA 19
        ||||| ||||| ||||| |||||
Db      809 TCAAGGAGGAGCGCTACGA 827

RESULT 7
US-09-252-991A-15932
; Sequence 15932, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONA:
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 15932
; LENGTH: 915
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-15932

Query Match          86.3%; Score 16.4; DB 4; Length 915;
Best Local Similarity 94.4%; Pred. No. 31;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 TCAAGGAGGAGCGCTACG 18
        ||||| ||||| ||||| |||||
Db      195 TCAAGGAGGAGCGCTACG 212

RESULT 8
US-09-252-991A-15765/c
; Sequence 15765, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONA:
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 15765
; LENGTH: 2814
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-15765

Query Match          86.3%; Score 16.4; DB 4; Length 2814;
Best Local Similarity 94.4%; Pred. No. 35;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1 TCAGGAGAGCGCTACG 18
|||||
Db 1553 TCAGGAGAGCGCTACG 1536

RESULT 9
US-09-252-991A-15868
; Sequence 15868, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 15868
; LENGTH: 3357
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-15868

Query Match 86.3%; Score 16.4; DB 4; Length 3357;
Best Local Similarity 94.4%; Pred. No. 35;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCAGGAGAGCGCTACG 18
|||||
Db 1907 TCAGGAGAGCGCTACG 1924

RESULT 10
US-08-961-527-360
; Sequence 360, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,527
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 360:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1958 base pairs

; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-961-527-360

Query Match 83.2%; Score 15.8; DB 4; Length 1958;
Best Local Similarity 89.5%; Pred. No. 66;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TCAGGAGAGCGCTACGA 19
|||||
Db 194 TCAGGAGAGCGCTACGA 212

RESULT 11
US-08-961-527-208
; Sequence 208, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,527
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 208:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3752 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-961-527-208

Query Match 83.2%; Score 15.8; DB 4; Length 3752;
Best Local Similarity 89.5%; Pred. No. 70;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TCAGGAGAGCGCTACGA 19
|||||
Db 2773 TCAGGAGAGCGCTACGA 2791

RESULT 12
US-08-961-527-178
; Sequence 178, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391

```
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,527
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 178:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4854 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
;
; US-08-961-527-178
;
; Query Match      83.2%; Score 15.8; DB 4; Length 4854;
; Best Local Similarity 89.5%; Pred. No. 72;
; Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
;
; QY      1 TCAAGGAGAGCGCTACGA 19
; DB      100 TCAAGAGAGAGCTACGA 118
;
; RESULT 13
; US-08-961-527-105/c
; Sequence 105, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,527
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 108:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11309 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
;
; US-08-961-527-108
;
; Query Match      83.2%; Score 15.8; DB 4; Length 11309;
; Best Local Similarity 89.5%; Pred. No. 78;
; Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
;
; QY      1 TCAAGGAGAGCGCTACGA 19
; DB      9043 TCAAGAGAGAGCTACGA 9025
;
; RESULT 15
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```
;
; REFERENCE/DOCKET NUMBER: PB340P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 105:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6516 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
;
; US-08-961-527-105
;
; Query Match      83.2%; Score 15.8; DB 4; Length 6516;
; Best Local Similarity 89.5%; Pred. No. 74;
; Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
;
; QY      1 TCAAGGAGAGCGCTACGA 19
; DB      5353 TCAAGAGAGAGCTACGA 5335
;
; RESULT 14
; US-08-961-527-108/c
; Sequence 108, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,527
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 108:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11309 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
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; US-08-961-527-108
;
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; Best Local Similarity 89.5%; Pred. No. 78;
; Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
;
; QY      1 TCAAGGAGAGCGCTACGA 19
; DB      9043 TCAAGAGAGAGCTACGA 9025
;
; RESULT 15
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US-09-396-243-356
; Sequence 356, Application US/09996243
; Patent No. 6478825
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary B.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C13
; CURRENT APPLICATION NUMBER: US/09/996,243
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
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; PRIOR FILING DATE: 1998-06-02
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; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: 60/088021
; PRIOR FILING DATE: 1998-06-04
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; PRIOR FILING DATE: 1998-06-04
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; PRIOR APPLICATION NUMBER: 60/088326
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088167
; PRIOR FILING DATE: 1998-06-05
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; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: 60/088734
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088738
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088742
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; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088824
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088826
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088858
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/088861
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/088876
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/089105
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: 60/089440
; PRIOR FILING DATE: 1998-06-16
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; PRIOR FILING DATE: 1998-06-16
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; PRIOR FILING DATE: 1998-06-16
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; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089538
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089598
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089599
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089600
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089653
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089907
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089908
; PRIOR FILING DATE: 1998-06-18
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; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/089948
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/089952
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/090246
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090252
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090254
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090349
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090355

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OM nucleic - nucleic search, using sw model

Run on: September 16, 2003, 16:37:04 ; Search time 154.436 Seconds
(without alignments)
302.640 Million cell updates/sec

Title: US-09-697-123B-25

Perfect score: 19

Sequence: 1 tcaaggagaagcgtacga 19

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Searched: 1660708 segs, 1229959015 residues

Total number of hits satisfying chosen parameters: 3321416

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications_NA:*

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- 3: /cgn2.6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
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- 10: /cgn2.6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
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- 12: /cgn2.6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2.6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2.6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2.6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 16: /cgn2.6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 17: /cgn2.6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	19	100.0	3519	10	US-09-712-363-30
3	16	84.2	212	10	US-09-833-381-29
4	15.8	83.2	255	9	US-09-294-093B-4362
5	15.8	83.2	281	9	US-09-294-093B-5081
6	15.8	83.2	1176	9	US-09-815-242-9077
7	15.8	83.2	4143	11	US-09-919-039-345
8	15.8	83.2	6082	10	US-09-880-107-2432
9	15.4	81.1	331	10	US-09-960-352-9053
10	15.4	81.1	355	10	US-09-960-352-6002
11	15.4	81.1	370	10	US-09-960-352-9968
12	15.4	81.1	375	10	US-09-960-352-12378
13	15.4	81.1	384	10	US-09-960-352-8128
14	15.4	81.1	386	10	US-09-960-352-11656
15	15.4	81.1	390	10	US-09-960-352-5030
16	15.4	81.1	405	10	US-09-960-352-8824

17	15.4	81.1	414	10	US-09-960-352-14725	Sequence 14725, A
18	15.4	81.1	422	10	US-09-960-352-4589	Sequence 4589, Ap
19	15.4	81.1	717	13	US-10-076-785-15	Sequence 15, Appl
20	15.4	81.1	935	13	US-10-076-785-19	Sequence 19, Appl
21	15.4	81.1	1072	9	US-09-853-386-105	Sequence 105, App
22	15.4	81.1	1143	10	US-09-738-626-1350	Sequence 1350, Ap
23	15.4	81.1	1230	9	US-09-960-288-1	Sequence 1, Appl
24	15.4	81.1	3309400	10	US-09-738-626-1	Sequence 1, Appl
25	15	78.9	477	12	US-10-258-105-48	Sequence 48, Appl
26	15	78.9	591	12	US-10-258-105-55	Sequence 55, Appl
27	15	78.9	663	12	US-10-258-105-56	Sequence 56, Appl
28	15	78.9	663	12	US-10-258-105-57	Sequence 57, Appl
29	15	78.9	669	12	US-10-258-105-59	Sequence 59, Appl
30	15	78.9	735	12	US-10-258-105-46	Sequence 46, Appl
31	15	78.9	741	12	US-10-258-105-60	Sequence 60, Appl
32	15	78.9	741	12	US-10-258-105-61	Sequence 61, Appl
33	15	78.9	813	12	US-10-258-105-45	Sequence 45, Appl
34	15	78.9	995	12	US-10-258-105-5	Sequence 5, Appl
35	15	78.9	1067	12	US-10-258-105-7	Sequence 7, Appl
36	15	78.9	1067	12	US-10-258-105-9	Sequence 9, Appl
37	15	78.9	1139	12	US-10-258-105-3	Sequence 3, Appl
38	15	78.9	1197	12	US-10-258-105-36	Sequence 36, Appl
39	15	78.9	1238	9	US-09-989-723-356	Sequence 356, App
40	15	78.9	1238	9	US-09-989-723-356	Sequence 356, App
41	15	78.9	1238	9	US-09-989-279-356	Sequence 356, App
42	15	78.9	1238	9	US-09-989-727-356	Sequence 356, App
43	15	78.9	1238	10	US-09-989-731-356	Sequence 356, App
44	15	78.9	1238	10	US-09-989-732-356	Sequence 356, App
45	15	78.9	1238	10	US-09-991-073-356	Sequence 356, App

ALIGNMENTS

RESULT 1
US-10-058-422-1
; Sequence 1, Application US/10058422
; Publication No. US20030108881A1
; GENERAL INFORMATION:
; APPLICANT: HyeYoung Lee, Hye Eun Bang, Sang-Nae Cho, Gill-Han BAI,
; APPLICANT: Sang-Jae Kim
; TITLE OF INVENTION: A method for identifying Micobacteria tuberculosis and
; TITLE OF INVENTION: non-tuberculosis Micobacteria, together with detecting resist
; TITLE OF INVENTION: to an antituberculosis drug of Micobacteria obtained by mutat
; TITLE OF INVENTION: of rpoB gene
; FILE REFERENCE: 0217-0008
; CURRENT APPLICATION NUMBER: US/10/058,422
; CURRENT FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: KopatentIn 1.71
; SEQ ID NO 1
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MOTT-rpo-long-B-5' primer for PCR amplification of rpoB gene
US-10-058-422-1

Query Match 100.0% Score 19; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAGGAGAAGCGCTACGA 19
|||||
Db 1 TCAAGGAGAAGCGCTACGA 19

RESULT 2.

US-09-712-363-30
; Sequence 30, Application US/09712363
; Patent No. US20020164588A1
; GENERAL INFORMATION:
; APPLICANT: Eisenberg, David

```

; APPLICANT: Rotstein, Sergio H.
; APPLICANT: Marcotte, Edward M.
; TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND
; FILE REFERENCE: 07419-032001
; CURRENT FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: US/09/712,363
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,531
; PRIOR FILING DATE: 2000-02-01
; PRIOR APPLICATION NUMBER: 60/117,844
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/118,206
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: 60/126,593
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/134,093
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/134,092
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/165,124
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/165,086
; PRIOR FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-09-712-363-30

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Query Match      100.0%; Score 19; DB 10; Length 3519;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAGGAGAGCGCTACGA 19
    |||||
DB 884 TCAGGAGAGCGCTACGA 902

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```

RESULT 3
US-09-833-381-29
; Sequence 29, Application US/09833381
; Patent No. US20020132090A1
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: No. US20020132090A1el Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-119
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516,448
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(212)
; OTHER INFORMATION: n = A,T,C or G
US-09-833-381-29

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Query Match      84.2%; Score 16; DB 10; Length 212;
Best Local Similarity 84.2%; Pred. No. 99;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TCAGGAGAGCGCTACGA 19
    |||
DB 75 TCAGGAGAGCGCTACGA 93

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RESULT 4
US-09-294-093B-4362
; Sequence 4362, Application US/09294093B
; Patent No. US20010051335A1
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath, V.
; APPLICANT: Ito, Laura, Y.
; APPLICANT: Sherman, Bradley, K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL
; FILE REFERENCE: PL-0009 US
; CURRENT FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 60/082,567
; PRIOR FILING DATE: April 21, 1998
; NUMBER OF SEQ ID NOS: 6207
; SOFTWARE: PERL Program
; SEQ ID NO 4362
; LENGTH: 265
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20010051335A1 700353887H1
; NAME/KEY: unsure
; LOCATION: 69, 75, 80, 87, 206
; OTHER INFORMATION: a, t, c, g, or other
US-09-294-093B-4362

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Query Match      83.2%; Score 15.8; DB 9; Length 265;
Best Local Similarity 89.5%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TCAGGAGAGCGCTACGA 19
    |||||
DB 140 TCAGGAGAGCGCTACGA 158

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RESULT 5
US-09-294-093B-5081
; Sequence 5081, Application US/09294093B
; Patent No. US20010051335A1
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath, V.
; APPLICANT: Ito, Laura, Y.
; APPLICANT: Sherman, Bradley, K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL
; FILE REFERENCE: PL-0009 US
; CURRENT FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 60/082,567
; PRIOR FILING DATE: April 21, 1998
; NUMBER OF SEQ ID NOS: 6207
; SOFTWARE: PERL Program
; SEQ ID NO 5081
; LENGTH: 281
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20010051335A1 700355754H1
; NAME/KEY: unsure
; LOCATION: 178, 205, 215
; OTHER INFORMATION: a, t, c, g, or other
US-09-294-093B-5081

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Query Match      83.2%; Score 15.8; DB 9; Length 281;
Best Local Similarity 89.5%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TCAGGAGAGCGCTACGA 19
    |||||

```

Query Match 81.1%; Score 15.4; DB 10; Length 331;

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Best Local Similarity 94.1%; Pred. No. 2e+02; 1; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CAAGGAGAGCGCTACG 18
    ||||| |||||
Db 327 CAAGGACAGCGCTACG 311

RESULT 10
US-09-960-352-6002/c
; Sequence 6002, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 6002
; LENGTH: 365
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 26-LIB3057-001-Q1-K1-G9
US-09-960-352-6002

Query Match 81.1%; Score 15.4; DB 10; Length 365;
Best Local Similarity 94.1%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CAAGGAGAGCGCTACG 18
    ||||| |||||
Db 309 CAAGGACAGCGCTACG 293

RESULT 11
US-09-960-352-9968/c
; Sequence 9968, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 9968
; LENGTH: 370
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 43-LIB3057-006-Q1-K1-C12
US-09-960-352-9968

Query Match 81.1%; Score 15.4; DB 10; Length 370;
Best Local Similarity 94.1%; Pred. No. 2e+02; 1; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CAAGGAGAGCGCTACG 18
    ||||| |||||
Db 321 CAAGGACAGCGCTACG 305

RESULT 12
US-09-960-352-12378/c
; Sequence 12378, Application US/09960352
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; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AN
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 12378
; LENGTH: 375
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 53-LIB3057-014-Q1-K1-F10
US-09-960-352-12378

Query Match 81.1%; Score 15.4; DB 10; Length 375;
Best Local Similarity 94.1%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CAAGGAGAGCGCTACG 18
    ||||| |||||
Db 319 CAAGGACAGCGCTACG 303

RESULT 13
US-09-960-352-8128/c
; Sequence 8128, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AN
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 8128
; LENGTH: 384
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (9)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: 35-LIB3057-006-Q1-K1-A12
US-09-960-352-8128

Query Match 81.1%; Score 15.4; DB 10; Length 384;
Best Local Similarity 94.1%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CAAGGAGAGCGCTACG 18
    ||||| |||||
Db 321 CAAGGACAGCGCTACG 305

RESULT 14
US-09-960-352-11656
; Sequence 11656, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AN
```

```

; TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960.352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 11656
; LENGTH: 386
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 50-LIB3057-003-Q1-K1-E10
US-09-960-352-11656

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Query Match      81.1%; Score 15.4; DB 10; Length 386;
Best Local Similarity 94.1%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      2 CAGGAGAGCGCTACG 18
        ||||| |||||
Db      201 CAGGACAGCGCTACG 217

```

RESULT 15

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US-09-960-352-5030
; Sequence 5030, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathalagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960.352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 5030
; LENGTH: 390
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 22-LIB3057-005-Q1-K1-F9
US-09-960-352-5030

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Query Match      81.1%; Score 15.4; DB 10; Length 390;
Best Local Similarity 94.1%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      2 CAGGAGAGCGCTACG 18
        ||||| |||||
Db      298 CAGGACAGCGCTACG 314

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Job time : 160.436 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 16, 2003, 16:37:01 ; Search time 46.1538 Seconds
(without alignments)
191.266 Million cell updates/sec

Title: US-09-697-123b-26
Perfect score: 20
Sequence: 1 ggatgttgatcagggtctgc 20

Scoring table: IDENTITY WOC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/prodata/2/ina/6A_COMB.seq.*
4: /cgn2_6/prodata/2/ina/6B_COMB.seq.*
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6: /cgn2_6/prodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
c 1	20	100.0	228	4	US-08-750-088A-69
c 2	20	100.0	254	4	US-08-750-088A-37
c 3	20	100.0	306	3	US-09-147-935A-1
c 4	20	100.0	306	3	US-09-147-935A-3
c 5	20	100.0	306	3	US-09-147-935A-4
c 6	20	100.0	306	3	US-09-147-935A-5
c 7	20	100.0	306	3	US-09-147-935A-8
c 8	20	100.0	306	3	US-09-147-935A-9
c 9	20	100.0	306	3	US-09-147-935A-10
c 10	20	100.0	306	3	US-09-147-935A-11
c 11	20	100.0	306	3	US-09-147-935A-12
c 12	20	100.0	306	3	US-09-147-935A-13
c 13	20	100.0	306	3	US-09-147-935A-14
c 14	20	100.0	306	3	US-09-147-935A-15
c 15	20	100.0	306	3	US-09-147-935A-17
c 16	20	100.0	306	3	US-09-147-935A-18
c 17	20	100.0	306	3	US-09-147-935A-22
c 18	20	100.0	306	3	US-09-147-935A-27
c 19	20	100.0	306	3	US-09-147-935A-28
c 20	20	100.0	306	3	US-09-147-935A-29
c 21	20	100.0	306	3	US-09-147-935A-30
c 22	20	100.0	306	3	US-09-147-935A-31
c 23	20	100.0	306	3	US-09-147-935A-32
c 24	20	100.0	306	3	US-09-147-935A-33
c 25	20	100.0	306	3	US-09-147-935A-35
c 26	20	100.0	306	3	US-09-147-935A-36
c 27	20	100.0	306	3	US-09-147-935A-37

c 28	20	100.0	306	3	US-09-147-935A-38	Sequence 38, Appl
c 29	20	100.0	306	3	US-09-147-935A-39	Sequence 39, Appl
c 30	20	100.0	306	3	US-09-147-935A-40	Sequence 40, Appl
c 31	20	100.0	306	3	US-09-147-935A-43	Sequence 43, Appl
c 32	20	100.0	306	3	US-09-147-935A-46	Sequence 46, Appl
c 33	20	100.0	306	3	US-09-147-935A-47	Sequence 47, Appl
c 34	20	100.0	319	4	US-08-750-088A-35	Sequence 35, Appl
c 35	20	100.0	324	4	US-08-750-088A-36	Sequence 36, Appl
c 36	18.4	92.0	306	3	US-09-147-935A-20	Sequence 20, Appl
c 37	18.4	92.0	306	3	US-09-147-935A-21	Sequence 21, Appl
c 38	18.4	92.0	306	3	US-09-147-935A-23	Sequence 23, Appl
c 39	18.4	92.0	306	3	US-09-147-935A-25	Sequence 25, Appl
c 40	18.4	92.0	306	3	US-09-147-935A-26	Sequence 26, Appl
c 41	18.4	92.0	306	3	US-09-147-935A-34	Sequence 34, Appl
c 42	18.4	92.0	306	3	US-09-147-935A-42	Sequence 42, Appl
c 43	18.4	92.0	306	3	US-09-147-935A-44	Sequence 44, Appl
c 44	16.8	84.0	306	3	US-09-147-935A-2	Sequence 2, Appl
c 45	16.8	84.0	306	3	US-09-147-935A-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-08-750-088A-69/G
; Sequence 69, Application US/08750088A
; Patent No. 6329138
; GENERAL INFORMATION:
; APPLICANT: DE BEENHOUWER, HANS
; APPLICANT: PORTAELS, FRAN OISE
; APPLICANT: MACHTELINCKX, LIEVE
; APPLICANT: JANNES, GEERT
; APPLICANT: ROSSAU, RUDI
; TITLE OF INVENTION: METHOD FOR DETECTION OF THE ANTIBIOTIC
; TITLE OF INVENTION: RESISTANCE SPECTRUM OF MYCOBACTERIUM SPECIES
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: US
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08750,088A
; FILING DATE: 21-FEB-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: GOLDSTEIN, JORGE A.
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 1657.0010000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 228 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-750-088A-69

Query Match 100.0% ; score 20; DB 4; Length 228;
Best Local Similarity 100.0% ; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGATGTGATCAGGGTCTGC 20

db 88 GGATGTTGATCAGGGTCG 69

RESULT 2
US-08-750-088A-37/c
: Sequence 37, Application US/08750088A
: Patent No. 6329138
: GENERAL INFORMATION:
: APPLICANT: DE BEENHOUWER, HANS
: APPLICANT: PORTAELS, FRAN OISE
: APPLICANT: MACHTELINCKX, LIEVE
: APPLICANT: JANNES, GEERT
: APPLICANT: ROSSAU, RUDI
: TITLE OF INVENTION: METHOD FOR DETECTION OF THE ANTIBIOTIC
: TITLE OF INVENTION: RESISTANCE SPECTRUM OF MYCOBACTERIUM SPECIES
: NUMBER OF SEQUENCES: 71
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: STERNÉ, KESSLER, GOLDSTEIN & FOX P.L.L.C.
: STREET: 1100 NEW YORK AVENUE, SUITE 600
: CITY: WASHINGTON
: STATE: D.C.
: COUNTRY: US
: ZIP: 20005-3934
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/750,088A
: FILING DATE: 21-FEB-1997
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: GOLDSTEIN, JORGE A.
: REGISTRATION NUMBER: 29,021
: REFERENCE/DOCKET NUMBER: 1657.0010000
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-371-2600
: TELEFAX: 202-371-2540
: INFORMATION FOR SEQ ID NO: 37:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 254 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: Double
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
US-08-750-088A-37

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; SOFTWARE: KOPATIN 1.0
; SEQ ID NO 1
; LENGTH: 306
; TYPE: DNA
; ORGANISM: Mycobacterium abscessus
US-09-147-935A-1

Query Match 100.0%; Score 20; DB 3; Length 306;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCATGTTGATCAGGGTCTCC 20
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Db 129 GCATGTTGATCAGGGTCTGC 110

RESULT 4
US-09-147-935A-3/c
; Sequence 3, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
; APPLICANT: KOOK, Yoon-Joon
; APPLICANT: KIM, Bum-Joon
; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
; TITLE OF INVENTION: COMPARATIVE SEQUENCE ANALYSIS OF IP0B GENE
; FILE REFERENCE: 0136/0f425
; CURRENT APPLICATION NUMBER: US/09/147,935A
; CURRENT FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/KR98/00228
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: KOPATIN 1.0
; SEQ ID NO 3
; LENGTH: 306
; TYPE: DNA
; ORGANISM: Mycobacterium asiaticum
US-09-147-935A-3

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RESULT 4
US-09-147-935A-3/c
; Sequence 3, Application US/09147995A
; Patent No. 624284
; GENERAL INFORMATION:
; APPLICANT: KOOK, Yoon-Hoh
; APPLICANT: KIM, Bum-Joon
; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
; TITLE OF INVENTION: COMPARATIVE SEQUENCE ANALYSIS OF rpoB GENE
; FILE REFERENCES: 0136/0F425
; CURRENT APPLICATION NUMBER: US/09/147,935A
; CURRENT FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/KR98/00228
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: KOPATIN 1.0
; SEQ ID NO 3
; LENGTH: 306
; TYPE: DNA
; ORGANISM: Mycobacterium asiaticum
US-09-147-935A-3

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RESULT 5
US-09-147-935A-4/c
; Sequence 4, Application US/09147935A
; Patent No. 624584
; GENERAL INFORMATION:
; APPLICANT: KOOK, Yoon-Hoh
; APPLICANT: KIM, Bum-Joon
; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
; TITLE OF INVENTION: COMPARATIVE SEQUENCE ANALYSIS OF rpoB GENE
; FILE REFERENCE: 0136/GF425
; CURRENT APPLICATION NUMBER: US/09/147,935A
; CURRENT FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/KR98/00228
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: KOPATIN 1.0
; SEQ ID NO 4
; LENGTH: 306
; TYPE: DNA
; ORGANISM: Mycobacterium aurum
US-09-147-935A-4

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RESULT 3
US-09-147-935A-1/c
; Sequence 1, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
; APPLICANT: KOOK, Yoon-Hoh
; APPLICANT: KIM, Bum-Joon
; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
; TITLE OF INVENTION: COMPARATIVE SEQUENCE ANALYSIS OF IPOB GENE
; FILE REFERENCE: 0136/OF425
; CURRENT APPLICATION NUMBER: US/09/147,935A
; CURRENT FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/KR98/00228
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 50

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QY 1 GGATGTTGATCAGGGTCTGC 20
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 Db 129 GGATGTTGATCAGGGTCTGC 110

RESULT 6

US-09-147-935A-5/c
 ; Sequence 5, Application US/09147935A
 ; Patent No. 6242584
 ; GENERAL INFORMATION:
 ; APPLICANT: KOOK, Yoon-Hoh
 ; APPLICANT: KIM, Bum-Joon
 ; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
 ; FILE REFERENCE: 0136/OF425
 ; CURRENT APPLICATION NUMBER: US/09/147,935A
 ; CURRENT FILING DATE: 1999-03-19
 ; PRIOR APPLICATION NUMBER: PCT/KR98/00228
 ; PRIOR FILING DATE: 1998-07-28
 ; NUMBER OF SEQ ID NOS: 50
 ; SOFTWARE: KOPATIN 1.0
 ; SEQ ID NO 5
 ; LENGTH: 306
 ; TYPE: DNA
 ; ORGANISM: Mycobacterium avium
 US-09-147-935A-5

Query Match 100.0%; Score 20; DB 3; Length 306;
 Best Local Similarity 100.0%; Pred. No. 1.5;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATGTTGATCAGGGTCTGC 20
 |||||
 Db 129 GGATGTTGATCAGGGTCTGC 110

RESULT 7

US-09-147-935A-8/c
 ; Sequence 8, Application US/09147935A
 ; Patent No. 6242584
 ; GENERAL INFORMATION:
 ; APPLICANT: KOOK, Yoon-Hoh
 ; APPLICANT: KIM, Bum-Joon
 ; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
 ; FILE REFERENCE: 0136/OF425
 ; CURRENT APPLICATION NUMBER: US/09/147,935A
 ; CURRENT FILING DATE: 1999-03-19
 ; PRIOR APPLICATION NUMBER: PCT/KR98/00228
 ; PRIOR FILING DATE: 1998-07-28
 ; NUMBER OF SEQ ID NOS: 50
 ; SOFTWARE: KOPATIN 1.0
 ; SEQ ID NO 8
 ; LENGTH: 306
 ; TYPE: DNA
 ; ORGANISM: Mycobacterium celatum Type1
 US-09-147-935A-8

Query Match 100.0%; Score 20; DB 3; Length 306;
 Best Local Similarity 100.0%; Pred. No. 1.5;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATGTTGATCAGGGTCTGC 20
 |||||
 Db 129 GGATGTTGATCAGGGTCTGC 110

RESULT 8

US-09-147-935A-9/c
 ; Sequence 9, Application US/09147935A
 ; Patent No. 6242584
 ; GENERAL INFORMATION:
 ; APPLICANT: KOOK, Yoon-Hoh

; APPLICANT: KIM, Bum-Joon
 ; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
 ; FILE REFERENCE: 0136/OF425
 ; CURRENT APPLICATION NUMBER: US/09/147,935A
 ; CURRENT FILING DATE: 1999-03-19
 ; PRIOR APPLICATION NUMBER: PCT/KR98/00228
 ; PRIOR FILING DATE: 1998-07-28
 ; NUMBER OF SEQ ID NOS: 50
 ; SOFTWARE: KOPATIN 1.0
 ; SEQ ID NO 9
 ; LENGTH: 306
 ; TYPE: DNA
 ; ORGANISM: Mycobacterium celatum Type2
 US-09-147-935A-9

Query Match 100.0%; Score 20; DB 3; Length 306;
 Best Local Similarity 100.0%; Pred. No. 1.5;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATGTTGATCAGGGTCTGC 20
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 Db 129 GGATGTTGATCAGGGTCTGC 110

RESULT 9

US-09-147-935A-10/c
 ; Sequence 10, Application US/09147935A
 ; Patent No. 6242584
 ; GENERAL INFORMATION:
 ; APPLICANT: KOOK, Yoon-Hoh
 ; APPLICANT: KIM, Bum-Joon
 ; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
 ; FILE REFERENCE: 0136/OF425
 ; CURRENT APPLICATION NUMBER: US/09/147,935A
 ; CURRENT FILING DATE: 1999-03-19
 ; PRIOR APPLICATION NUMBER: PCT/KR98/00228
 ; PRIOR FILING DATE: 1998-07-28
 ; NUMBER OF SEQ ID NOS: 50
 ; SOFTWARE: KOPATIN 1.0
 ; SEQ ID NO 10
 ; LENGTH: 306
 ; TYPE: DNA
 ; ORGANISM: Mycobacterium chelonae
 US-09-147-935A-10

Query Match 100.0%; Score 20; DB 3; Length 306;
 Best Local Similarity 100.0%; Pred. No. 1.5;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATGTTGATCAGGGTCTGC 20
 |||||
 Db 129 GGATGTTGATCAGGGTCTGC 110

RESULT 10

US-09-147-935A-11/c
 ; Sequence 11, Application US/09147935A
 ; Patent No. 6242584
 ; GENERAL INFORMATION:
 ; APPLICANT: KOOK, Yoon-Hoh
 ; APPLICANT: KIM, Bum-Joon
 ; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
 ; FILE REFERENCE: 0136/OF425
 ; CURRENT APPLICATION NUMBER: US/09/147,935A
 ; CURRENT FILING DATE: 1999-03-19
 ; PRIOR APPLICATION NUMBER: PCT/KR98/00228
 ; PRIOR FILING DATE: 1998-07-28
 ; NUMBER OF SEQ ID NOS: 50
 ; SOFTWARE: KOPATIN 1.0
 ; SEQ ID NO 11

; LENGTH: 306
 ; TYPE: DNA
 ; ORGANISM: Mycobacterium chitae
 ; US-09-147-935A-11

Query Match 100.0%; Score 20; DB 3; Length 306;
 Best Local Similarity 100.0%; Pred. No. 1.5;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATGTTGATCAGGGTCTGC 20
 |||||
 Db 129 GGATGTTGATCAGGGTCTGC 110

RESULT 11

US-09-147-935A-12/c
 ; Sequence 12, Application US/09147935A
 ; Patent No. 6242584
 ; GENERAL INFORMATION:
 ; APPLICANT: KOOK, Yoon-Hoh
 ; APPLICANT: KIM, Bum-Joon
 ; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
 ; FILE REFERENCE: 0136/0F425
 ; CURRENT APPLICATION NUMBER: US/09/147,935A
 ; CURRENT FILING DATE: 1999-03-19
 ; PRIOR APPLICATION NUMBER: PCT/KR98/00228
 ; PRIOR FILING DATE: 1998-07-28
 ; NUMBER OF SEQ ID NOS: 50
 ; SOFTWARE: KOPATIN 1.0
 ; SEQ ID NO 12
 ; LENGTH: 306
 ; TYPE: DNA
 ; ORGANISM: Mycobacterium fallax
 ; US-09-147-935A-12

Query Match 100.0%; Score 20; DB 3; Length 306;
 Best Local Similarity 100.0%; Pred. No. 1.5;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATGTTGATCAGGGTCTGC 20
 |||||
 Db 129 GGATGTTGATCAGGGTCTGC 110

RESULT 12

US-09-147-935A-13/c
 ; Sequence 13, Application US/09147935A
 ; Patent No. 6242584
 ; GENERAL INFORMATION:
 ; APPLICANT: KOOK, Yoon-Hoh
 ; APPLICANT: KIM, Bum-Joon
 ; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
 ; FILE REFERENCE: 0136/0F425
 ; CURRENT APPLICATION NUMBER: US/09/147,935A
 ; CURRENT FILING DATE: 1999-03-19
 ; PRIOR APPLICATION NUMBER: PCT/KR98/00228
 ; PRIOR FILING DATE: 1998-07-28
 ; NUMBER OF SEQ ID NOS: 50
 ; SOFTWARE: KOPATIN 1.0
 ; SEQ ID NO 13
 ; LENGTH: 306
 ; TYPE: DNA
 ; ORGANISM: Mycobacterium flavescens
 ; US-09-147-935A-13

Query Match 100.0%; Score 20; DB 3; Length 306;
 Best Local Similarity 100.0%; Pred. No. 1.5;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATGTTGATCAGGGTCTGC 20
 |||||

Db 129 GGATGTTGATCAGGGTCTGC 110

RESULT 13

US-09-147-935A-14/c
 ; Sequence 14, Application US/09147935A
 ; Patent No. 6242584
 ; GENERAL INFORMATION:
 ; APPLICANT: KOOK, Yoon-Hoh
 ; APPLICANT: KIM, Bum-Joon
 ; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
 ; FILE REFERENCE: 0136/0F425
 ; CURRENT APPLICATION NUMBER: US/09/147,935A
 ; CURRENT FILING DATE: 1999-03-19
 ; PRIOR APPLICATION NUMBER: PCT/KR98/00228
 ; PRIOR FILING DATE: 1998-07-28
 ; NUMBER OF SEQ ID NOS: 50
 ; SOFTWARE: KOPATIN 1.0
 ; SEQ ID NO 14
 ; LENGTH: 306
 ; TYPE: DNA
 ; ORGANISM: Mycobacterium fortuitum
 ; US-09-147-935A-14

Query Match 100.0%; Score 20; DB 3; Length 306;
 Best Local Similarity 100.0%; Pred. No. 1.5;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATGTTGATCAGGGTCTGC 20
 |||||
 Db 129 GGATGTTGATCAGGGTCTGC 110

RESULT 14

US-09-147-935A-15/c
 ; Sequence 15, Application US/09147935A
 ; Patent No. 6242584
 ; GENERAL INFORMATION:
 ; APPLICANT: KOOK, Yoon-Hoh
 ; APPLICANT: KIM, Bum-Joon
 ; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
 ; FILE REFERENCE: 0136/0F425
 ; CURRENT APPLICATION NUMBER: US/09/147,935A
 ; CURRENT FILING DATE: 1999-03-19
 ; PRIOR APPLICATION NUMBER: PCT/KR98/00228
 ; PRIOR FILING DATE: 1998-07-28
 ; NUMBER OF SEQ ID NOS: 50
 ; SOFTWARE: KOPATIN 1.0
 ; SEQ ID NO 15
 ; LENGTH: 306
 ; TYPE: DNA
 ; ORGANISM: Mycobacterium fortuitum 49403
 ; US-09-147-935A-15

Query Match 100.0%; Score 20; DB 3; Length 306;
 Best Local Similarity 100.0%; Pred. No. 1.5;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATGTTGATCAGGGTCTGC 20
 |||||
 Db 129 GGATGTTGATCAGGGTCTGC 110

RESULT 15

US-09-147-935A-17/c
 ; Sequence 17, Application US/09147935A
 ; Patent No. 6242584
 ; GENERAL INFORMATION:
 ; APPLICANT: KOOK, Yoon-Hoh
 ; APPLICANT: KIM, Bum-Joon
 ; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY

; TITLE OF INVENTION: COMPARATIVE SEQUENCE ANALYSIS OF rpoB GENE
; FILE REFERENCE: 0136/0F425
; CURRENT APPLICATION NUMBER: US/09/147,935A
; CURRENT FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/KR98/00228
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: KOPATIN 1.0
; SEQ ID NO 17
; LENGTH: 306
; TYPE: DNA
; ORGANISM: Mycobacterium genavense
US-09-147-935A-17

Query Match 100.0%; Score 20; DB 3; Length 306;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATGTTGATCAGGGTCTGC 20
|||||
Db 129 GGATGTTGATCAGGGTCTGC 110

Search completed: September 16, 2003, 16:39:15
Job time : 46.1538 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 16, 2003, 16:37:04 ; Search time 162.564 Seconds
(without alignments)
302.640 Million cell updates/sec

Title: US-09-697-123b-26

Perfect score: 20

Sequence: 1 ggatgttgcagggtctgc 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1660708 seqs, 1229959015 residues

Total number of hits satisfying chosen parameters: 3321416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Published Applications NA:

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3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
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16: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
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c 2	20	100.0	254	12	US-10-339-604-37
c 3	20	100.0	319	12	US-10-339-604-35
c 4	20	100.0	324	12	US-10-339-604-36
c 5	20	100.0	652	10	US-09-285-306-30
c 6	20	100.0	652	10	US-09-285-306-38
c 7	20	100.0	687	10	US-09-285-306-18
c 8	20	100.0	687	10	US-09-285-306-19
c 9	20	100.0	687	10	US-09-285-306-20
c 10	20	100.0	687	10	US-09-285-306-21
c 11	20	100.0	687	10	US-09-285-306-22
c 12	20	100.0	687	10	US-09-285-306-23
c 13	20	100.0	687	10	US-09-285-306-25
c 14	20	100.0	687	10	US-09-285-306-26
c 15	20	100.0	687	10	US-09-285-306-27
c 16	20	100.0	687	10	US-09-285-306-48

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c 17 20 100.0 687 10 US-09-285-306-49
c 18 20 100.0 687 10 US-09-285-306-50
c 19 20 100.0 687 10 US-09-285-306-58
c 20 20 100.0 687 10 US-09-285-306-59
c 21 20 100.0 687 10 US-09-285-306-60
c 22 20 100.0 687 10 US-09-285-306-61
c 23 20 100.0 687 10 US-09-285-306-62
c 24 20 100.0 687 10 US-09-285-306-63
c 25 20 100.0 687 10 US-09-285-306-80
c 26 20 100.0 687 10 US-09-285-306-81
c 27 20 100.0 687 10 US-09-285-306-82
c 28 20 100.0 687 10 US-09-285-306-97
c 29 20 100.0 687 10 US-09-285-306-98
c 30 20 100.0 687 10 US-09-285-306-99
c 31 20 100.0 687 10 US-09-285-306-100
c 32 20 100.0 687 10 US-09-285-306-137
c 33 20 100.0 687 10 US-09-285-306-138
c 34 20 100.0 687 10 US-09-285-306-139
c 35 20 100.0 687 10 US-09-285-306-140
c 36 20 100.0 687 10 US-09-285-306-141
c 37 20 100.0 687 10 US-09-285-306-142
c 38 20 100.0 687 10 US-09-285-306-145
c 39 20 100.0 687 10 US-09-285-306-146
c 40 20 100.0 687 10 US-09-285-306-148
c 41 20 100.0 687 10 US-09-285-306-149
c 42 20 100.0 687 10 US-09-285-306-150
c 43 20 100.0 687 10 US-09-285-306-151
c 44 20 100.0 687 10 US-09-285-306-152
c 45 20 100.0 687 10 US-09-285-306-158
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ALIGNMENTS

RESULT 1

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US-10-339-604-69/c
; Sequence 69, Application US/10339604
; Publication No. US20030152982A1
; GENERAL INFORMATION:
; APPLICANT: DE BEENHOUWER, HANS
; APPLICANT: PORTAELS, FRANCOISE
; APPLICANT: MACHTELINCKX, LIEVE
; APPLICANT: JANNES, GEERT
; APPLICANT: ROSSAU, RUDI
; TITLE OF INVENTION: Oligonucleotide Molecules for Use in Detection of Mycobacteri
; FILE OF INVENTION: Antibiotic Resistance
; FILE REFERENCE: 1657.0010001
; CURRENT APPLICATION NUMBER: US/10/339,604
; CURRENT FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: US/09/722,319
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 08/750,088
; PRIOR FILING DATE: 1996-12-06
; PRIOR APPLICATION NUMBER: PCT/EP95/02230
; PRIOR FILING DATE: 1995-06-09
; PRIOR APPLICATION NUMBER: EP 94870093.5
; PRIOR FILING DATE: 1994-06-09
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 69
; LENGTH: 228
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe
; NAME/KEY: misc_feature
; LOCATION: (8)..(8)
; OTHER INFORMATION: n can be any nucleotide
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (33)..(33)
; OTHER INFORMATION: n can be any nucleotide
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US-10-339-604-69

Query Match 100.0%; Score 20; DB 12; Length 228;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGATGTTGATCAGGGTCTGC 20
Db 88 GGATGTTGATCAGGGTCTGC 69

RESULT 2

US-10-339-604-37/c
; Sequence 37, Application US/10339604
; Publication No. US20030152982A1
; GENERAL INFORMATION:
; APPLICANT: DE BEENHOUWER, HANS
; APPLICANT: PORTAELS, FRANCOISE
; APPLICANT: MACHTELINCKX, LIEVE
; APPLICANT: JANNES, GEERT
; APPLICANT: ROSSAU, RUDI
; TITLE OF INVENTION: Oligonucleotide Molecules for Use in Detection of Mycobacterium
; TITLE OF INVENTION: Antibiotic Resistance
; FILE REFERENCE: 1657.0010001
; CURRENT APPLICATION NUMBER: US/10/339,604
; CURRENT FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: US/09/722,319
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 08/750,088
; PRIOR FILING DATE: 1996-12-06
; PRIOR APPLICATION NUMBER: PCT/EP95/02230
; PRIOR FILING DATE: 1995-06-09
; PRIOR APPLICATION NUMBER: EP 94870093.5
; PRIOR FILING DATE: 1994-06-09
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
; LENGTH: 254
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (169)..(169)
; OTHER INFORMATION: n can be any nucleotide
US-10-339-604-37

Query Match 100.0%; Score 20; DB 12; Length 254;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGATGTTGATCAGGGTCTGC 20
Db 94 GGATGTTGATCAGGGTCTGC 75

RESULT 3

US-10-339-604-35/c
; Sequence 35, Application US/10339604
; Publication No. US20030152982A1
; GENERAL INFORMATION:
; APPLICANT: DE BEENHOUWER, HANS
; APPLICANT: PORTAELS, FRANCOISE
; APPLICANT: MACHTELINCKX, LIEVE
; APPLICANT: JANNES, GEERT
; APPLICANT: ROSSAU, RUDI
; TITLE OF INVENTION: Oligonucleotide Molecules for Use in Detection of Mycobacterium
; TITLE OF INVENTION: Antibiotic Resistance
; FILE REFERENCE: 1657.0010001
; CURRENT APPLICATION NUMBER: US/10/339,604
; CURRENT FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: US/09/722,319

; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 08/750,088
; PRIOR FILING DATE: 1996-12-06
; PRIOR APPLICATION NUMBER: PCT/EP95/02230
; PRIOR FILING DATE: 1995-06-09
; PRIOR APPLICATION NUMBER: EP 94870093.5
; PRIOR FILING DATE: 1994-06-09
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
; LENGTH: 319
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (38)..(38)
; OTHER INFORMATION: n can be any nucleotide
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (52)..(52)
; OTHER INFORMATION: n can be any nucleotide
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (62)..(62)
; OTHER INFORMATION: n can be any nucleotide
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (131)..(131)
; OTHER INFORMATION: n can be any nucleotide
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (207)..(207)
; OTHER INFORMATION: n can be any nucleotide
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (254)..(254)
; OTHER INFORMATION: n can be any nucleotide
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (261)..(261)
; OTHER INFORMATION: n can be any nucleotide
US-10-339-604-35

Query Match 100.0%; Score 20; DB 12; Length 319;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGATGTTGATCAGGGTCTGC 20
Db 96 GGATGTTGATCAGGGTCTGC 77

RESULT 4

US-10-339-604-36/c
; Sequence 36, Application US/10339604
; Publication No. US20030152982A1
; GENERAL INFORMATION:
; APPLICANT: DE BEENHOUWER, HANS
; APPLICANT: PORTAELS, FRANCOISE
; APPLICANT: MACHTELINCKX, LIEVE
; APPLICANT: JANNES, GEERT
; APPLICANT: ROSSAU, RUDI
; TITLE OF INVENTION: Oligonucleotide Molecules for Use in Detection of Mycobacterium
; TITLE OF INVENTION: Antibiotic Resistance
; FILE REFERENCE: 1657.0010001
; CURRENT APPLICATION NUMBER: US/10/339,604
; CURRENT FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: US/09/722,319
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 08/750,088
; PRIOR FILING DATE: 1996-12-06

```

; PRIOR APPLICATION NUMBER: PCI/EP95/02230
; PRIOR FILING DATE: 1995-06-09
; PRIOR APPLICATION NUMBER: EP 94870093.5
; PRIOR FILING DATE: 1994-06-09
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
; LENGTH: 324
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe
US-10-339-604-36

```

```

Query Match      100.0%; Score 20; DB 12; Length 324;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 GGATGTTGATCAGGCTCTGC 20
        |||||
Db      78 GGATGTTGATCAGGCTCTGC 59

```

RESULT 5

```

US-09-285-306-30/c
; Sequence 30, Application US/09285306A
; Publication No. US20020187467A1
; GENERAL INFORMATION:
; APPLICANT: Gingeras, Thomas
; APPLICANT: Drenkow, Jorg
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Mycobacterial rpoB Sequences
; FILE REFERENCE: 018547-018570US
; CURRENT APPLICATION NUMBER: US/09/285,306A
; CURRENT FILING DATE: 1999-04-02
; EARLIER APPLICATION NUMBER: US 60/080,616
; EARLIER FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 181
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 652
; TYPE: DNA
; ORGANISM: Mycobacterium chelonae
US-09-285-306-30

```

```

Query Match      100.0%; Score 20; DB 10; Length 652;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 GGATGTTGATCAGGCTCTGC 20
        |||||
Db      21 GGATGTTGATCAGGCTCTGC 2

```

RESULT 6

```

US-09-285-306-38/c
; Sequence 38, Application US/09285306A
; Publication No. US20020187467A1
; GENERAL INFORMATION:
; APPLICANT: Gingeras, Thomas
; APPLICANT: Drenkow, Jorg
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Mycobacterial rpoB Sequences
; FILE REFERENCE: 018547-018570US
; CURRENT APPLICATION NUMBER: US/09/285,306A
; CURRENT FILING DATE: 1999-04-02
; EARLIER APPLICATION NUMBER: US 60/080,616
; EARLIER FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 181
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 38
; LENGTH: 652
; TYPE: DNA

```

```

; ORGANISM: Mycobacterium chelonae
US-09-285-306-38

```

```

Query Match      100.0%; Score 20; DB 10; Length 652;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 GGATGTTGATCAGGCTCTGC 20
        |||||
Db      20 GGATGTTGATCAGGCTCTGC 1

```

RESULT 7

```

US-09-285-306-18/c
; Sequence 18, Application US/09285306A
; Publication No. US20020187467A1
; GENERAL INFORMATION:
; APPLICANT: Gingeras, Thomas
; APPLICANT: Drenkow, Jorg
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Mycobacterial rpoB Sequences
; FILE REFERENCE: 018547-018570US
; CURRENT APPLICATION NUMBER: US/09/285,306A
; CURRENT FILING DATE: 1999-04-02
; EARLIER APPLICATION NUMBER: US 60/080,616
; EARLIER FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 181
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 687
; TYPE: DNA
; ORGANISM: Mycobacterium avium
US-09-285-306-18

```

```

Query Match      100.0%; Score 20; DB 10; Length 687;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 GGATGTTGATCAGGCTCTGC 20
        |||||
Db      35 GGATGTTGATCAGGCTCTGC 16

```

RESULT 8

```

US-09-285-306-19/c
; Sequence 19, Application US/09285306A
; Publication No. US20020187467A1
; GENERAL INFORMATION:
; APPLICANT: Gingeras, Thomas
; APPLICANT: Drenkow, Jorg
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Mycobacterial rpoB Sequences
; FILE REFERENCE: 018547-018570US
; CURRENT APPLICATION NUMBER: US/09/285,306A
; CURRENT FILING DATE: 1999-04-02
; EARLIER APPLICATION NUMBER: US 60/080,616
; EARLIER FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 181
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 687
; TYPE: DNA
; ORGANISM: Mycobacterium avium
US-09-285-306-19

```

```

Query Match      100.0%; Score 20; DB 10; Length 687;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 GGATGTTGATCAGGCTCTGC 20
        |||||
Db      35 GGATGTTGATCAGGCTCTGC 16

```

```

RESULT 9
US-09-285-306-20/c
; Sequence 20, Application US/09285306A
; Publication No. US20020187467A1
; GENERAL INFORMATION:
; APPLICANT: Gingeras, Thomas
; APPLICANT: Drenkow, Jorg
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Mycobacterial rpoB Sequences
; FILE REFERENCE: 018547-0185700S
; CURRENT APPLICATION NUMBER: US/09/285,306A
; CURRENT FILING DATE: 1999-04-02
; EARLIER APPLICATION NUMBER: US 60/080,616
; EARLIER FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 181
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 687
; TYPE: DNA
; ORGANISM: Mycobacterium avium
US-09-285-306-20

Query Match      100.0%; Score 20; DB 10; Length 687;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGATGTTGATCAGGGTCTGC 20
      |||||||
Db      35 GGATGTTGATCAGGGTCTGC 16

RESULT 10
US-09-285-306-21/c
; Sequence 21, Application US/09285306A
; Publication No. US20020187467A1
; GENERAL INFORMATION:
; APPLICANT: Gingeras, Thomas
; APPLICANT: Drenkow, Jorg
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Mycobacterial rpoB Sequences
; FILE REFERENCE: 018547-0185700S
; CURRENT APPLICATION NUMBER: US/09/285,306A
; CURRENT FILING DATE: 1999-04-02
; EARLIER APPLICATION NUMBER: US 60/080,616
; EARLIER FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 181
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 687
; TYPE: DNA
; ORGANISM: Mycobacterium avium
US-09-285-306-21

Query Match      100.0%; Score 20; DB 10; Length 687;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGATGTTGATCAGGGTCTGC 20
      |||||||
Db      35 GGATGTTGATCAGGGTCTGC 16

RESULT 11
US-09-285-306-22/c
; Sequence 22, Application US/09285306A
; Publication No. US20020187467A1
; GENERAL INFORMATION:
; APPLICANT: Gingeras, Thomas
; APPLICANT: Drenkow, Jorg
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Mycobacterial rpoB Sequences
; FILE REFERENCE: 018547-0185700S
; CURRENT APPLICATION NUMBER: US/09/285,306A
; CURRENT FILING DATE: 1999-04-02
; EARLIER APPLICATION NUMBER: US 60/080,616
; EARLIER FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 181
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 687
; TYPE: DNA
; ORGANISM: Mycobacterium avium
US-09-285-306-22

Query Match      100.0%; Score 20; DB 10; Length 687;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGATGTTGATCAGGGTCTGC 20
      |||||||
Db      35 GGATGTTGATCAGGGTCTGC 16

RESULT 12
US-09-285-306-23/c
; Sequence 23, Application US/09285306A
; Publication No. US20020187467A1
; GENERAL INFORMATION:
; APPLICANT: Gingeras, Thomas
; APPLICANT: Drenkow, Jorg
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Mycobacterial rpoB Sequences
; FILE REFERENCE: 018547-0185700S
; CURRENT APPLICATION NUMBER: US/09/285,306A
; CURRENT FILING DATE: 1999-04-02
; EARLIER APPLICATION NUMBER: US 60/080,616
; EARLIER FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 181
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 687
; TYPE: DNA
; ORGANISM: Mycobacterium avium
US-09-285-306-23

Query Match      100.0%; Score 20; DB 10; Length 687;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGATGTTGATCAGGGTCTGC 20
      |||||||
Db      35 GGATGTTGATCAGGGTCTGC 16

RESULT 13
US-09-285-306-25/c
; Sequence 25, Application US/09285306A
; Publication No. US20020187467A1
; GENERAL INFORMATION:
; APPLICANT: Gingeras, Thomas
; APPLICANT: Drenkow, Jorg
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Mycobacterial rpoB Sequences
; FILE REFERENCE: 018547-0185700S
; CURRENT APPLICATION NUMBER: US/09/285,306A
; CURRENT FILING DATE: 1999-04-02
; EARLIER APPLICATION NUMBER: US 60/080,616
; EARLIER FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 181
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 687
; TYPE: DNA
; ORGANISM: Mycobacterium avium
US-09-285-306-25

```

Job time : 163.564 secs

Query Match 100.0%; Score 20; DB 10; Length 687;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATGTTGATCAGGGTCTGC 20
|||||
Db 35 GGATGTTGATCAGGGTCTGC 16

RESULT 14
US-09-285-306-26/c
; Sequence 26, Application US/09285306A
; Publication No. US20020187467A1
; GENERAL INFORMATION:
; APPLICANT: Gingeras, Thomas
; APPLICANT: Drenkow, Jorg
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Mycobacterial rpoB Sequences
; FILE REFERENCE: 018547-018570US
; CURRENT APPLICATION NUMBER: US/09/285,306A
; CURRENT FILING DATE: 1999-04-02
; EARLIER APPLICATION NUMBER: US 60/080,616
; EARLIER FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 181
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 687
; TYPE: DNA
; ORGANISM: Mycobacterium avium
US-09-285-306-26

Query Match 100.0%; Score 20; DB 10; Length 687;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATGTTGATCAGGGTCTGC 20
|||||
Db 35 GGATGTTGATCAGGGTCTGC 16

RESULT 15
US-09-285-306-27/c
; Sequence 27, Application US/09285306A
; Publication No. US20020187467A1
; GENERAL INFORMATION:
; APPLICANT: Gingeras, Thomas
; APPLICANT: Drenkow, Jorg
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Mycobacterial rpoB Sequences
; FILE REFERENCE: 018547-018570US
; CURRENT APPLICATION NUMBER: US/09/285,306A
; CURRENT FILING DATE: 1999-04-02
; EARLIER APPLICATION NUMBER: US 60/080,616
; EARLIER FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 181
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 687
; TYPE: DNA
; ORGANISM: Mycobacterium avium complex (MAC)
US-09-285-306-27

Query Match 100.0%; Score 20; DB 10; Length 687;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATGTTGATCAGGGTCTGC 20
|||||
Db 35 GGATGTTGATCAGGGTCTGC 16

Search completed: September 16, 2003, 18:22:48